

Testing examples in saemix 3.0

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Setup

- set up work directories
- two versions toggled by testMode
 - if testMode is FALSE, load the functions in R
 - if testMode is TRUE, load the library in a dev_mode environment
- aim: check the examples used in the online documentation
 - all examples must run without error

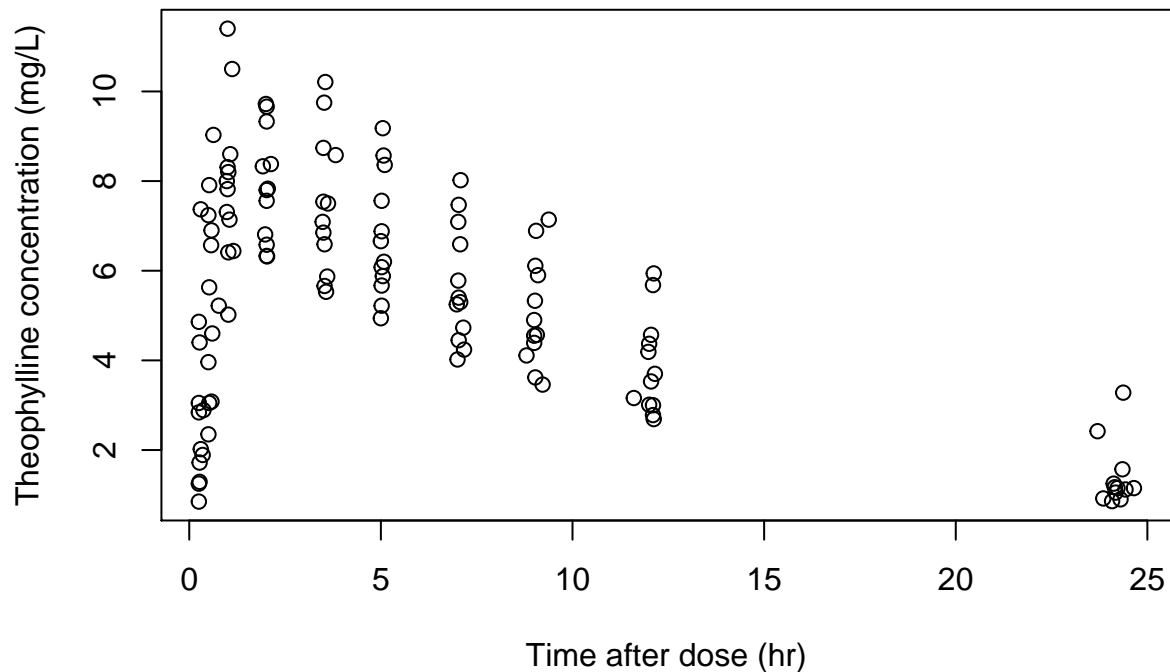
Testing library

Continuous response model

Theophylline

```
if(testMode)
  data(theo.saemix) else
  theo.saemix<-read.table(file.path(datDir, "theo.saemix.tab"), header=TRUE)

#Plotting the theophylline data
plot(Concentration~Time,data=theo.saemix,xlab="Time after dose (hr)",
ylab="Theophylline concentration (mg/L)")
```



```
saemix.data<-saemixData(name.data=theo.saemix,header=TRUE,sep=" ",na=NA,
  name.group=c("Id"),name.predictors=c("Dose","Time"),
  name.response=c("Concentration"),name.covariates=c("Weight","Sex"),
  units=list(x="hr",y="mg/L",covariates=c("kg","-")), name.X="Time")
```

```
## [1] "Weight" "Sex"
##
##
## The following SaemixData object was successfully created:
##
## Object of class SaemixData
##   longitudinal data for use with the SAEM algorithm
## Dataset theo.saemix
##   Structured data: Concentration ~ Dose + Time | Id
##   X variable for graphs: Time (hr)
##   covariates: Weight (kg), Sex (-)
##   reference class for covariate Sex : 0
```

```
model1cpt<-function(psi,id,xidep) {
  dose<-xidep[,1]
  tim<-xidep[,2]
  ka<-psi[id,1]
  V<-psi[id,2]
  CL<-psi[id,3]
  k<-CL/V
  ypred<-dose*ka/(V*(ka-k))*(exp(-k*tim)-exp(-ka*tim))
  return(ypred)
}
# Default model, no covariate
saemix.model<-saemixModel(model=model1cpt,
  description="One-compartment model with first-order absorption",
  psi0=matrix(c(1.,20,0.5,0.1,0,-0.01),ncol=3,byrow=TRUE,
  dimnames=list(NULL, c("ka","V","CL"))),transform.par=c(1,1,1))
```

```

##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
## Model function: One-compartment model with first-order absorption Model type: structural
## function(psi,id,xidep) {
##     dose<-xidep[,1]
##     tim<-xidep[,2]
##     ka<-psi[id,1]
##     V<-psi[id,2]
##     CL<-psi[id,3]
##     k<-CL/V
##     ypred<-dose*ka/(V*(ka-k))*(exp(-k*tim)-exp(-ka*tim))
##     return(ypred)
## }
## Nb of parameters: 3
##     parameter names: ka V CL
##     distribution:
##     Parameter Distribution Estimated
## [1,] ka          log-normal Estimated
## [2,] V           log-normal Estimated
## [3,] CL          log-normal Estimated
## Variance-covariance matrix:
##     ka V CL
## ka  1 0 0
## V   0 1 0
## CL  0 0 1
## Error model: constant , initial values: a.1=1
## No covariate in the model.
## Initial values
##           ka V CL
## Pop.CondInit 1.0 20 0.50
## Cov.CondInit 0.1 0 -0.01

# Note: remove the options save=FALSE and save.graphs=FALSE
# to save the results and graphs
saemix.options<-list(seed=632545,save=FALSE,save.graphs=FALSE, displayProgress=FALSE)

saemix.fit<-saemix(saemix.model,saemix.data,saemix.options)

## Nonlinear mixed-effects model fit by the SAEM algorithm
## -----
## ---- Data ----
## -----
## Object of class SaemixData
## longitudinal data for use with the SAEM algorithm
## Dataset theo.saemix
## Structured data: Concentration ~ Dose + Time | Id
## X variable for graphs: Time (hr)
## covariates: Weight (kg), Sex (-)
## reference class for covariate Sex : 0
## Dataset characteristics:
## number of subjects: 12
## number of observations: 120

```

```

##      average/min/max nb obs: 10.00 / 10 / 10
## First 10 lines of data:
##      Id      Dose  Time Concentration Weight Sex mdv cens occ ytype
## 1      1 319.992 0.25          2.84   79.6   1  0    0  1    1
## 2      1 319.992 0.57          6.57   79.6   1  0    0  1    1
## 3      1 319.992 1.12         10.50   79.6   1  0    0  1    1
## 4      1 319.992 2.02          9.66   79.6   1  0    0  1    1
## 5      1 319.992 3.82          8.58   79.6   1  0    0  1    1
## 6      1 319.992 5.10          8.36   79.6   1  0    0  1    1
## 7      1 319.992 7.03          7.47   79.6   1  0    0  1    1
## 8      1 319.992 9.05          6.89   79.6   1  0    0  1    1
## 9      1 319.992 12.12         5.94   79.6   1  0    0  1    1
## 10     1 319.992 24.37          3.28   79.6   1  0    0  1    1
## -----
## ----          Model          ----
## -----
## Nonlinear mixed-effects model
## Model function: One-compartment model with first-order absorption Model type: structural
## function(psi,id,xidep) {
##     dose<-xidep[,1]
##     tim<-xidep[,2]
##     ka<-psi[id,1]
##     V<-psi[id,2]
##     CL<-psi[id,3]
##     k<-CL/V
##     ypred<-dose*ka/(V*(ka-k))*(exp(-k*tim)-exp(-ka*tim))
##     return(ypred)
## }
## <bytecode: 0x564ed24aa9c8>
## Nb of parameters: 3
##     parameter names: ka V CL
##     distribution:
##     Parameter Distribution Estimated
## [1,] ka      log-normal Estimated
## [2,] V      log-normal Estimated
## [3,] CL      log-normal Estimated
## Variance-covariance matrix:
##     ka V CL
## ka  1 0  0
## V   0 1  0
## CL  0 0  1
## Error model: constant , initial values: a.1=1
## No covariate in the model.
## Initial values
##     ka V CL
## Pop.CondInit 1 20 0.5
## -----
## ---- Key algorithm options ----
## -----
## Estimation of individual parameters (MAP)
## Estimation of standard errors and linearised log-likelihood
## Estimation of log-likelihood by importance sampling
## Number of iterations: K1=300, K2=100
## Number of chains: 5

```

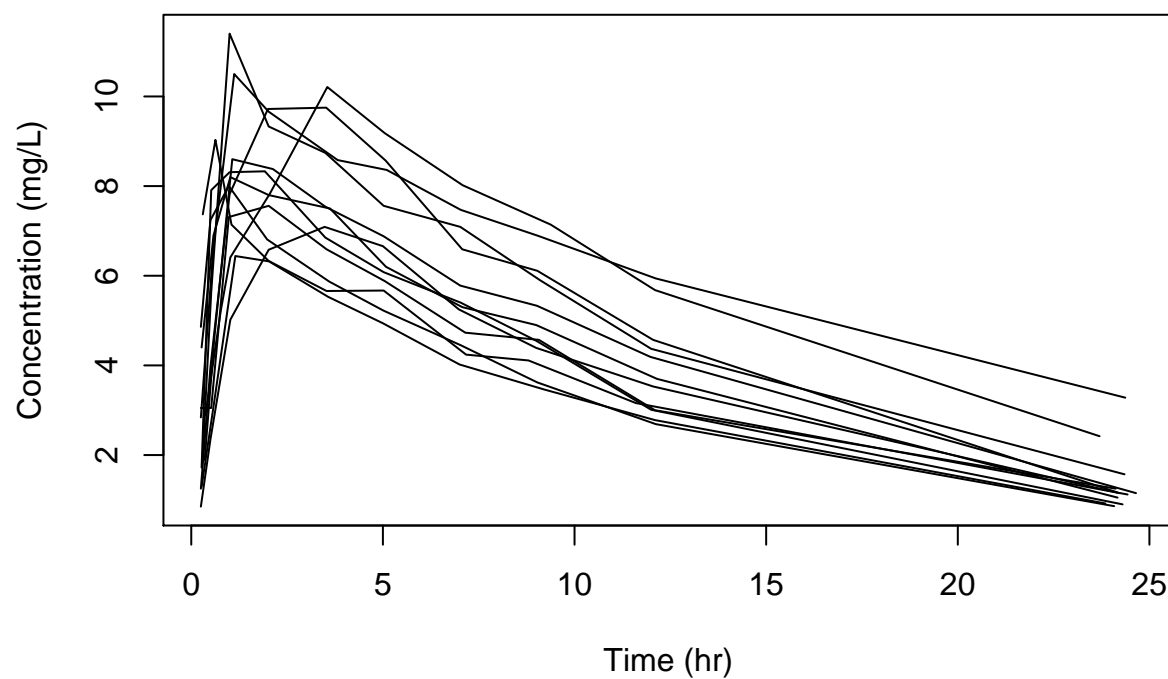
```

##      Seed: 632545
##      Number of MCMC iterations for IS: 5000
##      Simulations:
##          nb of simulated datasets used for npde: 1000
##          nb of simulated datasets used for VPC: 100
##      Input/output
##          save the results to a file: FALSE
##          save the graphs to files: FALSE
## -----
## ----- Results -----
## -----
## ----- Fixed effects -----
## -----
##      Parameter Estimate SE      CV(%)
## [1,] ka          1.57   0.304 19.3
## [2,] V          31.47   1.423  4.5
## [3,] CL          2.77   0.239  8.7
## [4,] a.1         0.74   0.057  7.7
## -----
## ----- Variance of random effects -----
## -----
##      Parameter Estimate SE      CV(%)
## ka omega2.ka 0.397   0.1790 45
## V  omega2.V  0.017   0.0096 58
## CL omega2.CL 0.074   0.0360 49
## -----
## ----- Correlation matrix of random effects -----
## -----
##      omega2.ka omega2.V omega2.CL
## omega2.ka 1      0      0
## omega2.V  0      1      0
## omega2.CL 0      0      1
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
##      -2LL= 344.1136
##      AIC = 358.1136
##      BIC = 361.5079
##
## Likelihood computed by importance sampling
##      -2LL= 345.4329
##      AIC = 359.4329
##      BIC = 362.8273
## -----

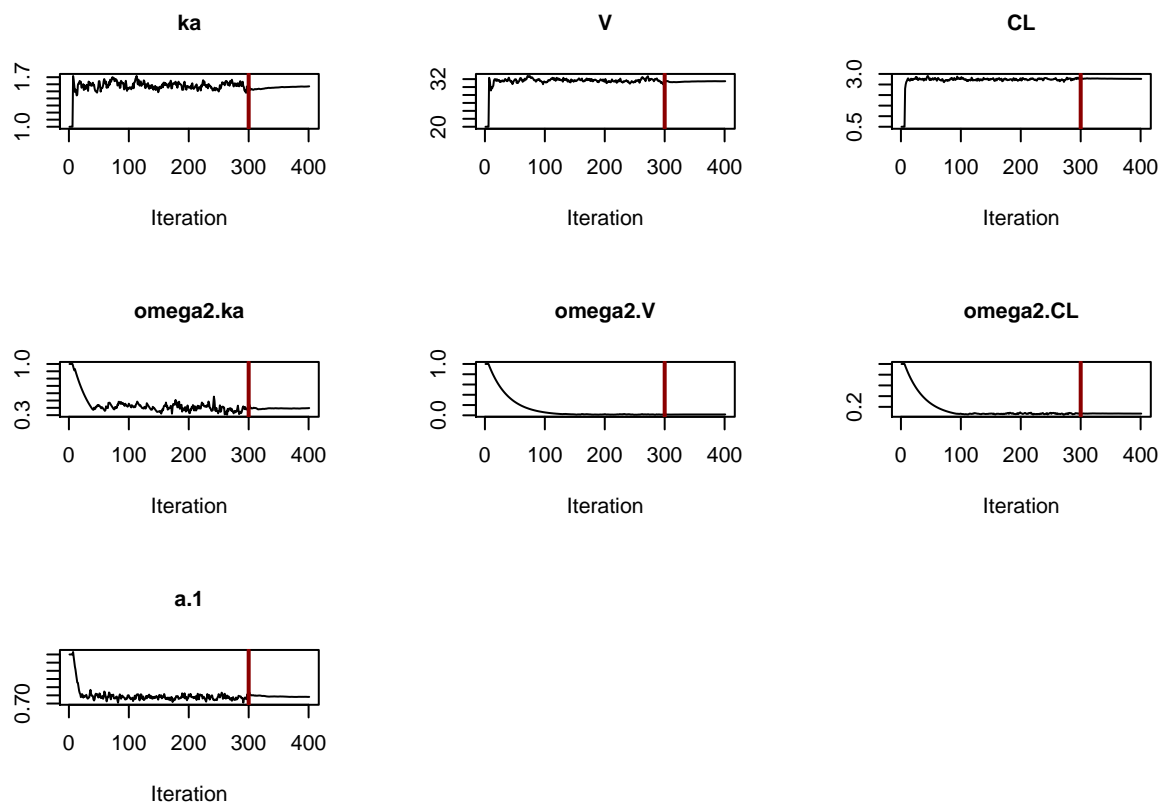
```

```
plot(saemix.fit)
```

```
## Plotting the data
```

