

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

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Abstract

Rpackage **FME** (?) 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 simulation model, solved with integration routines from package **deSolve**

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

`vignette("FMEcmc")` 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 (?) for a description of reaction-transport models.

The constitutive equations are:

$$\begin{aligned}\frac{\partial O_2}{\partial t} &= -\frac{\partial Flux}{\partial x} - cons \cdot \frac{O_2}{O_2 + k_s} \\ Flux &= -D \cdot \frac{\partial O_2}{\partial x} \\ O_2(x=0) &= upO2\end{aligned}$$

```
> 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
```

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```
+          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** ((?)) does this in a very efficient way (see (?)).

```
> 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`).

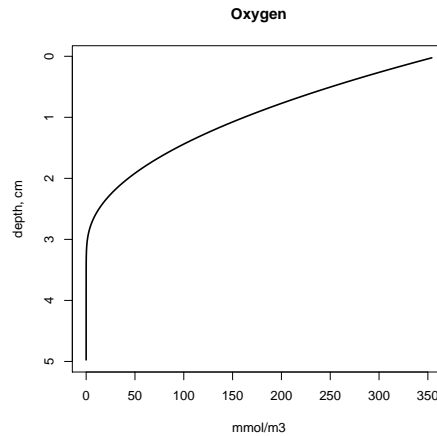


Figure 1: The modeled oxygen profile - see text for R-code

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

```
user  system elapsed
0.97   0.00   0.98
```

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 analysis 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)
```

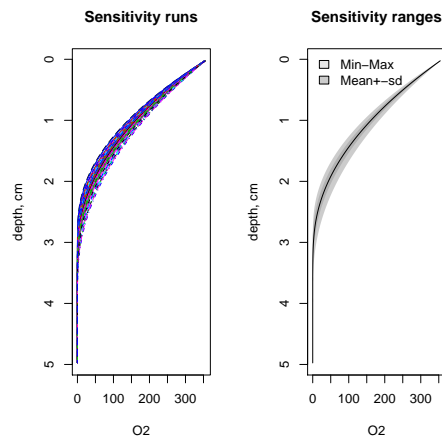


Figure 2: Results of the sensitivity run - left: all model runs, right: summary - see text for R-code

	value	scale	L1	L2	Mean	Min	Max	N
up02	360	360	6.7	0.83	6.7	1.0e+00	12.5653	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	8.1	1.14	8.1	8.4e-03	22.0312	100

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

```
> pairs(O2sens)
```

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

	up02	cons	ks	D
up02	1.0000000	-0.9744572	0.8267094	0.9744572
cons	-0.9744572	1.0000000	-0.9317287	-1.0000000
ks	0.8267094	-0.9317287	1.0000000	0.9317287
D	0.9744572	-1.0000000	0.9317287	1.0000000

Multivariate sensitivity is done by estimating the collinearity between parameter sets (?).

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

```
> Coll
```

	up02	cons	ks	D	N	collinearity
1	1	1	0	0	2	7.1
2	1	0	1	0	2	2.8
3	1	0	0	1	2	7.1

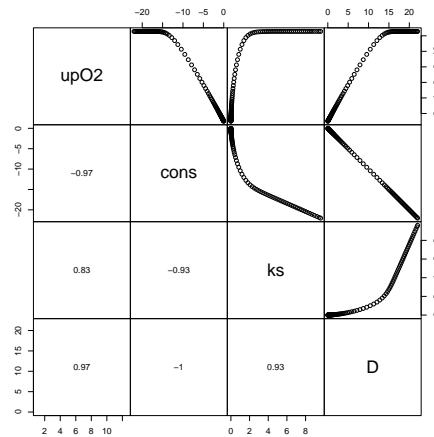


Figure 3: pairs plot - see text for R-code

```

4      0      1      1      0      2      4.4
5      0      1      0      1      2      54794158.0
6      0      0      1      1      2      4.4
7      1      1      1      0      3      23.1
8      1      1      0      1      3      NaN
9      1      0      1      1      3      23.1
10     0      1      1      1      3      NaN
11     1      1      1      1      4      NaN

```

```
> 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)
+ {
+   derivs <- function(t, O2, pars)

```

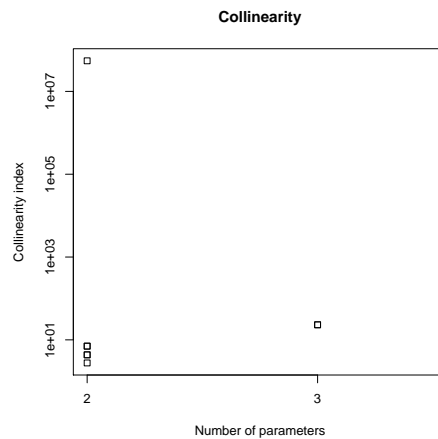


Figure 4: collinearity - see text for R-code

```
+ {
+   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=02flux,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=parms)
+ ))