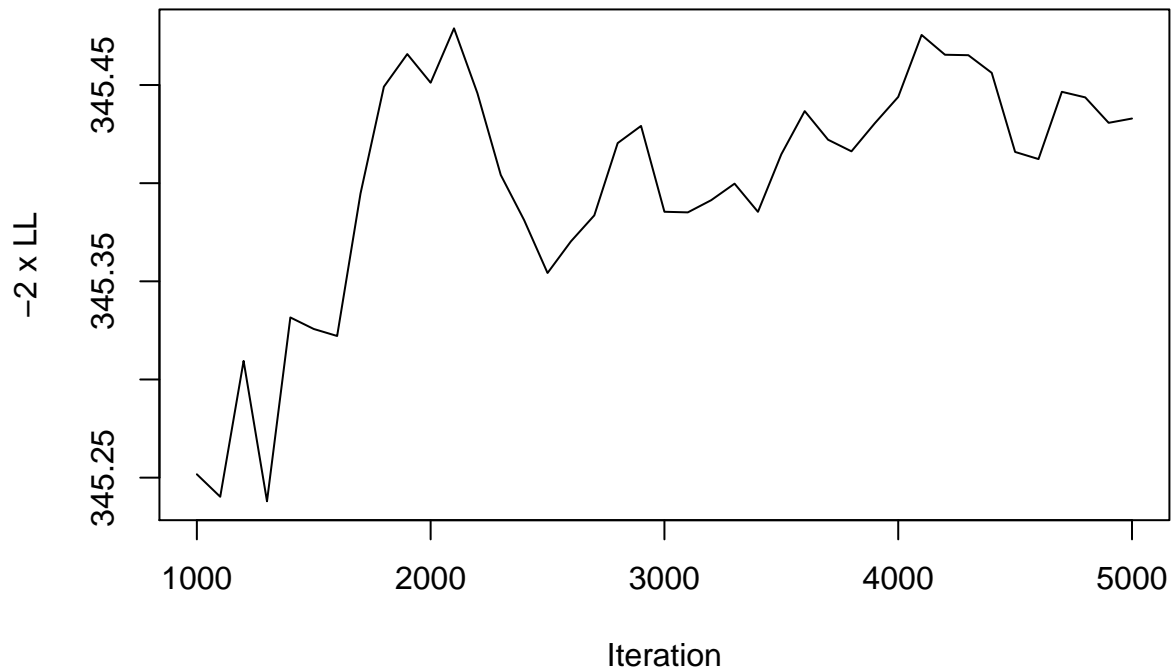


Plotting convergence plots



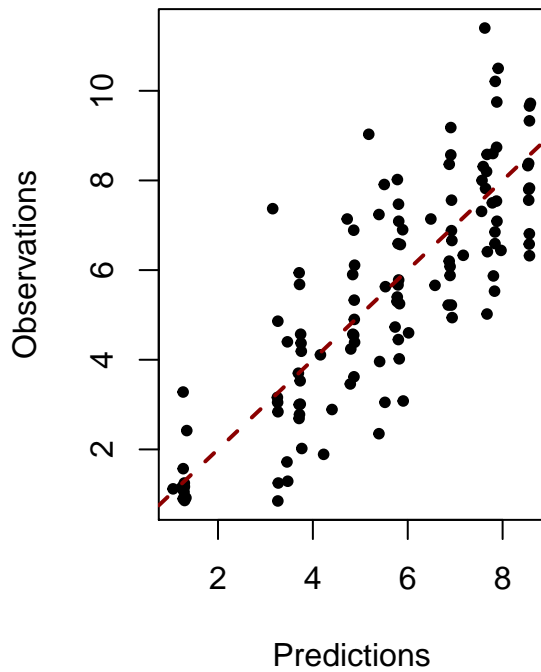
Plotting the likelihood

-2xLL by Importance Sampling

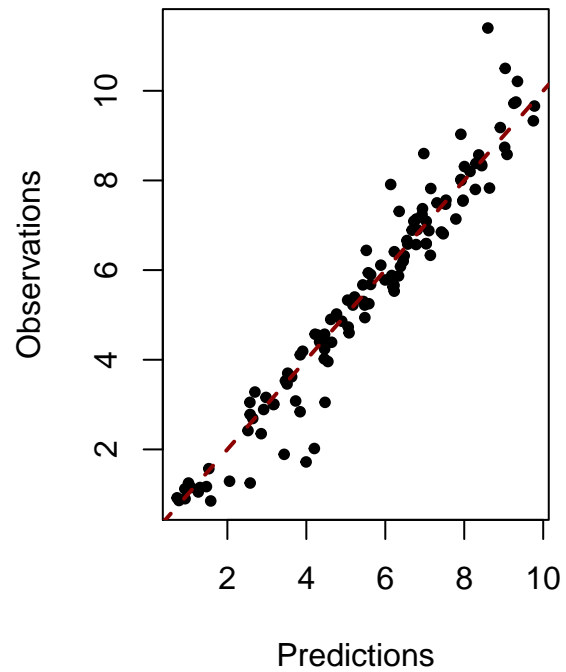


Plotting observations versus predictions

Population predictions



Individual predictions, MAP



```
# Model with covariates
saemix.model<-saemixModel(model=model1cpt,
                           description="One-compartment model with first-order absorption",
                           psi0=matrix(c(1.,20,0.5,0.1,0,-0.01),ncol=3,byrow=TRUE,
```

```

dimnames=list(NULL, c("ka", "V", "CL")),transform.par=c(1,1,1),
covariate.model=matrix(c(0,0,1,0,0,0),ncol=3,byrow=TRUE),fixed.estim=c(1,1,1),
covariance.model=matrix(c(1,0,0,0,1,1,0,1,1),ncol=3,byrow=TRUE),
omega.init=matrix(c(1,0,0,0,1,0,0,0,1),ncol=3,byrow=TRUE),error.model="combined"

##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
## Model function: One-compartment model with first-order absorption Model type: structural
## function(psi,id,xidep) {
##   dose<-xidep[,1]
##   tim<-xidep[,2]
##   ka<-psi[id,1]
##   V<-psi[id,2]
##   CL<-psi[id,3]
##   k<-CL/V
##   ypred<-dose*ka/(V*(ka-k))*(exp(-k*tim)-exp(-ka*tim))
##   return(ypred)
## }
## <bytecode: 0x564ed24aa9c8>
## Nb of parameters: 3
## parameter names: ka V CL
## distribution:
## Parameter Distribution Estimated
## [1,] ka log-normal Estimated
## [2,] V log-normal Estimated
## [3,] CL log-normal Estimated
## Variance-covariance matrix:
## ka V CL
## ka 1 0 0
## V 0 1 1
## CL 0 1 1
## Error model: combined , initial values: a.1=1 b.1=1
## Covariate model:
## ka V CL
## [1,] 0 0 1
## [2,] 0 0 0
## Initial values
## ka V CL
## Pop.CondInit 1.0 20 0.50
## Cov.CondInit 0.1 0 -0.01

saemix.options<-list(seed=39546,save=FALSE,save.graphs=FALSE, displayProgress=FALSE)
saemix.fit<-saemix(saemix.model,saemix.data,saemix.options)

## Nonlinear mixed-effects model fit by the SAEM algorithm
## -----
## ---- Data ----
## -----
## Object of class SaemixData
## longitudinal data for use with the SAEM algorithm
## Dataset theo.saemix

```



```

##      Structured data: Concentration ~ Dose + Time | Id
##      X variable for graphs: Time (hr)
##      covariates: Weight (kg), Sex (-)
##      reference class for covariate Sex : 0
## Dataset characteristics:
##      number of subjects:      12
##      number of observations: 120
##      average/min/max nb obs: 10.00 / 10 / 10
## First 10 lines of data:
##      Id      Dose  Time Concentration Weight Sex mdv cens occ ytype
## 1      1 319.992 0.25          2.84   79.6   1  0    0  1    1
## 2      1 319.992 0.57          6.57   79.6   1  0    0  1    1
## 3      1 319.992 1.12         10.50   79.6   1  0    0  1    1
## 4      1 319.992 2.02          9.66   79.6   1  0    0  1    1
## 5      1 319.992 3.82          8.58   79.6   1  0    0  1    1
## 6      1 319.992 5.10          8.36   79.6   1  0    0  1    1
## 7      1 319.992 7.03          7.47   79.6   1  0    0  1    1
## 8      1 319.992 9.05          6.89   79.6   1  0    0  1    1
## 9      1 319.992 12.12         5.94   79.6   1  0    0  1    1
## 10     1 319.992 24.37          3.28   79.6   1  0    0  1    1
## -----
## ----          Model          ----
## -----
## Nonlinear mixed-effects model
##      Model function: One-compartment model with first-order absorption Model type: structural
## function(psi,id,xidep) {
##      dose<-xidep[,1]
##      tim<-xidep[,2]
##      ka<-psi[id,1]
##      V<-psi[id,2]
##      CL<-psi[id,3]
##      k<-CL/V
##      ypred<-dose*ka/(V*(ka-k))*(exp(-k*tim)-exp(-ka*tim))
##      return(ypred)
##      }
## <bytecode: 0x564ed24aa9c8>
##      Nb of parameters: 3
##      parameter names: ka V CL
##      distribution:
##      Parameter Distribution Estimated
## [1,] ka          log-normal Estimated
## [2,] V          log-normal Estimated
## [3,] CL          log-normal Estimated
##      Variance-covariance matrix:
##      ka V CL
## ka  1 0 0
## V   0 1 1
## CL  0 1 1
##      Error model: combined , initial values: a.1=1 b.1=1
##      Covariate model:
##      [,1] [,2] [,3]
## Weight  0  0  1
##      Initial values
##      ka V CL

```

```

## Pop.CondInit 1.0 20 0.50
## Cov.CondInit 0.1 0 -0.01
## -----
## ---- Key algorithm options ----
## -----
## Estimation of individual parameters (MAP)
## Estimation of standard errors and linearised log-likelihood
## Estimation of log-likelihood by importance sampling
## Number of iterations: K1=300, K2=100
## Number of chains: 5
## Seed: 39546
## Number of MCMC iterations for IS: 5000
## Simulations:
## nb of simulated datasets used for npde: 1000
## nb of simulated datasets used for VPC: 100
## Input/output
## save the results to a file: FALSE
## save the graphs to files: FALSE
## -----
## ---- Results ----
## -----
## ----- Fixed effects -----
## -----
## Parameter Estimate SE CV(%) p-value
## [1,] ka 1.5565 0.3050 19.6 -
## [2,] V 31.6621 1.4946 4.7 -
## [3,] CL 4.4308 1.9206 43.3 -
## [4,] beta_Weight(CL) -0.0067 0.0061 91.3 0.14
## [5,] a.1 0.5734 0.1211 21.1 -
## [6,] b.1 0.0748 0.0223 29.8 -
## -----
## ----- Variance of random effects -----
## -----
## Parameter Estimate SE CV(%)
## ka omega2.ka 0.412 0.179 44
## V omega2.V 0.019 0.011 56
## CL omega2.CL 0.064 0.031 48
## covar cov.V.CL 0.035 0.016 45
## -----
## ----- Correlation matrix of random effects -----
## -----
## omega2.ka omega2.V omega2.CL
## omega2.ka 1 0 0
## omega2.V 0 1 1
## omega2.CL 0 1 1
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
## -2LL= 330.7213
## AIC = 350.7213
## BIC = 355.5704
##
## Likelihood computed by importance sampling

```

```
##      -2LL= 333.9945
##      AIC = 353.9945
##      BIC = 358.8436
## -----
```

Simulated PD

```
if(testMode) {
  data(PD1.saemix)
  data(PD2.saemix)
} else {
  PD1.saemix<-read.table(file.path(datDir, "PD1.saemix.tab"), header=TRUE)
  PD2.saemix<-read.table(file.path(datDir, "PD1.saemix.tab"), header=TRUE)
}

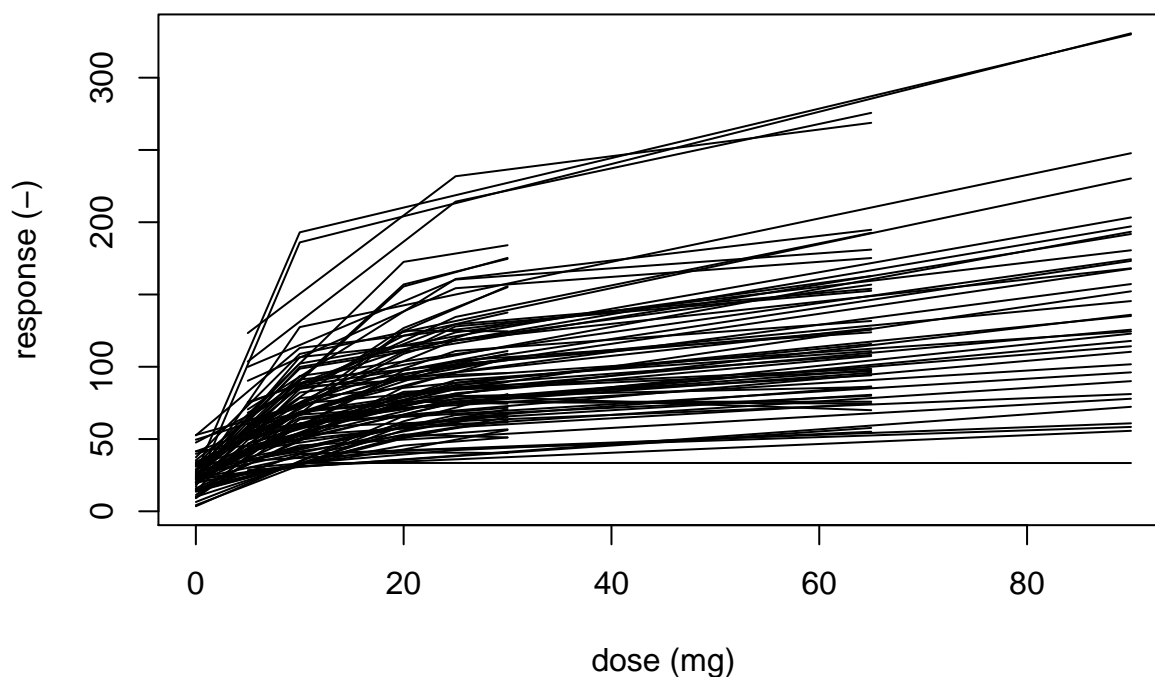
saemix.data<-saemixData(name.data=PD1.saemix,header=TRUE,name.group=c("subject"),
  name.predictors=c("dose"),name.response=c("response"),
  name.covariates=c("gender"), units=list(x="mg",y="-",covariates=c("-")))

## [1] "gender"
##
##
## The following SaemixData object was successfully created:
##
## Object of class SaemixData
##   longitudinal data for use with the SAEM algorithm
## Dataset PD1.saemix
##   Structured data: response ~ dose | subject
##   Predictor: dose (mg)
##   covariates: gender (-)
##   reference class for covariate gender : 0

modelemax<-function(psi,id,xidep) {
  # input:
  #   psi : matrix of parameters (3 columns, E0, Emax, EC50)
  #   id : vector of indices
  #   xidep : dependent variables (same nb of rows as length of id)
  # returns:
  #   a vector of predictions of length equal to length of id
  dose<-xidep[,1]
  e0<-psi[id,1]
  emax<-psi[id,2]
  e50<-psi[id,3]
  f<-e0+emax*dose/(e50+dose)
  return(f)
}

# Plotting the data
plot(saemix.data,main="Simulated data PD1")
```