```

```

      user  system elapsed
      0.11    0.00    0.11

```

```

> summary(sF)

```

	value	scale	L1	L2	Mean	Min	Max	N
up02	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)

```

	up02	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("up02","cons","ks"))

```

	up02	cons	ks	D	N	collinearity
1	1	1	1	0	3	14

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```
> print(system.time(
+ Fit<-modFit(p=c(up02=360,cons=80,ks=1),
+             f=Objective,lower=c(0,0,0))
+             ))

      user  system elapsed
      0.75    0.00    0.75

> (SFit<-summary(Fit))

Parameters:
      Estimate Std. Error t value Pr(>|t|)
up02   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:
      up02   cons    ks
up02 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
> mod02 <- 02fun(Pars)

> plot(02depth$y,02depth$x,ylim=rev(range(02depth$x)),pch=18,
+      main="Oxygen-fitted", xlab="mmol/m3",ylab="depth, cm")
> lines(mod02$02,mod02$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
```

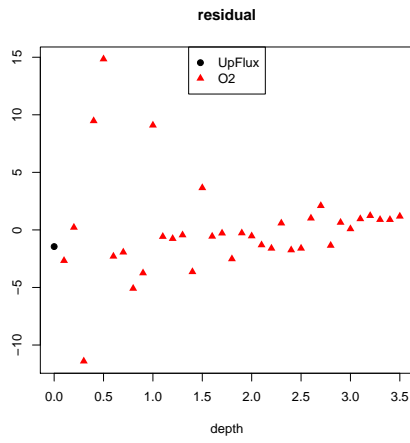



Figure 5: residuals - see text for R-code

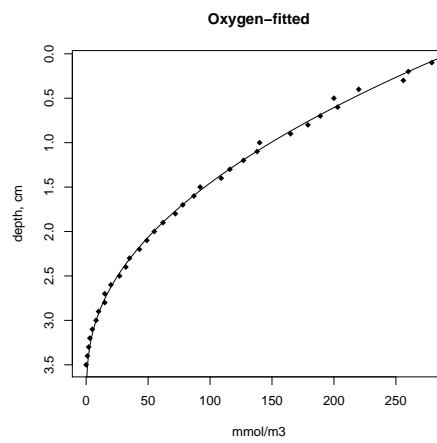


Figure 6: Best fit model - see text for R-code

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: 642 out of 1000 (64.2%)

	user	system	elapsed
	30.02	0.01	30.38

```
> MCMC$count
```

	dr_steps	Alfasteps	num_accepted	num_covupdate
	719	2157	642	10

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	294.325441	53.434001	3.7863391	410.07662
sd	4.570607	5.369264	3.2230949	4047.17061
min	282.804016	45.272009	0.1380697	1.67834
max	318.343606	80.569464	17.6821727	114933.27503
q025	291.650102	50.097000	1.4658009	11.37898
q050	293.556448	51.895676	2.6959854	29.25143
q075	295.523590	54.931174	5.2125728	95.82216