Simulated data PD1



```
# Compare models with and without covariates with LL by Importance Sampling
modell1<-saemixModel(model=modelemax,description="Emax growth model",
  psi0=matrix(c(20,300,20,0,0,0),ncol=3,byrow=TRUE,dimnames=list(NULL,
    c("E0","Emax","EC50"))), transform.par=c(1,1,1),
  covariate.model=matrix(c(0,0,0), ncol=3,byrow=TRUE),fixed.estim=c(1,1,1))
```

```
##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
## Model function: Emax growth model Model type: structural
## function(psi,id,xidep) {
## # input:
## #   psi : matrix of parameters (3 columns, E0, Emax, EC50)
## #   id : vector of indices
## #   xidep : dependent variables (same nb of rows as length of id)
## # returns:
## #   a vector of predictions of length equal to length of id
## dose<-xidep[,1]
## e0<-psi[id,1]
## emax<-psi[id,2]
## e50<-psi[id,3]
## f<-e0+emax*dose/(e50+dose)
## return(f)
## }
## Nb of parameters: 3
## parameter names: E0 Emax EC50
## distribution:
## Parameter Distribution Estimated
```

```

## [1,] E0          log-normal  Estimated
## [2,] Emax        log-normal  Estimated
## [3,] EC50        log-normal  Estimated
##   Variance-covariance matrix:
##       E0 Emax EC50
## E0    1    0    0
## Emax  0    1    0
## EC50  0    0    1
##   Error model: constant , initial values: a.1=1
##   No covariate in the model.
##   Initial values
##       E0 Emax EC50
## Pop.CondInit 20 300 20
## Cov.CondInit 0  0  0

model2<-saemixModel(model=modelemax,description="Emax growth model",
  psi0=matrix(c(20,300,20,0,0,0),ncol=3,byrow=TRUE,dimnames=list(NULL,
    c("E0","Emax","EC50"))), transform.par=c(1,1,1),
  covariate.model=matrix(c(0,0,1), ncol=3,byrow=TRUE),fixed.estim=c(1,1,1))

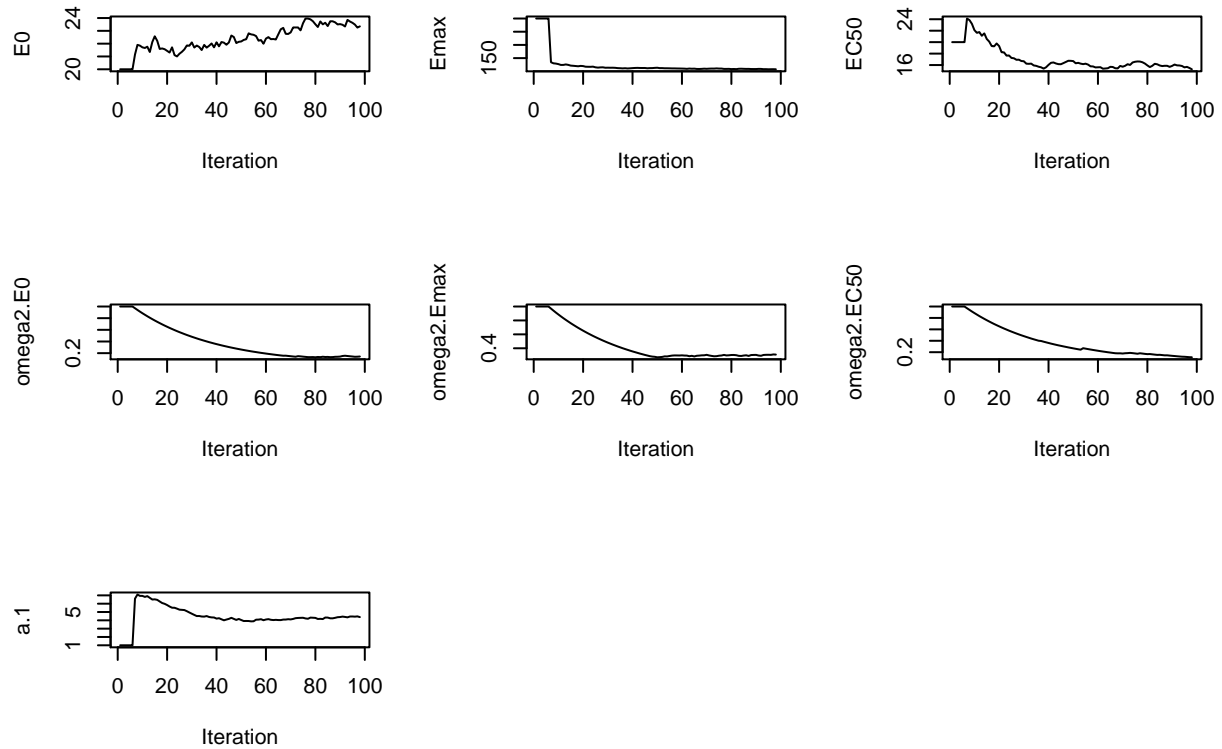
##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
##   Model function:  Emax growth model  Model type:  structural
## function(psi,id,xidep) {
## # input:
## #   psi : matrix of parameters (3 columns, E0, Emax, EC50)
## #   id  : vector of indices
## #   xidep : dependent variables (same nb of rows as length of id)
## # returns:
## #   a vector of predictions of length equal to length of id
##   dose<-xidep[,1]
##   e0<-psi[id,1]
##   emax<-psi[id,2]
##   e50<-psi[id,3]
##   f<-e0+emax*dose/(e50+dose)
##   return(f)
## }
##   Nb of parameters: 3
##       parameter names:  E0 Emax EC50
##       distribution:
##       Parameter Distribution Estimated
## [1,] E0          log-normal  Estimated
## [2,] Emax        log-normal  Estimated
## [3,] EC50        log-normal  Estimated
##   Variance-covariance matrix:
##       E0 Emax EC50
## E0    1    0    0
## Emax  0    1    0
## EC50  0    0    1
##   Error model: constant , initial values: a.1=1
##   Covariate model:
##       E0 Emax EC50

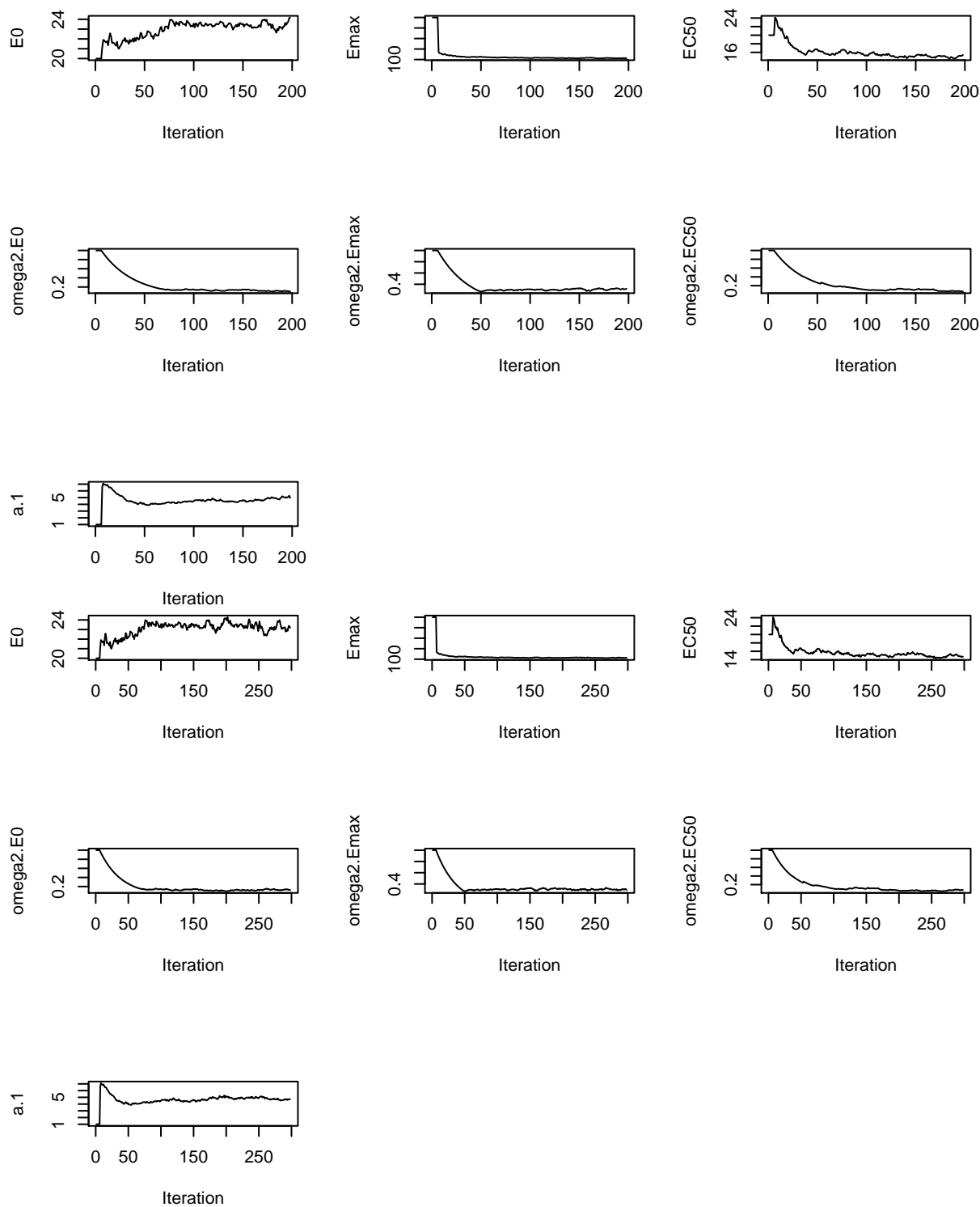
```

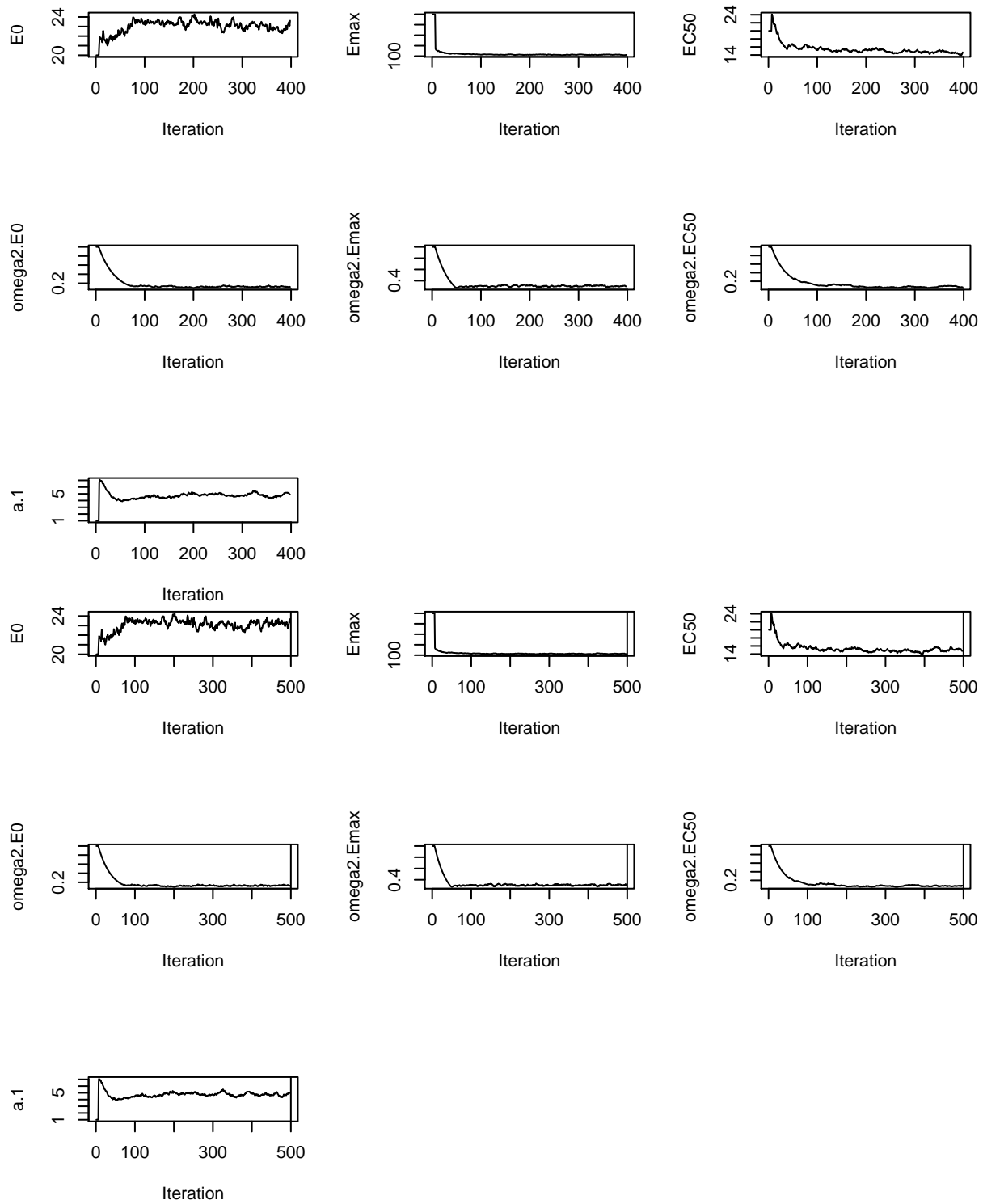
```
## [1,] 0 0 1
##      Initial values
##      E0 Emax EC50
## Pop.CondInit 20 300 20
## Cov.CondInit 0 0 0

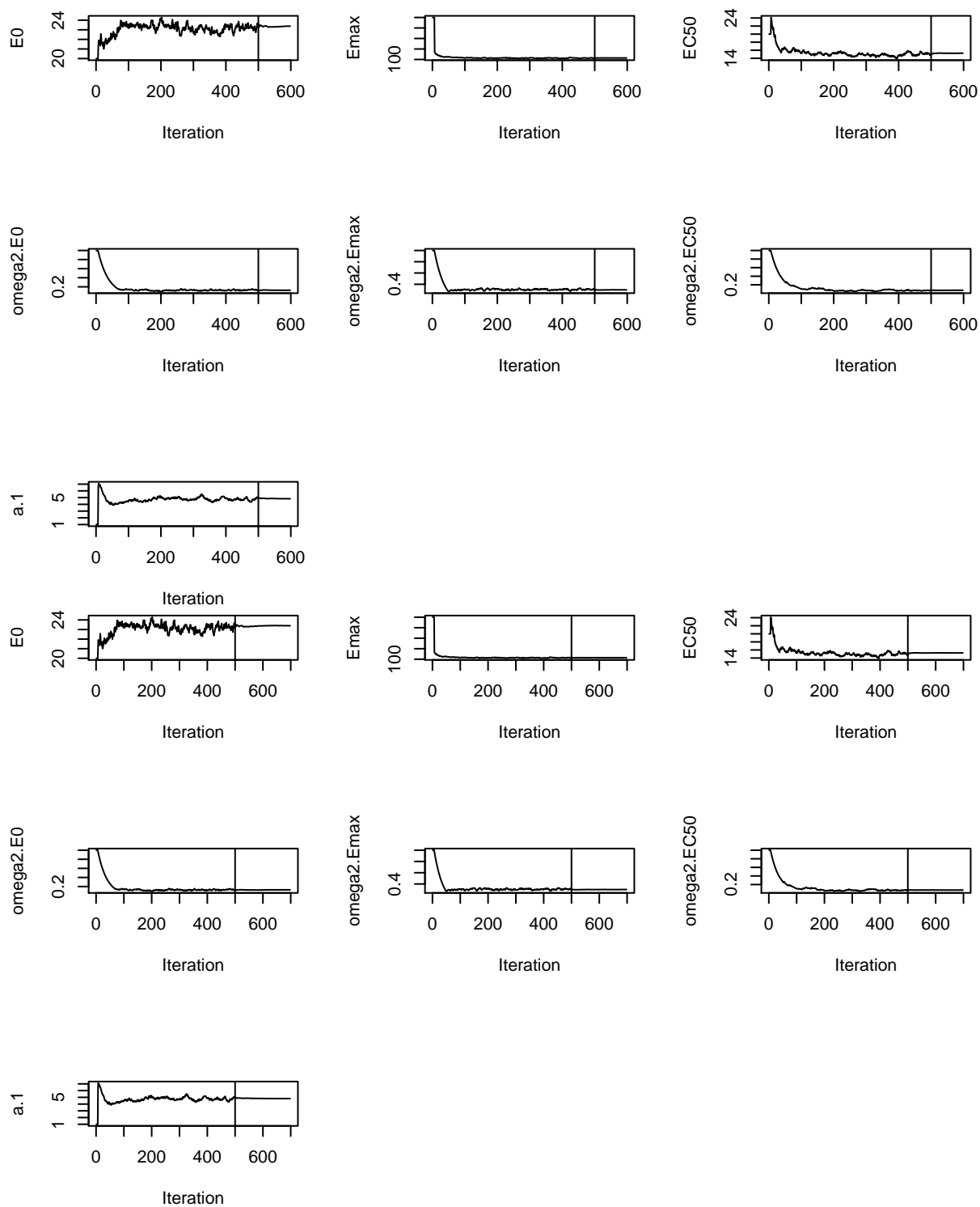
# SE not computed as not needed for the test
saemix.options<-list(algorithms=c(0,1,1),nb.chains=3,seed=765754,
  nbiter.saemix=c(500,300),save=FALSE,save.graphs=FALSE)

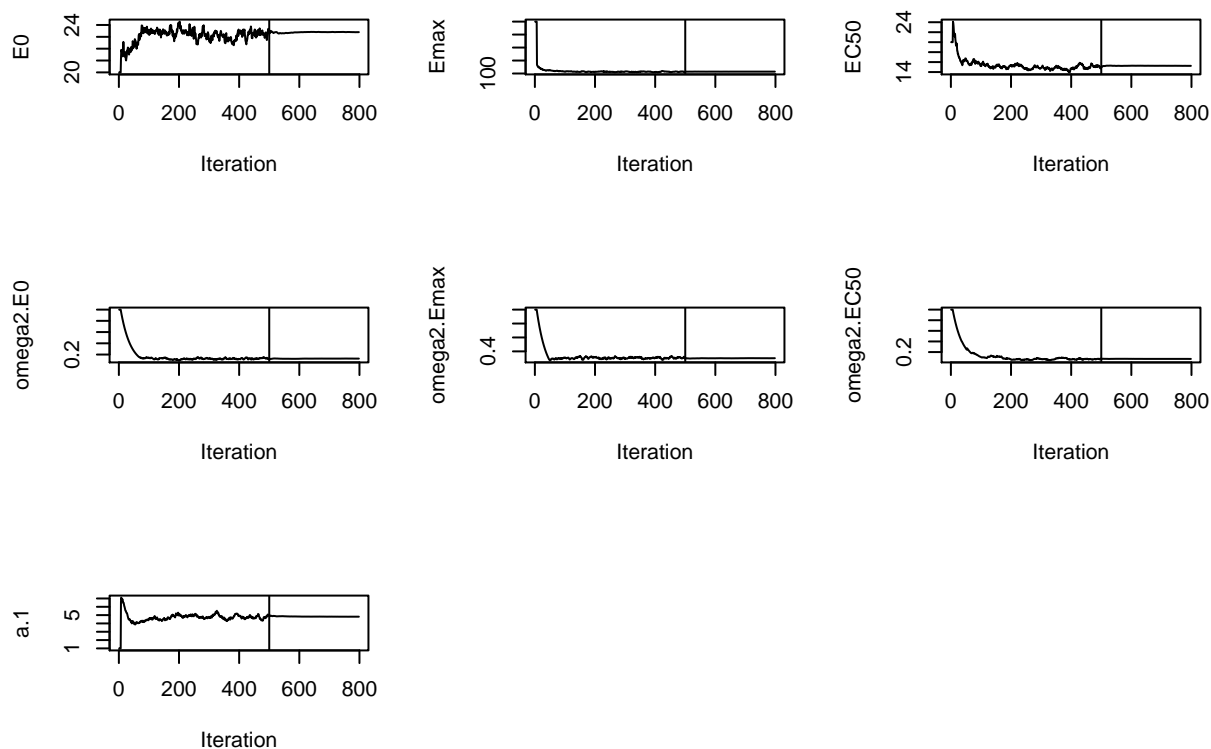
fit1<-saemix(model1,saemix.data,saemix.options)
```











```
## Nonlinear mixed-effects model fit by the SAEM algorithm
```

```
## -----
```

```
## ----          Data          ----
```

```
## -----
```

```
## Object of class SaemixData
```

```
##   longitudinal data for use with the SAEM algorithm
```

```
## Dataset PD1.saemix
```

```
##   Structured data: response ~ dose | subject
```

```
##   Predictor: dose (mg)
```

```
##   covariates: gender (-)
```

```
##   reference class for covariate gender : 0
```

```
## Dataset characteristics:
```

```
##   number of subjects:      100
```

```
##   number of observations: 300
```

```
##   average/min/max nb obs: 3.00 / 3 / 3
```

```
## First 10 lines of data:
```

```
##   subject dose response gender mdv cens occ ytype
```

## 1	1	0	11.2870	1	0	0	1	1
## 2	1	10	63.6114	1	0	0	1	1
## 3	1	90	122.9170	1	0	0	1	1
## 4	2	0	15.0514	1	0	0	1	1
## 5	2	10	39.5296	1	0	0	1	1
## 6	2	90	60.8522	1	0	0	1	1
## 7	3	0	25.5390	1	0	0	1	1
## 8	3	10	58.0035	1	0	0	1	1
## 9	3	90	81.1173	1	0	0	1	1
## 10	4	0	22.1446	1	0	0	1	1

```
## -----
```

```
## ----          Model          ----
```

```
## -----
```

```

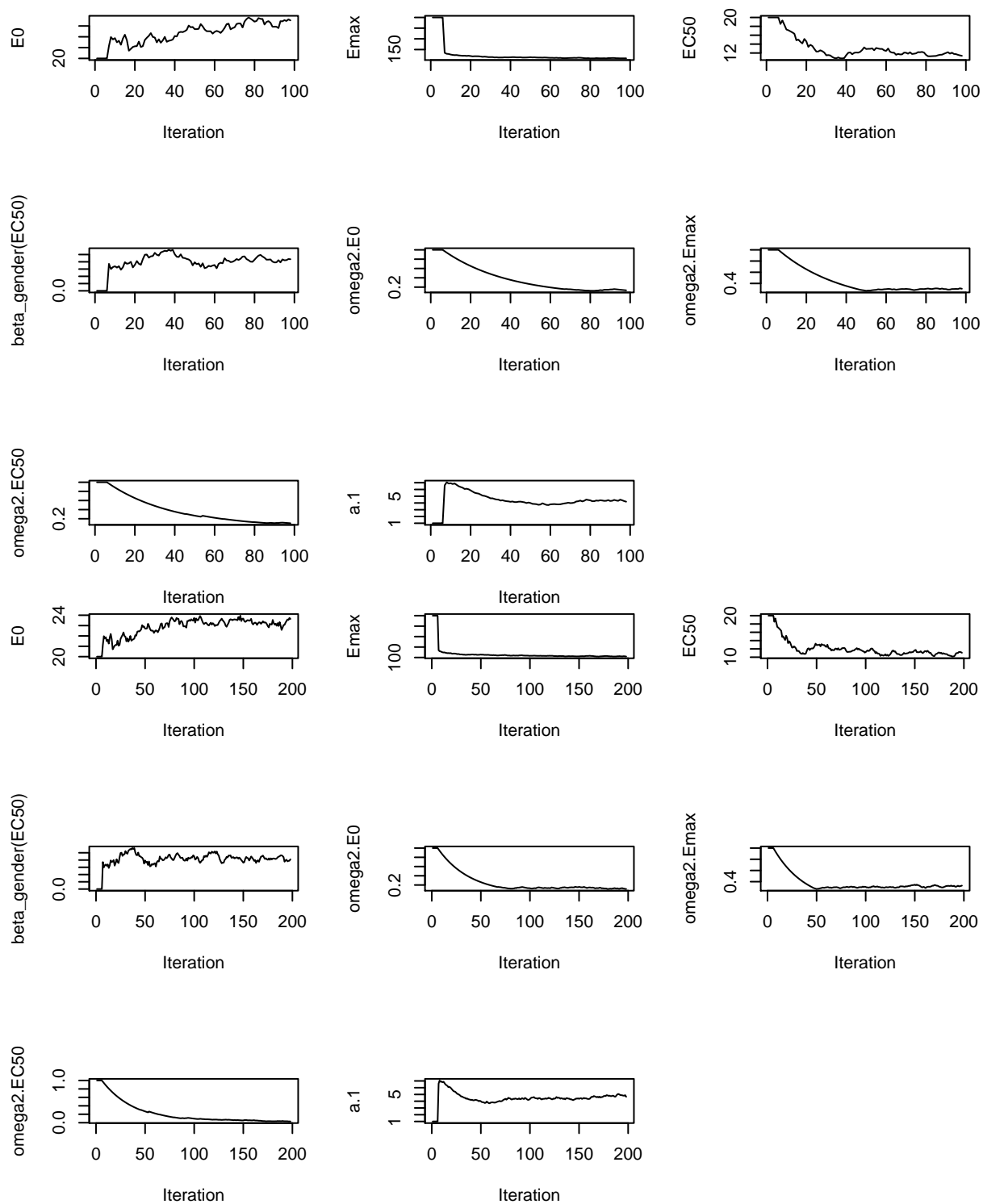
## Nonlinear mixed-effects model
##   Model function: Emax growth model   Model type: structural
## function(psi,id,xidep) {
##   # input:
##   #   psi : matrix of parameters (3 columns, E0, Emax, EC50)
##   #   id  : vector of indices
##   #   xidep : dependent variables (same nb of rows as length of id)
##   # returns:
##   #   a vector of predictions of length equal to length of id
##   dose<-xidep[,1]
##   e0<-psi[id,1]
##   emax<-psi[id,2]
##   e50<-psi[id,3]
##   f<-e0+emax*dose/(e50+dose)
##   return(f)
## }
## <bytecode: 0x564ed5e224b0>
##   Nb of parameters: 3
##     parameter names:  E0 Emax EC50
##     distribution:
##     Parameter Distribution Estimated
## [1,] E0      log-normal Estimated
## [2,] Emax    log-normal Estimated
## [3,] EC50    log-normal Estimated
##   Variance-covariance matrix:
##     E0 Emax EC50
## E0    1    0    0
## Emax  0    1    0
## EC50  0    0    1
##   Error model: constant , initial values: a.1=1
##   No covariate in the model.
##   Initial values
##           E0 Emax EC50
## Pop.CondInit 20  300  20
## -----
## ----   Key algorithm options   ----
## -----
##   Estimation of individual parameters (MAP)
##   Estimation of standard errors and linearised log-likelihood
##   Estimation of log-likelihood by importance sampling
##   Number of iterations:  K1=500, K2=300
##   Number of chains:  3
##   Seed: 765754
##   Number of MCMC iterations for IS:  5000
##   Simulations:
##     nb of simulated datasets used for npde:  1000
##     nb of simulated datasets used for VPC:  100
##   Input/output
##     save the results to a file:  FALSE
##     save the graphs to files:  FALSE
## -----
## ----                               Results                               ----
## -----
## ----- Fixed effects -----

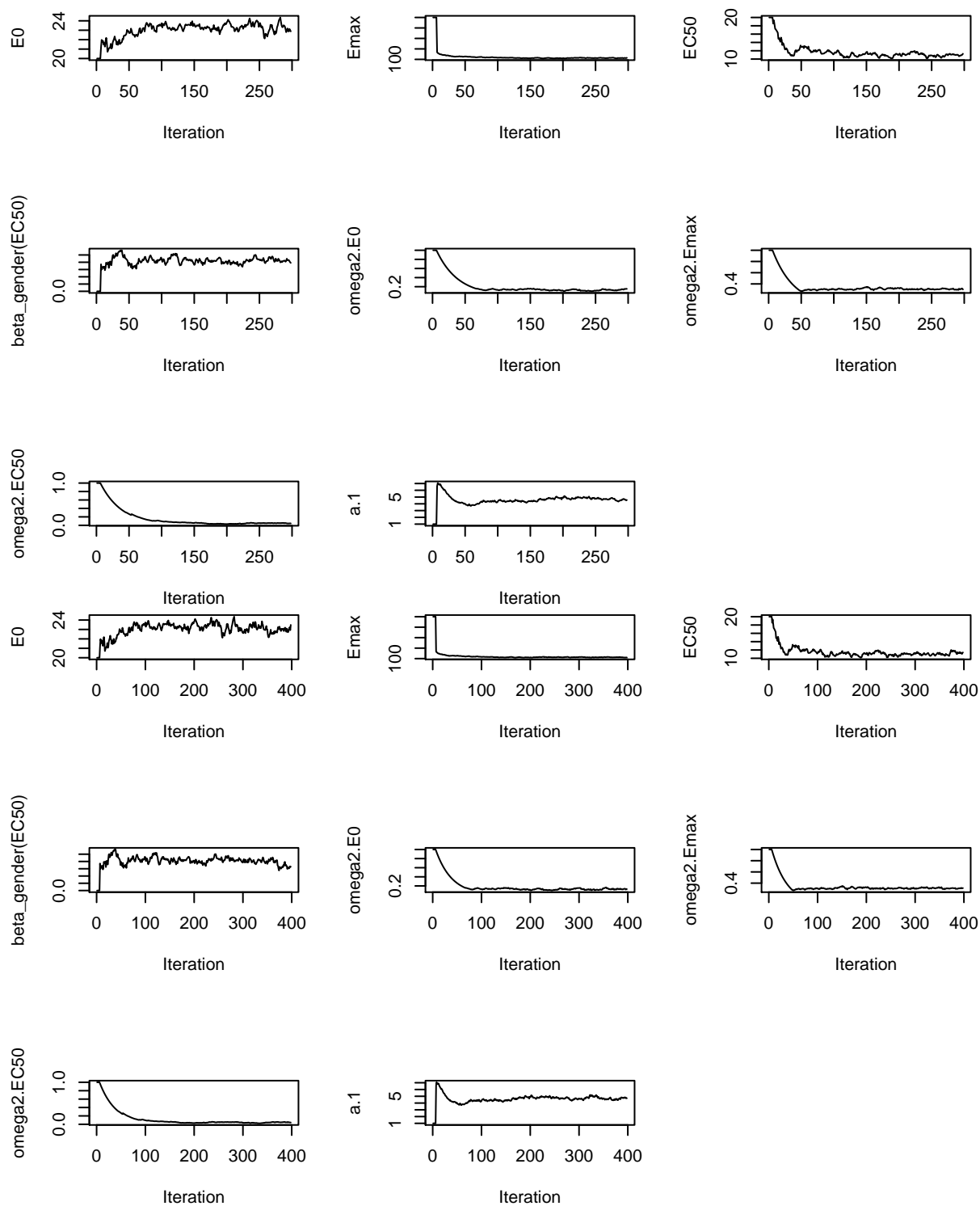
```