```
> cor(MCMC$pars)
```

	up02	cons	ks
up02	1.0000000	0.7493331	0.4515089
cons	0.7493331	1.0000000	0.8663396
ks	0.4515089	0.8663396	1.0000000

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

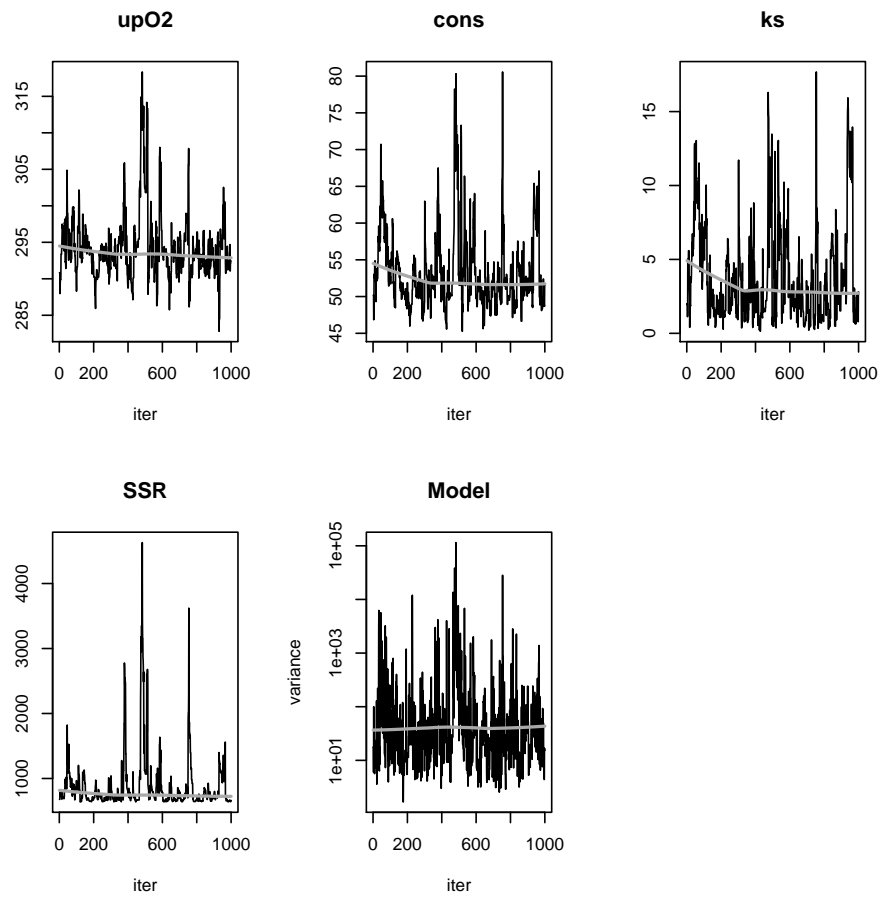


Figure 7: MCMC plot results - see text for R-code

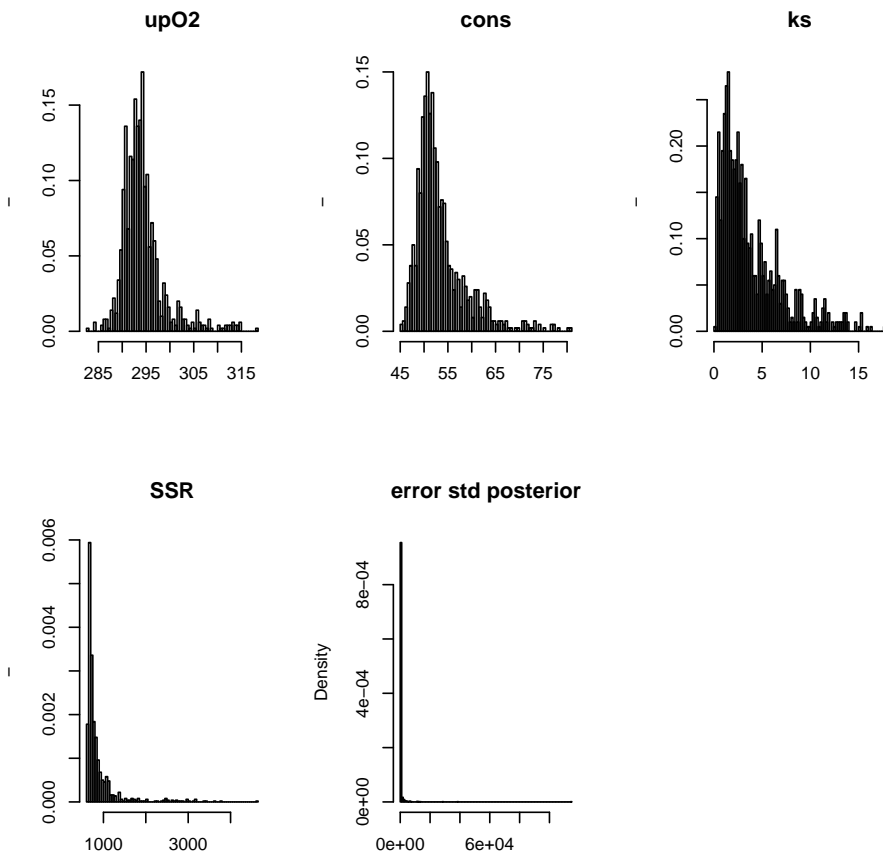


Figure 8: MCMC histogram results - see text for R-code