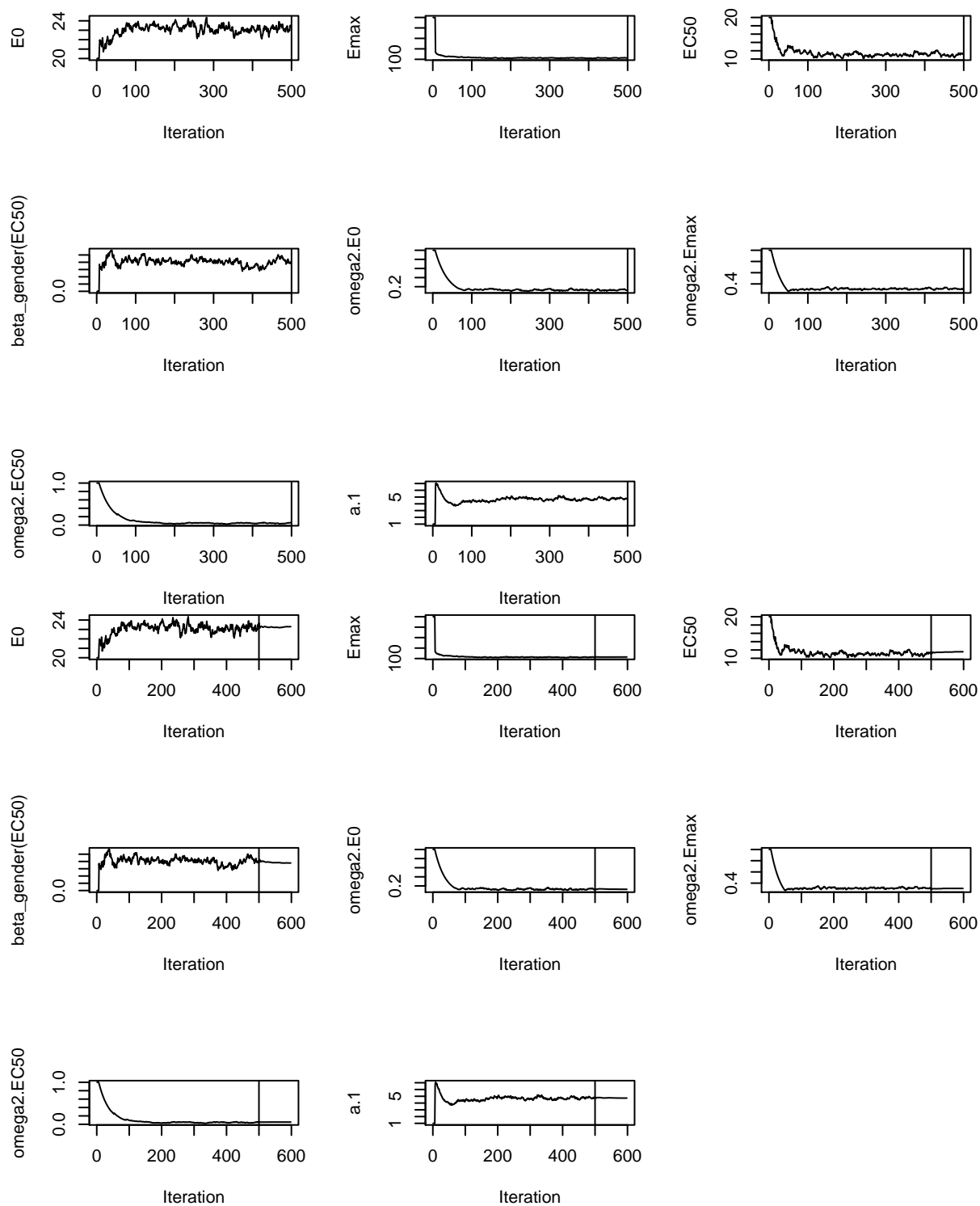
```

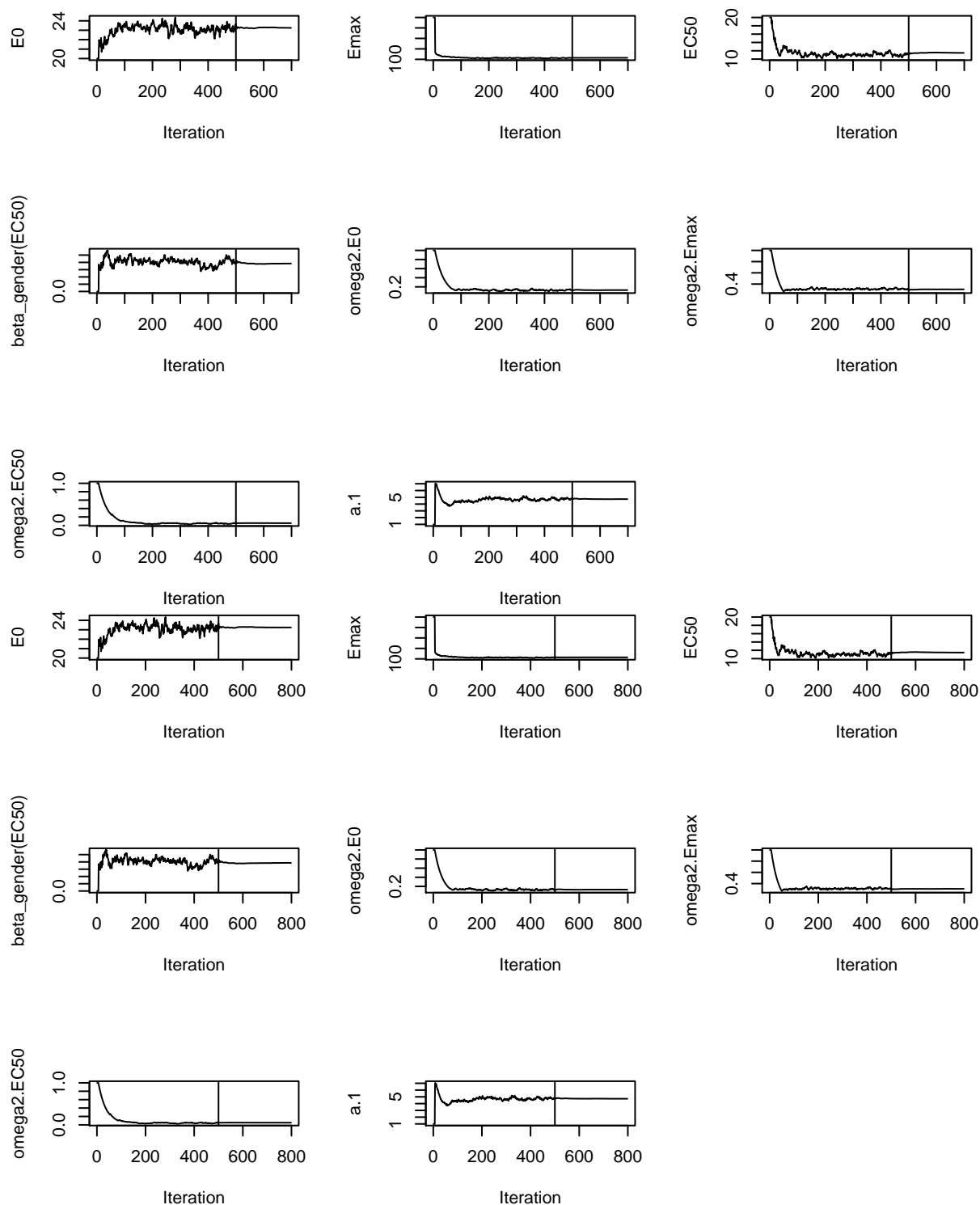
## -----
##      Parameter Estimate SE   CV(%)
## [1,] E0          23.4   1.08 4.6
## [2,] Emax        107.2   6.09 5.7
## [3,] EC50         15.2   0.77 5.0
## [4,] a.1          4.8   0.42 8.8
## -----
## ----- Variance of random effects -----
## -----
##      Parameter   Estimate SE    CV(%)
## E0  omega2.E0    0.128   0.028 22
## Emax omega2.Emax 0.302   0.045 15
## EC50 omega2.EC50 0.071   0.027 38
## -----
## ----- Correlation matrix of random effects -----
## -----
##      omega2.E0 omega2.Emax omega2.EC50
## omega2.E0    1          0          0
## omega2.Emax  0          1          0
## omega2.EC50  0          0          1
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
##      -2LL= 2463.063
##      AIC = 2477.063
##      BIC = 2495.299
##
## Likelihood computed by importance sampling
##      -2LL= 2466.154
##      AIC = 2480.154
##      BIC = 2498.39
## -----
fit2<-saemix(model2,saemix.data,saemix.options)

```









```
## Nonlinear mixed-effects model fit by the SAEM algorithm
## -----
## ---- Data ----
## -----
## Object of class SaemixData
## longitudinal data for use with the SAEM algorithm
## Dataset PD1.saemix
```



```

##      Structured data: response ~ dose | subject
##      Predictor: dose (mg)
##      covariates: gender (-)
##      reference class for covariate gender : 0
## Dataset characteristics:
##      number of subjects:      100
##      number of observations: 300
##      average/min/max nb obs: 3.00 / 3 / 3
## First 10 lines of data:
##      subject dose response gender mdv cens occ ytype
## 1          1    0  11.2870      1  0    0    1    1
## 2          1   10  63.6114      1  0    0    1    1
## 3          1   90 122.9170      1  0    0    1    1
## 4          2    0  15.0514      1  0    0    1    1
## 5          2   10  39.5296      1  0    0    1    1
## 6          2   90  60.8522      1  0    0    1    1
## 7          3    0  25.5390      1  0    0    1    1
## 8          3   10  58.0035      1  0    0    1    1
## 9          3   90  81.1173      1  0    0    1    1
## 10         4    0  22.1446      1  0    0    1    1
## -----
## ----          Model          ----
## -----
## Nonlinear mixed-effects model
##      Model function: Emax growth model  Model type: structural
## function(psi,id,xidep) {
## # input:
## #   psi : matrix of parameters (3 columns, E0, Emax, EC50)
## #   id  : vector of indices
## #   xidep : dependent variables (same nb of rows as length of id)
## # returns:
## #   a vector of predictions of length equal to length of id
##   dose<-xidep[,1]
##   e0<-psi[id,1]
##   emax<-psi[id,2]
##   e50<-psi[id,3]
##   f<-e0+emax*dose/(e50+dose)
##   return(f)
## }
## <bytecode: 0x564ed5e224b0>
##      Nb of parameters: 3
##      parameter names:  E0 Emax EC50
##      distribution:
##      Parameter Distribution Estimated
## [1,] E0          log-normal  Estimated
## [2,] Emax        log-normal  Estimated
## [3,] EC50        log-normal  Estimated
##      Variance-covariance matrix:
##      E0 Emax EC50
## E0    1    0    0
## Emax  0    1    0
## EC50  0    0    1
##      Error model: constant , initial values: a.1=1
##      Covariate model:

```

```

##      [,1] [,2] [,3]
## gender    0    0    1
##      Initial values
##              E0 Emax EC50
## Pop.CondInit 20  300  20
## Cov.CondInit  0    0    0
## -----
## ----      Key algorithm options      ----
## -----
##      Estimation of individual parameters (MAP)
##      Estimation of standard errors and linearised log-likelihood
##      Estimation of log-likelihood by importance sampling
##      Number of iterations:  K1=500, K2=300
##      Number of chains:  3
##      Seed:  765754
##      Number of MCMC iterations for IS:  5000
##      Simulations:
##          nb of simulated datasets used for npde:  1000
##          nb of simulated datasets used for VPC:  100
##      Input/output
##          save the results to a file:  FALSE
##          save the graphs to files:  FALSE
## -----
## ----                        Results                        ----
## -----
## -----      Fixed effects      -----
## -----
##      Parameter          Estimate SE      CV(%) p-value
## [1,] E0                  23.24  1.072  4.6  -
## [2,] Emax                 107.20  6.120  5.7  -
## [3,] EC50                 11.45  0.980  8.6  -
## [4,] beta_gender(EC50)    0.39   0.099 25.6  4.7e-05
## [5,] a.1                  4.72   0.407  8.6  -
## -----
## -----      Variance of random effects      -----
## -----
##      Parameter  Estimate SE      CV(%)
## E0  omega2.E0   0.129   0.028  22
## Emax omega2.Emax 0.307   0.045  15
## EC50 omega2.EC50 0.052   0.022  43
## -----
## -----      Correlation matrix of random effects      -----
## -----
##      omega2.E0  omega2.Emax  omega2.EC50
## omega2.E0    1          0          0
## omega2.Emax  0          1          0
## omega2.EC50  0          0          1
## -----
## -----      Statistical criteria      -----
## -----
## Likelihood computed by linearisation
##      -2LL= 2448.635
##      AIC = 2464.635
##      BIC = 2485.477

```

```
##
## Likelihood computed by importance sampling
##      -2LL= 2452.279
##      AIC = 2468.279
##      BIC = 2489.121
## -----
wstat<-(-2)*(fit1["results"]["ll.is"]-fit2["results"]["ll.is"])
cat("LRT test for covariate effect on EC50: p-value=",1-pchisq(wstat,1),"\n")

## LRT test for covariate effect on EC50: p-value= 0.0001954234
```

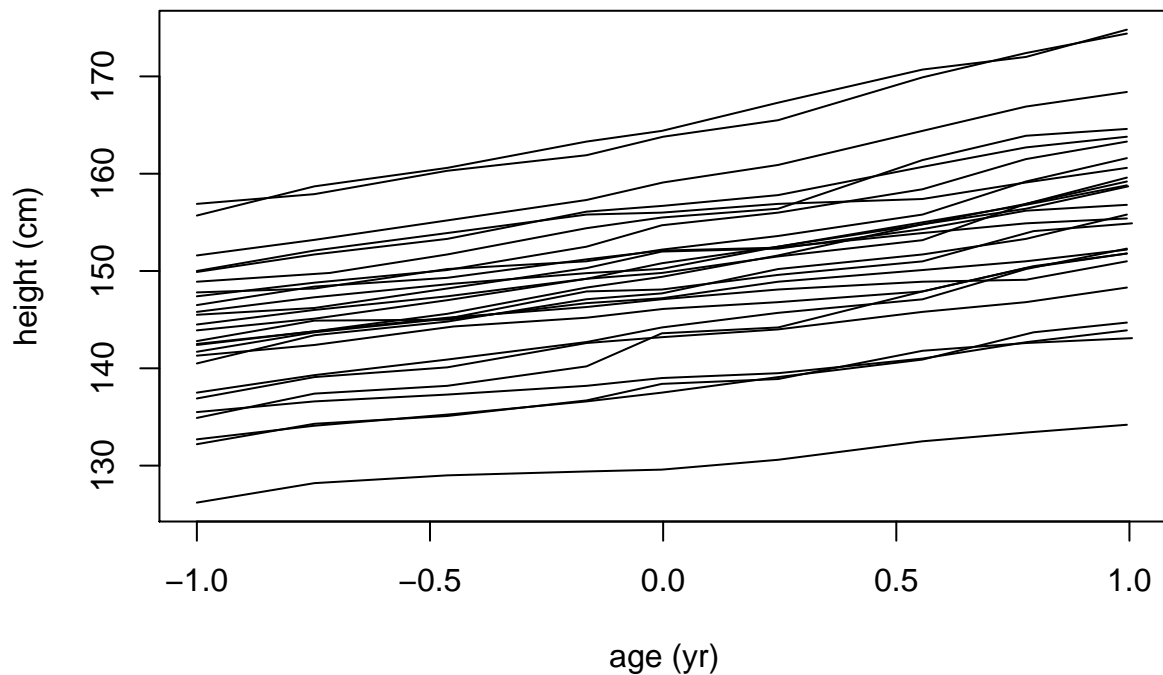
Oxford boys

```
if(testMode)
  data(oxboys.saemix) else
  oxboys.saemix<-read.table(file.path(datDir, "oxboys.saemix.tab"), header=TRUE)

saemix.data<-saemixData(name.data=oxboys.saemix,header=TRUE,
  name.group=c("Subject"),name.predictors=c("age"),name.response=c("height"),
  units=list(x="yr",y="cm"))

##
##
## The following SaemixData object was successfully created:
##
## Object of class SaemixData
##      longitudinal data for use with the SAEM algorithm
## Dataset oxboys.saemix
##      Structured data: height ~ age | Subject
##      Predictor: age (yr)

# plot the data
plot(saemix.data)
```



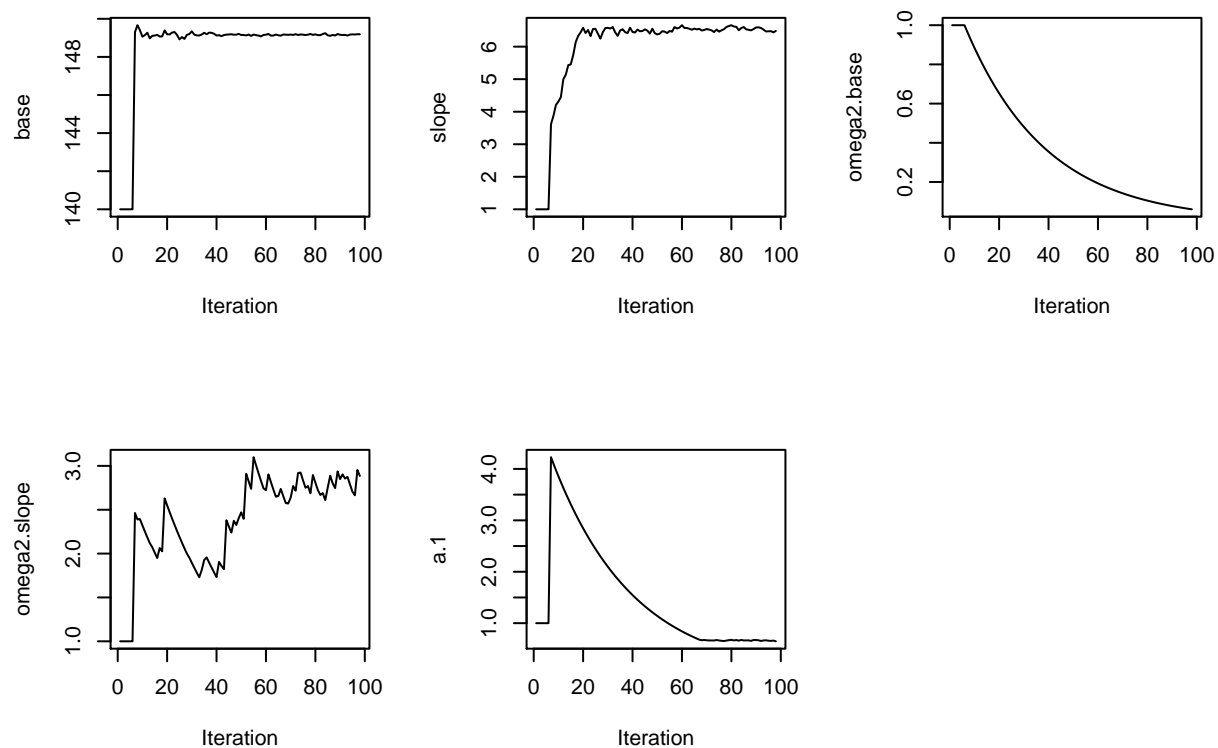
```
growth.linear<-function(psi,id,xidep) {
  x<-xidep[,1]
  base<-psi[id,1]
  slope<-psi[id,2]
  f<-base+slope*x
  return(f)
}
saemix.model<-saemixModel(model=growth.linear,description="Linear model",
  psi0=matrix(c(140,1),ncol=2,byrow=TRUE,dimnames=list(NULL,c("base","slope"))),
  transform.par=c(1,0),covariance.model=matrix(c(1,1,1,1),ncol=2,byrow=TRUE),
  error.model="constant")
```