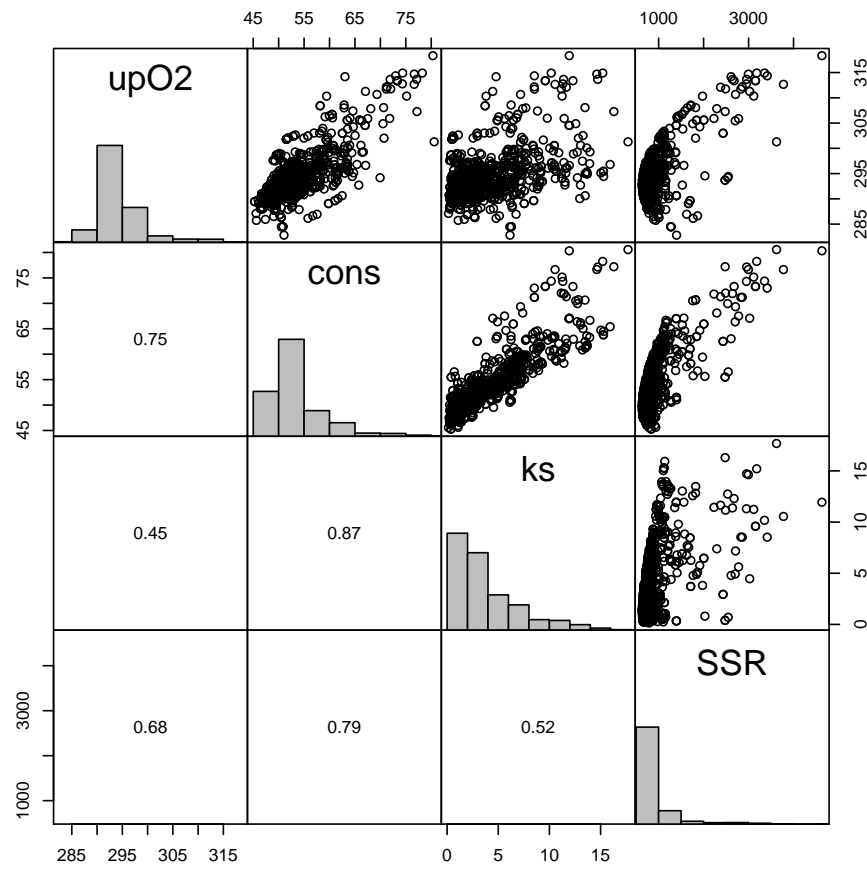


Figure 9: MCMC pairs plot - see text for R-code

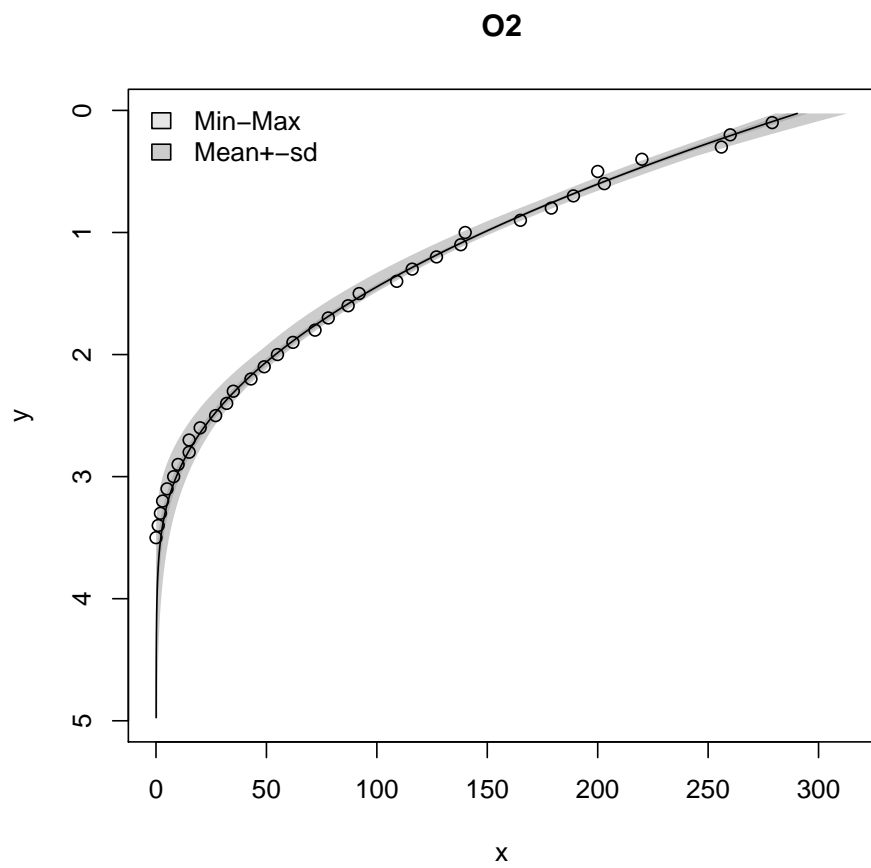


Figure 10: MCMC range plot - see text for R-code

```
> 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 (?) translation of part of the **FME** examples.

References

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