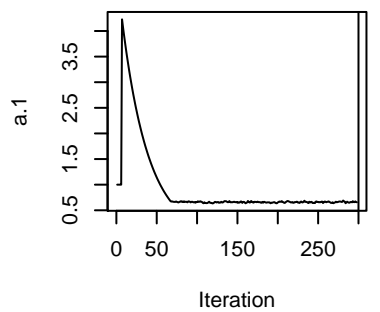
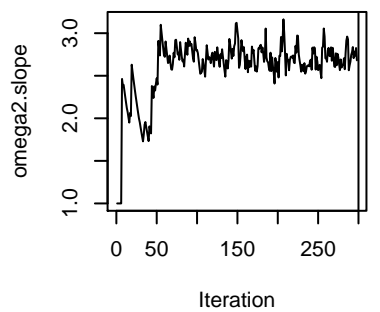
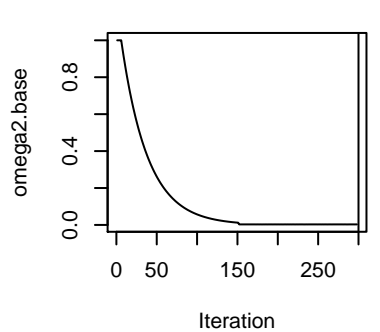
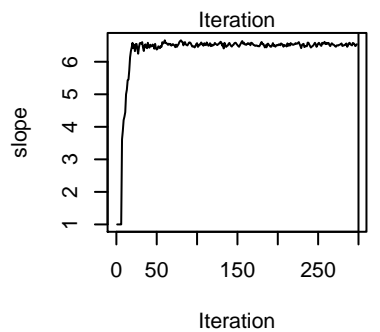
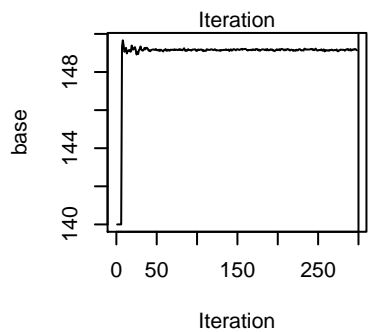
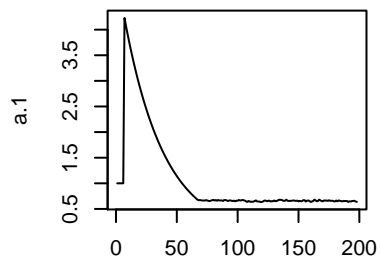
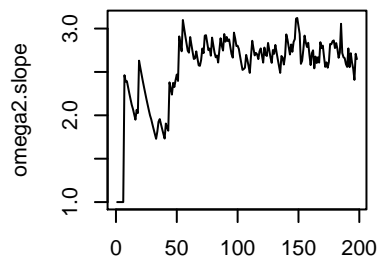
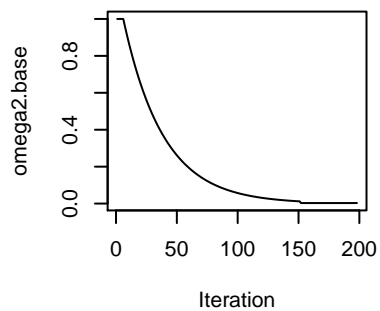
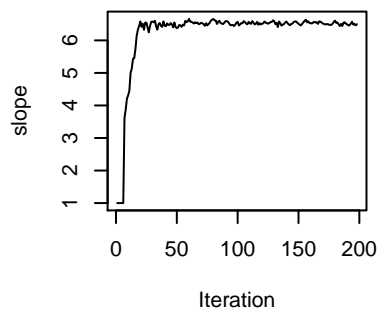
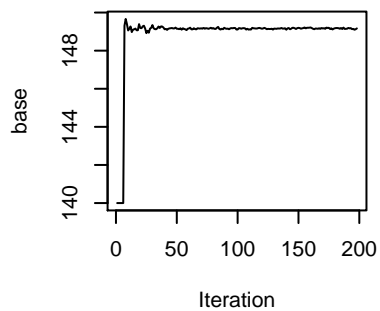
```
##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
##   Model function:  Linear model   Model type:  structural
## function(psi,id,xidep) {
##   x<-xidep[,1]
##   base<-psi[id,1]
##   slope<-psi[id,2]
##   f<-base+slope*x
##   return(f)
## }
##   Nb of parameters: 2
##       parameter names:  base slope
##       distribution:
##       Parameter Distribution Estimated
## [1,] base      log-normal   Estimated
## [2,] slope     normal      Estimated
```

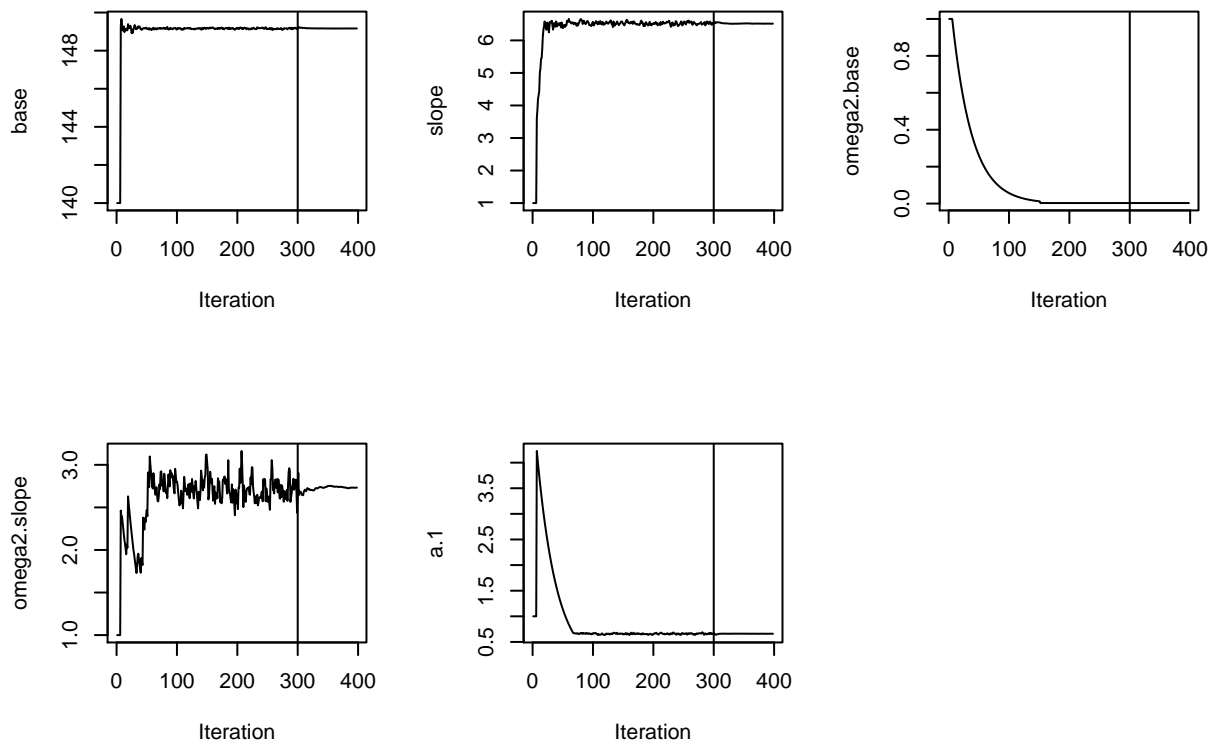
```
## Variance-covariance matrix:
## base slope
## base 1 1
## slope 1 1
## Error model: constant , initial values: a.1=1
## No covariate in the model.
## Initial values
## base slope
## Pop.CondInit 140 1

saemix.options<-list(algorithms=c(1,1,1),nb.chains=1,seed=201004,
  save=FALSE,save.graphs=FALSE)
saemix.fit<-saemix(saemix.model,saemix.data,saemix.options)
```

The number of subjects is small, increasing the number of chains to 2 to improve convergence







```
## Nonlinear mixed-effects model fit by the SAEM algorithm
```

```
## -----
```

```
## ---- Data ----
```

```
## -----
```

```
## Object of class SaemixData
```

```
## longitudinal data for use with the SAEM algorithm
```

```
## Dataset oxboys.saemix
```

```
## Structured data: height ~ age | Subject
```

```
## Predictor: age (yr)
```

```
## Dataset characteristics:
```

```
## number of subjects: 26
```

```
## number of observations: 234
```

```
## average/min/max nb obs: 9.00 / 9 / 9
```

```
## First 10 lines of data:
```

```
## Subject age height mdv cens occ ytype
## 1 1 -1.0000 140.5 0 0 1 1
## 2 1 -0.7479 143.4 0 0 1 1
## 3 1 -0.4630 144.8 0 0 1 1
## 4 1 -0.1643 147.1 0 0 1 1
## 5 1 -0.0027 147.7 0 0 1 1
## 6 1 0.2466 150.2 0 0 1 1
## 7 1 0.5562 151.7 0 0 1 1
## 8 1 0.7781 153.3 0 0 1 1
## 9 1 0.9945 155.8 0 0 1 1
## 10 2 -1.0000 136.9 0 0 1 1
```

```
## -----
```

```
## ---- Model ----
```

```
## -----
```

```
## Nonlinear mixed-effects model
```

```
## Model function: Linear model Model type: structural
```

```

## function(psi,id,xidep) {
##   x<-xidep[,1]
##   base<-psi[id,1]
##   slope<-psi[id,2]
##   f<-base+slope*x
##   return(f)
## }
## <bytecode: 0x564edb2fc9a8>
##   Nb of parameters: 2
##     parameter names:  base slope
##     distribution:
##     Parameter Distribution Estimated
## [1,] base      log-normal  Estimated
## [2,] slope     normal      Estimated
##   Variance-covariance matrix:
##     base slope
## base      1      1
## slope     1      1
##   Error model: constant , initial values: a.1=1
##   No covariate in the model.
##   Initial values
##           base slope
## Pop.CondInit  140      1
## -----
## ----   Key algorithm options   ----
## -----
##   Estimation of individual parameters (MAP)
##   Estimation of standard errors and linearised log-likelihood
##   Estimation of log-likelihood by importance sampling
##   Number of iterations:  K1=300, K2=100
##   Number of chains:  2
##   Seed:  201004
##   Number of MCMC iterations for IS:  5000
##   Simulations:
##     nb of simulated datasets used for npde:  1000
##     nb of simulated datasets used for VPC:  100
##   Input/output
##     save the results to a file:  FALSE
##     save the graphs to files:  FALSE
## -----
## ----                               Results                               ----
## -----
## ----- Fixed effects -----
## -----
##   Parameter Estimate SE      CV(%)
## [1,] base      149.16  1.563 1.0
## [2,] slope      6.51  0.331 5.1
## [3,] a.1        0.66  0.035 5.2
## -----
## ----- Variance of random effects -----
## -----
##   Parameter      Estimate SE      CV(%)
## base omega2.base  0.0029  0.00079 28
## slope omega2.slope 2.7361  0.79109 29

```



```
## covar cov.base.slope 0.0564    0.02087 37
## -----
## ----- Correlation matrix of random effects -----
## -----
##              omega2.base omega2.slope
## omega2.base  1.00          0.64
## omega2.slope 0.64          1.00
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
##      -2LL= 726.5422
##      AIC = 738.5422
##      BIC = 746.0908
##
## Likelihood computed by importance sampling
##      -2LL= 726.5619
##      AIC = 738.5619
##      BIC = 746.1105
## -----
```

Cow

```
if(testMode)
  data(cow.saemix) else
  cow.saemix<-read.table(file.path(datDir, "cow.saemix.tab"), header=TRUE)

saemix.data<-saemixData(name.data=cow.saemix,header=TRUE,name.group=c("cow"),
  name.predictors=c("time"),name.response=c("weight"),
  name.covariates=c("birthyear","twin","birthrank"),
  units=list(x="days",y="kg",covariates=c("yr","-","-")))

## [1] "birthyear" "twin"      "birthrank"
##
##
## The following SaemixData object was successfully created:
##
## Object of class SaemixData
##      longitudinal data for use with the SAEM algorithm
## Dataset cow.saemix
##      Structured data: weight ~ time | cow
##      Predictor: time (days)
##      covariates: birthyear (yr), twin (-), birthrank (-)
##      reference class for covariate twin : 1

growthcow<-function(psi,id,xidep) {
  x<-xidep[,1]
  a<-psi[id,1]
  b<-psi[id,2]
  k<-psi[id,3]
  f<-a*(1-b*exp(-k*x))
  return(f)
}
```

```

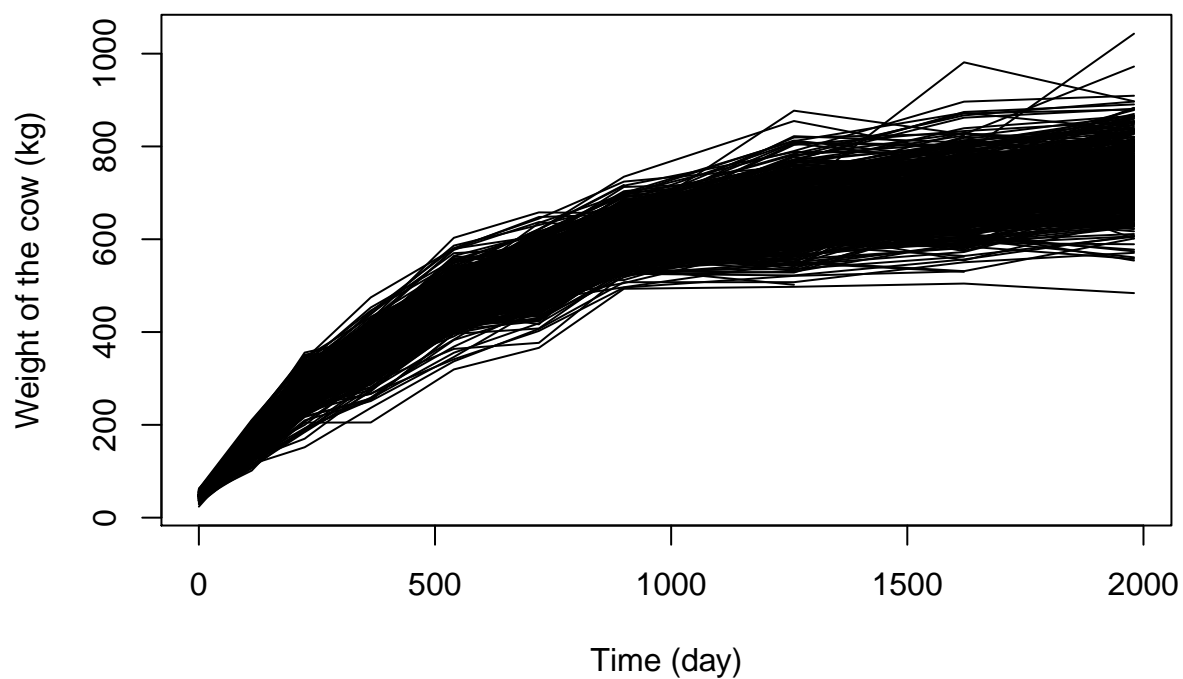
saemix.model<-saemixModel(model=growthcow,
  description="Exponential growth model",
  psi0=matrix(c(700,0.9,0.02,0,0,0),ncol=3,byrow=TRUE,
    dimnames=list(NULL,c("A","B","k"))),transform.par=c(1,1,1),fixed.estim=c(1,1,1),
  covariate.model=matrix(c(0,0,0),ncol=3,byrow=TRUE),
  covariance.model=matrix(c(1,0,0,0,1,0,0,0,1),ncol=3,byrow=TRUE),
  omega.init=matrix(c(1,0,0,0,1,0,0,0,1),ncol=3,byrow=TRUE),error.model="constant")

##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
## Model function: Exponential growth model Model type: structural
## function(psi,id,xidep) {
##   x<-xidep[,1]
##   a<-psi[id,1]
##   b<-psi[id,2]
##   k<-psi[id,3]
##   f<-a*(1-b*exp(-k*x))
##   return(f)
## }
## Nb of parameters: 3
## parameter names: A B k
## distribution:
## Parameter Distribution Estimated
## [1,] A log-normal Estimated
## [2,] B log-normal Estimated
## [3,] k log-normal Estimated
## Variance-covariance matrix:
## A B k
## A 1 0 0
## B 0 1 0
## k 0 0 1
## Error model: constant , initial values: a.1=1
## No covariate in the model.
## Initial values
## A B k
## Pop.CondInit 700 0.9 0.02
## Cov.CondInit 0 0.0 0.00

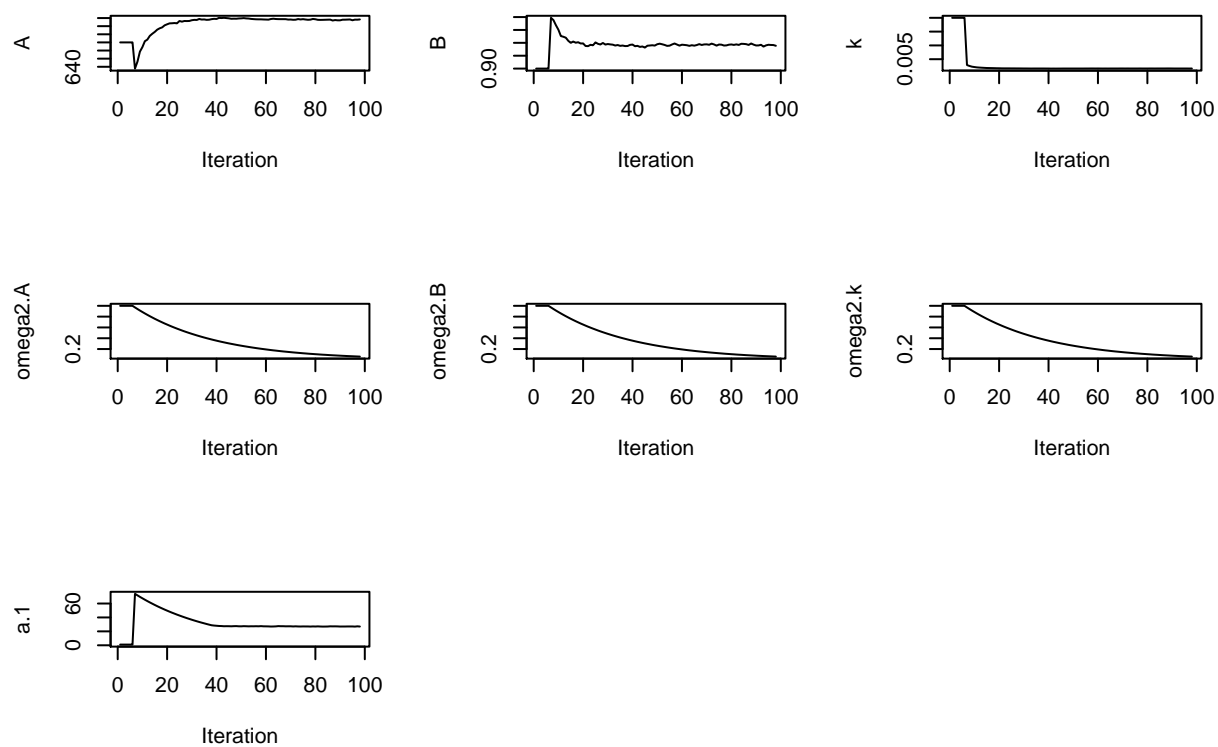
saemix.options<-list(algorithms=c(1,1,1),nb.chains=1,nbiter.saemix=c(200,100),
  seed=4526,save=FALSE,save.graphs=FALSE)

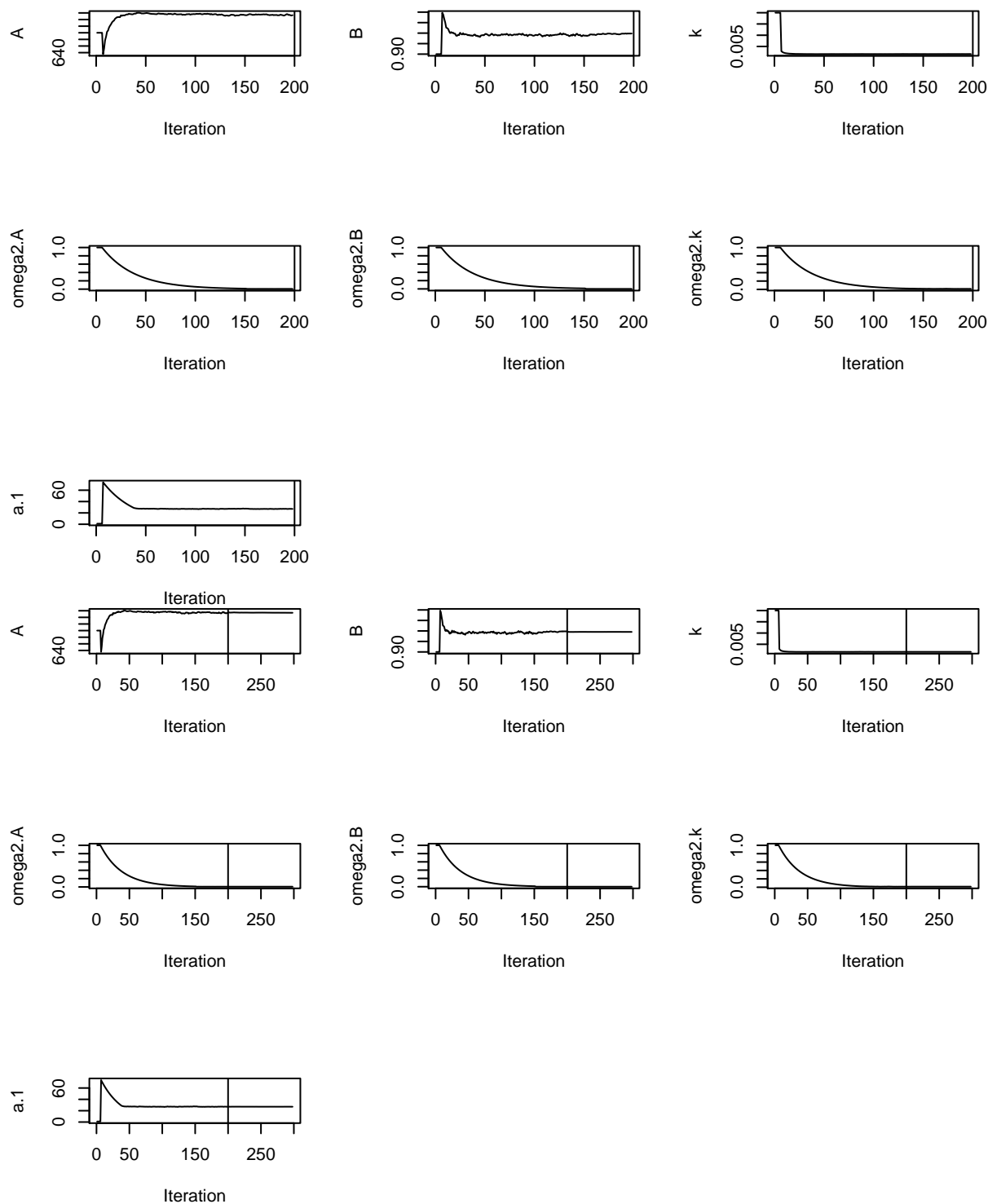
# Plotting the data
plot(saemix.data,xlab="Time (day)",ylab="Weight of the cow (kg)")

```



```
saemix.fit<-saemix(saemix.model,saemix.data,saemix.options)
```





```
## Nonlinear mixed-effects model fit by the SAEM algorithm
## -----
## ---- Data ----
## -----
## Object of class SaemixData
## longitudinal data for use with the SAEM algorithm
## Dataset cow.saemix
```

```

##      Structured data: weight ~ time | cow
##      Predictor: time (days)
##      covariates: birthyear (yr), twin (-), birthrank (-)
##      reference class for covariate twin : 1
## Dataset characteristics:
##      number of subjects:      560
##      number of observations: 5455
##      average/min/max nb obs: 9.74 / 7 / 10
## First 10 lines of data:
##      cow time weight birthyear twin birthrank mdv cens occ ytype
## 1 1988005 0 44.0 1988 1 3 0 0 1 1
## 2 1988005 112 173.4 1988 1 3 0 0 1 1
## 3 1988005 224 292.8 1988 1 3 0 0 1 1
## 4 1988005 364 364.6 1988 1 3 0 0 1 1
## 5 1988005 540 490.4 1988 1 3 0 0 1 1
## 6 1988005 720 522.0 1988 1 3 0 0 1 1
## 7 1988005 900 601.1 1988 1 3 0 0 1 1
## 8 1988005 1260 698.1 1988 1 3 0 0 1 1
## 9 1988005 1620 657.7 1988 1 3 0 0 1 1
## 10 1988005 1980 776.7 1988 1 3 0 0 1 1
## -----
## ----          Model          ----
## -----
## Nonlinear mixed-effects model
## Model function: Exponential growth model Model type: structural
## function(psi,id,xidep) {
##   x<-xidep[,1]
##   a<-psi[id,1]
##   b<-psi[id,2]
##   k<-psi[id,3]
##   f<-a*(1-b*exp(-k*x))
##   return(f)
## }
## <bytecode: 0x564eda496fb8>
## Nb of parameters: 3
## parameter names: A B k
## distribution:
## Parameter Distribution Estimated
## [1,] A log-normal Estimated
## [2,] B log-normal Estimated
## [3,] k log-normal Estimated
## Variance-covariance matrix:
## A B k
## A 1 0 0
## B 0 1 0
## k 0 0 1
## Error model: constant , initial values: a.1=1
## No covariate in the model.
## Initial values
## A B k
## Pop.CondInit 700 0.9 0.02
## -----
## ---- Key algorithm options ----
## -----

```

```

## Estimation of individual parameters (MAP)
## Estimation of standard errors and linearised log-likelihood
## Estimation of log-likelihood by importance sampling
## Number of iterations: K1=200, K2=100
## Number of chains: 1
## Seed: 4526
## Number of MCMC iterations for IS: 5000
## Simulations:
##     nb of simulated datasets used for npde: 1000
##     nb of simulated datasets used for VPC: 100
## Input/output
##     save the results to a file: FALSE
##     save the graphs to files: FALSE
## -----
## ----- Results -----
## -----
## ----- Fixed effects -----
## -----
## Parameter Estimate SE      CV(%)
## [1,] A          7.5e+02 2.9e+00 0.38
## [2,] B          9.4e-01 1.2e-03 0.13
## [3,] k          1.6e-03 1.2e-05 0.72
## [4,] a.1        2.7e+01 3.0e-01 1.11
## -----
## ----- Variance of random effects -----
## -----
## Parameter Estimate SE      CV(%)
## A omega2.A 6.4e-03 4.4e-04 7.0
## B omega2.B 4.7e-05 5.2e-05 110.6
## k omega2.k 1.4e-02 1.4e-03 9.8
## -----
## ----- Correlation matrix of random effects -----
## -----
## omega2.A omega2.B omega2.k
## omega2.A 1      0      0
## omega2.B 0      1      0
## omega2.k 0      0      1
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
##     -2LL= 53706.64
##     AIC = 53720.64
##     BIC = 53750.93
##
## Likelihood computed by importance sampling
##     -2LL= 53731.51
##     AIC = 53745.51
##     BIC = 53775.8
## -----

```

Wheat yield

```
if(testMode)
  data(yield.saemix) else
    yield.saemix<-read.table(file.path(datDir, "yield.saemix.tab"), header=TRUE)
saemix.data<-saemixData(name.data=yield.saemix,header=TRUE,name.group=c("site"),
  name.predictors=c("dose"),name.response=c("yield"),
  name.covariates=c("soil.nitrogen"),units=list(x="kg/ha",y="t/ha",covariates=c("kg/ha")))

## [1] "soil.nitrogen"
##
##
## The following SaemixData object was successfully created:
##
## Object of class SaemixData
##   longitudinal data for use with the SAEM algorithm
## Dataset yield.saemix
##   Structured data: yield ~ dose | site
##   Predictor: dose (kg/ha)
##   covariates: soil.nitrogen (kg/ha)

# Model: linear + plateau
yield.LP<-function(psi,id,xidep) {
  x<-xidep[,1]
  ymax<-psi[id,1]
  xmax<-psi[id,2]
  slope<-psi[id,3]
  f<-ymax+slope*(x-xmax)
  #' cat(length(f)," ",length(ymax),"\\n")
  f[x>xmax]<-ymax[x>xmax]
  return(f)
}

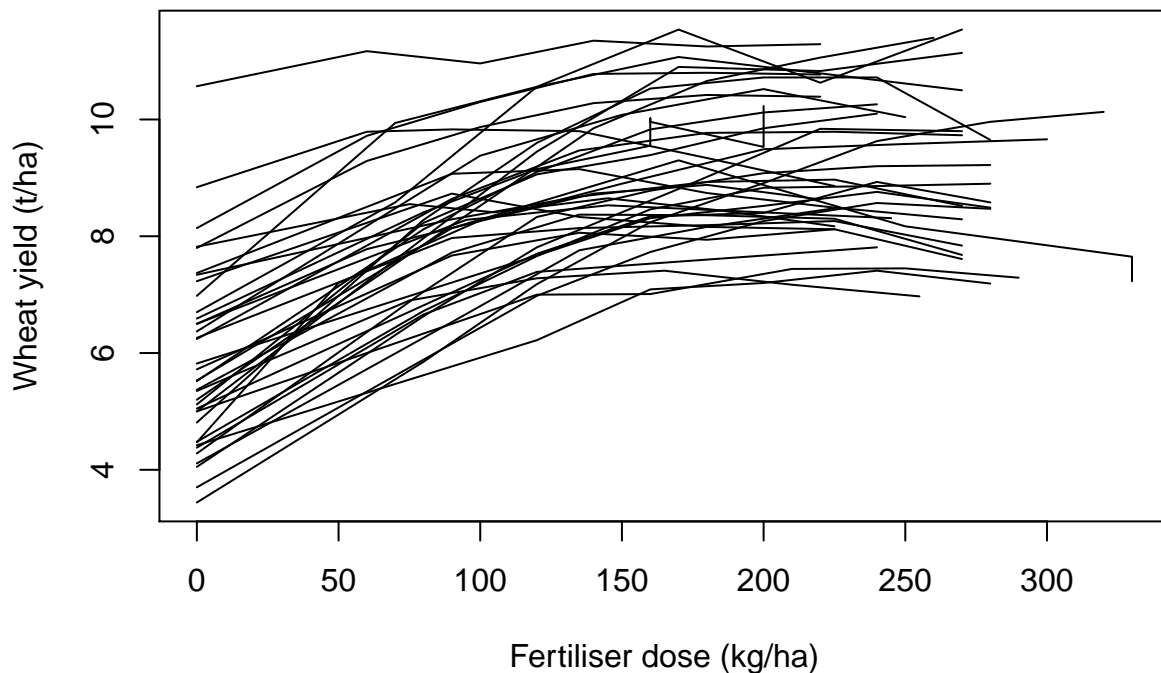
saemix.model<-saemixModel(model=yield.LP,description="Linear plus plateau model",
  psi0=matrix(c(8,100,0.2,0,0,0),ncol=3,byrow=TRUE,dimnames=list(NULL,
    c("Ymax","Xmax","slope"))),covariate.model=matrix(c(0,0,0),ncol=3,byrow=TRUE),
  transform.par=c(0,0,0),covariance.model=matrix(c(1,0,0,0,1,0,0,0,1),ncol=3,
    byrow=TRUE),error.model="constant")

##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
##   Model function: Linear plus plateau model   Model type: structural
## function(psi,id,xidep) {
##   x<-xidep[,1]
##   ymax<-psi[id,1]
##   xmax<-psi[id,2]
##   slope<-psi[id,3]
##   f<-ymax+slope*(x-xmax)
##   #' cat(length(f)," ",length(ymax),"\\n")
##   f[x>xmax]<-ymax[x>xmax]
##   return(f)
## }
```

```
## Nb of parameters: 3
##   parameter names: Ymax Xmax slope
##   distribution:
##   Parameter Distribution Estimated
## [1,] Ymax      normal      Estimated
## [2,] Xmax      normal      Estimated
## [3,] slope     normal      Estimated
## Variance-covariance matrix:
##      Ymax Xmax slope
## Ymax   1    0    0
## Xmax   0    1    0
## slope  0    0    1
## Error model: constant , initial values: a.1=1
## No covariate in the model.
## Initial values
##      Ymax Xmax slope
## Pop.CondInit   8 100 0.2
## Cov.CondInit   0  0 0.0

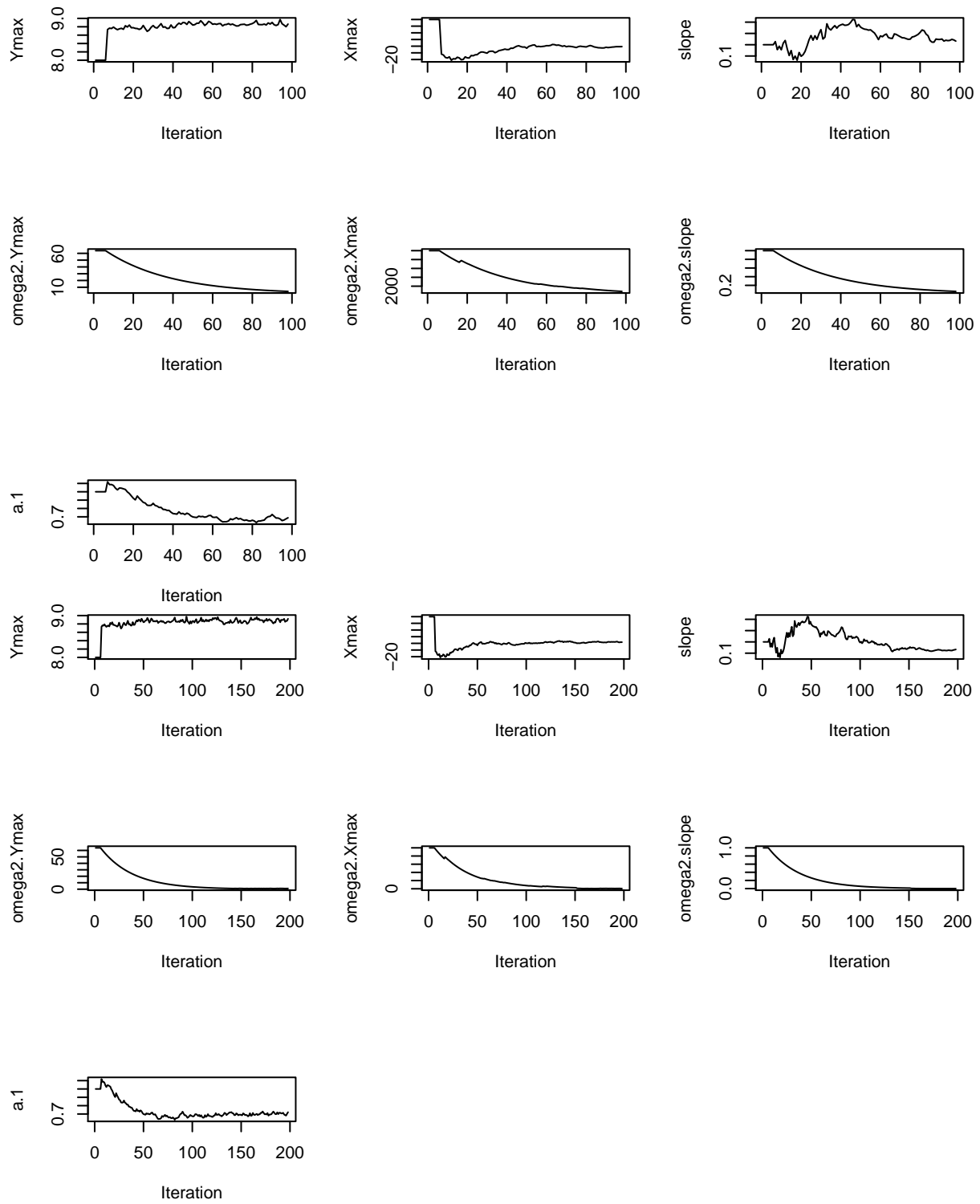
saemix.options<-list(algorithms=c(1,1,1),nb.chains=1,seed=666,
  save=FALSE,save.graphs=FALSE)

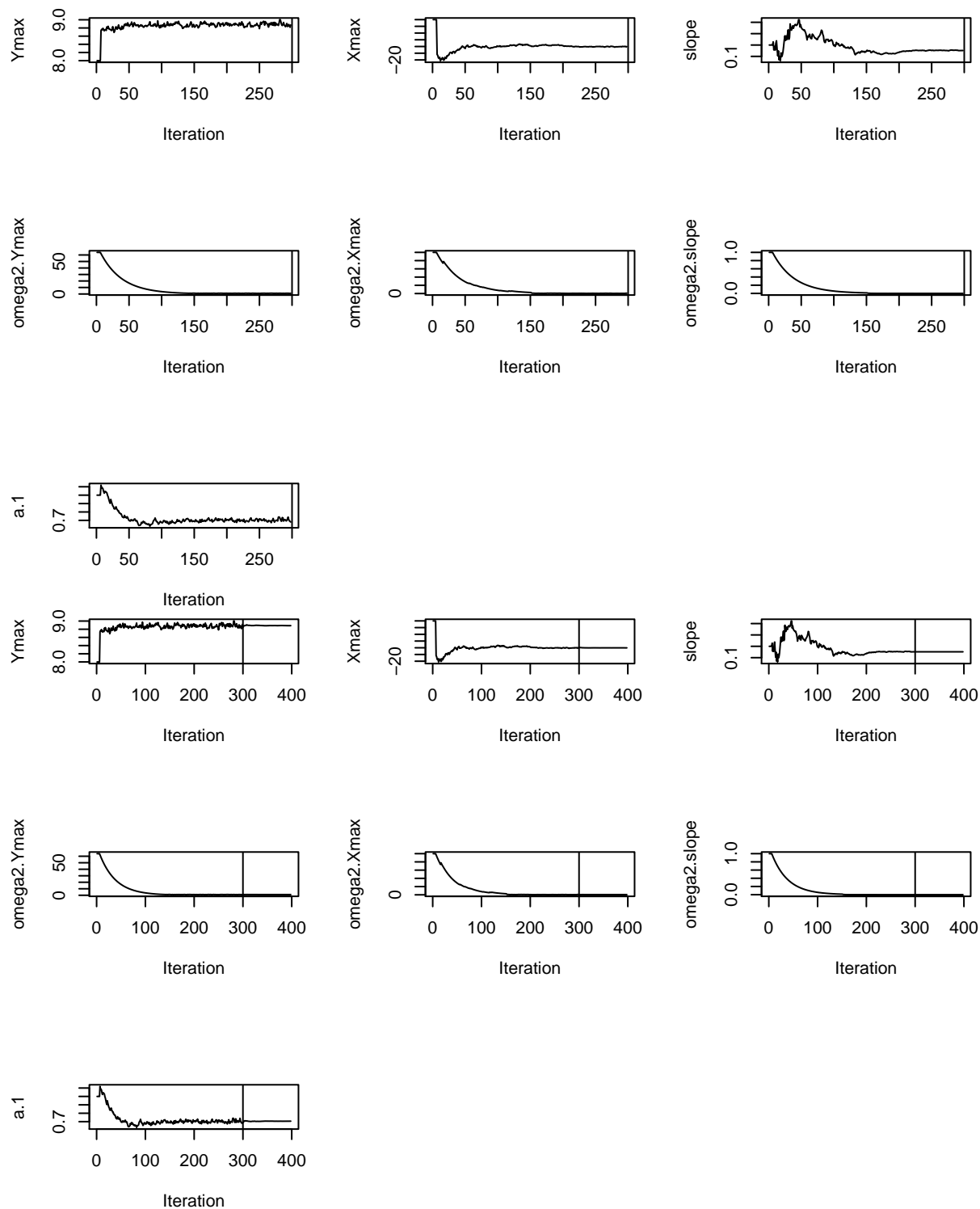
# Plotting the data
plot(saemix.data,xlab="Fertiliser dose (kg/ha)", ylab="Wheat yield (t/ha)")
```



```
saemix.fit<-saemix(saemix.model,saemix.data,saemix.options)
```

```
## The number of subjects is small, increasing the number of chains to 2 to improve convergence
```



```
## Nonlinear mixed-effects model fit by the SAEM algorithm
## -----
##      Data
## -----
## Object of class SaemixData
##      longitudinal data for use with the SAEM algorithm
## Dataset yield.saemix
```

```

##      Structured data: yield ~ dose | site
##      Predictor: dose (kg/ha)
##      covariates: soil.nitrogen (kg/ha)
## Dataset characteristics:
##      number of subjects:      37
##      number of observations: 224
##      average/min/max nb obs: 6.05 / 5 / 8
## First 10 lines of data:
##      site dose yield soil.nitrogen mdv cens occ ytype
## 1  1901    0  6.70          70    0    0    1    1
## 2  1901   70  8.58          70    0    0    1    1
## 3  1901  120 10.56          70    0    0    1    1
## 4  1901  170 11.54          70    0    0    1    1
## 5  1901  220 10.63          70    0    0    1    1
## 6  1901  270 11.54          70    0    0    1    1
## 7  1902    0  6.98          80    0    0    1    1
## 8  1902   70  9.94          80    0    0    1    1
## 9  1902  120 10.56          80    0    0    1    1
## 10 1902  170 11.07          80    0    0    1    1
## -----
## ----          Model          ----
## -----
## Nonlinear mixed-effects model
##      Model function: Linear plus plateau model  Model type: structural
## function(psi,id,xidep) {
##   x<-xidep[,1]
##   ymax<-psi[id,1]
##   xmax<-psi[id,2]
##   slope<-psi[id,3]
##   f<-ymax+slope*(x-xmax)
##   #' cat(length(f)," ",length(ymax),"\\n")
##   f[x>xmax]<-ymax[x>xmax]
##   return(f)
## }
## <bytecode: 0x564ed7e8b568>
##      Nb of parameters: 3
##      parameter names: Ymax Xmax slope
##      distribution:
##      Parameter Distribution Estimated
## [1,] Ymax      normal      Estimated
## [2,] Xmax      normal      Estimated
## [3,] slope     normal      Estimated
##      Variance-covariance matrix:
##      Ymax Xmax slope
## Ymax    1    0    0
## Xmax    0    1    0
## slope   0    0    1
##      Error model: constant , initial values: a.1=1
##      No covariate in the model.
##      Initial values
##      Ymax Xmax slope
## Pop.CondInit    8 100 0.2
## -----
## ----      Key algorithm options      ----

```

```

## -----
## Estimation of individual parameters (MAP)
## Estimation of standard errors and linearised log-likelihood
## Estimation of log-likelihood by importance sampling
## Number of iterations: K1=300, K2=100
## Number of chains: 2
## Seed: 666
## Number of MCMC iterations for IS: 5000
## Simulations:
##     nb of simulated datasets used for npde: 1000
##     nb of simulated datasets used for VPC: 100
## Input/output
##     save the results to a file: FALSE
##     save the graphs to files: FALSE
## -----
## ----- Results -----
## -----
## ----- Fixed effects -----
## -----
## Parameter Estimate SE CV(%)
## [1,] Ymax      8.89  0.176 2.0
## [2,] Xmax     19.75  5.089 25.8
## [3,] slope      0.15  0.037 24.7
## [4,] a.1        0.71  0.041 5.8
## -----
## ----- Variance of random effects -----
## -----
## Parameter Estimate SE CV(%)
## Ymax omega2.Ymax 1.0e+00 0.2659 25
## Xmax omega2.Xmax 5.3e+01 38.0311 72
## slope omega2.slope 9.2e-06 0.0018 19486
## -----
## ----- Correlation matrix of random effects -----
## -----
## omega2.Ymax omega2.Xmax omega2.slope
## omega2.Ymax 1 0 0
## omega2.Xmax 0 1 0
## omega2.slope 0 0 1
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
## -2LL= 616.5701
## AIC = 630.5701
## BIC = 641.8466
##
## Likelihood computed by importance sampling
## -2LL= 616.5048
## AIC = 630.5048
## BIC = 641.7812
## -----
# Comparing the likelihoods obtained by linearisation and importance sampling
# to the likelihood obtained by Gaussian Quadrature

```

```

saemix.fit<-llgq.saemix(saemix.fit)
{
  cat("LL by Importance sampling, LL_IS=",saemix.fit["results"]["ll.is"],"\n")
  cat("LL by linearisation, LL_lin=",saemix.fit["results"]["ll.lin"],"\n")
  cat("LL by Gaussian Quadrature, LL_GQ=",saemix.fit["results"]["ll.gq"],"\n")
}

## LL by Importance sampling, LL_IS= -308.2524
## LL by linearisation, LL_lin= -308.2851
## LL by Gaussian Quadrature, LL_GQ= -308.2772

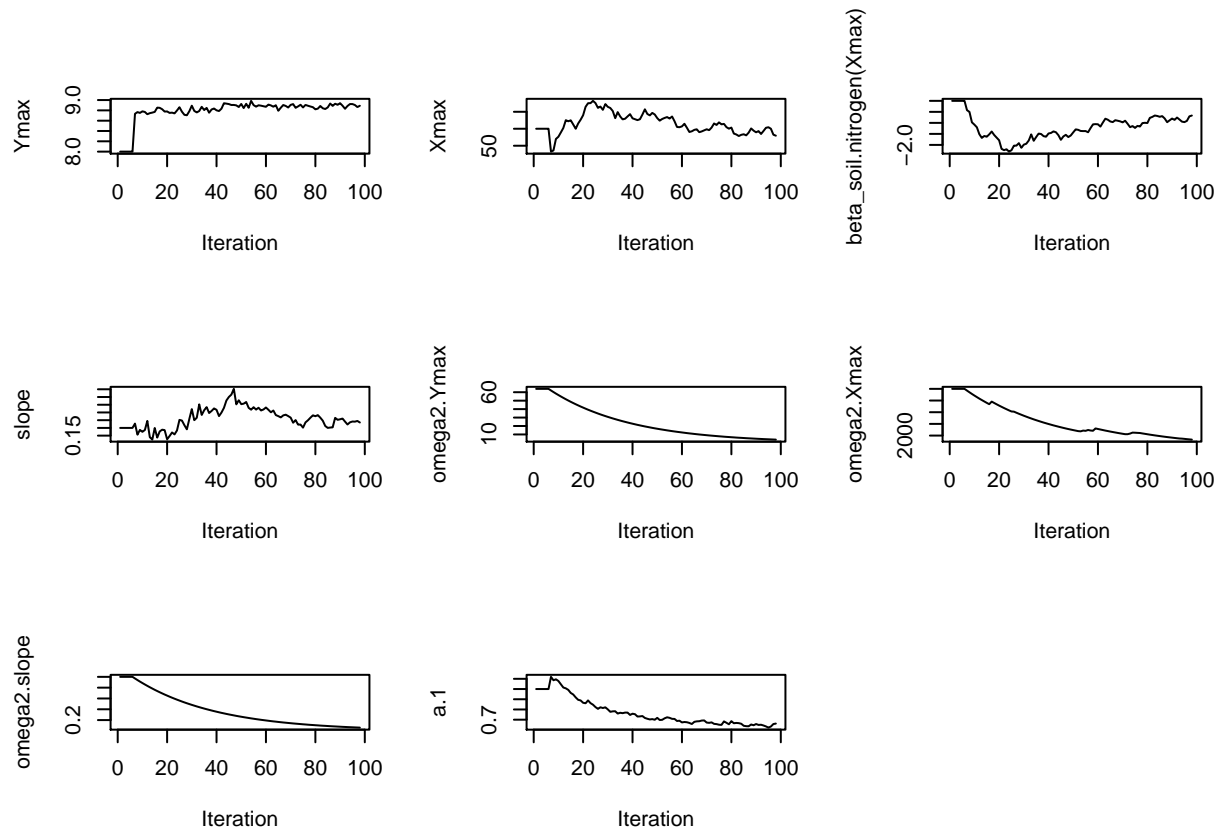
# Testing for an effect of covariate soil.nitrogen on Xmax
saemix.model2<-saemixModel(model=yield.LP,description="Linear plus plateau model",
  psi0=matrix(c(8,100,0.2,0,0,0),ncol=3,byrow=TRUE,dimnames=list(NULL,
    c("Ymax","Xmax","slope"))),covariate.model=matrix(c(0,1,0),ncol=3,byrow=TRUE),
  transform.par=c(0,0,0),covariance.model=matrix(c(1,0,0,0,1,0,0,0,1),ncol=3,
    byrow=TRUE),error.model="constant")

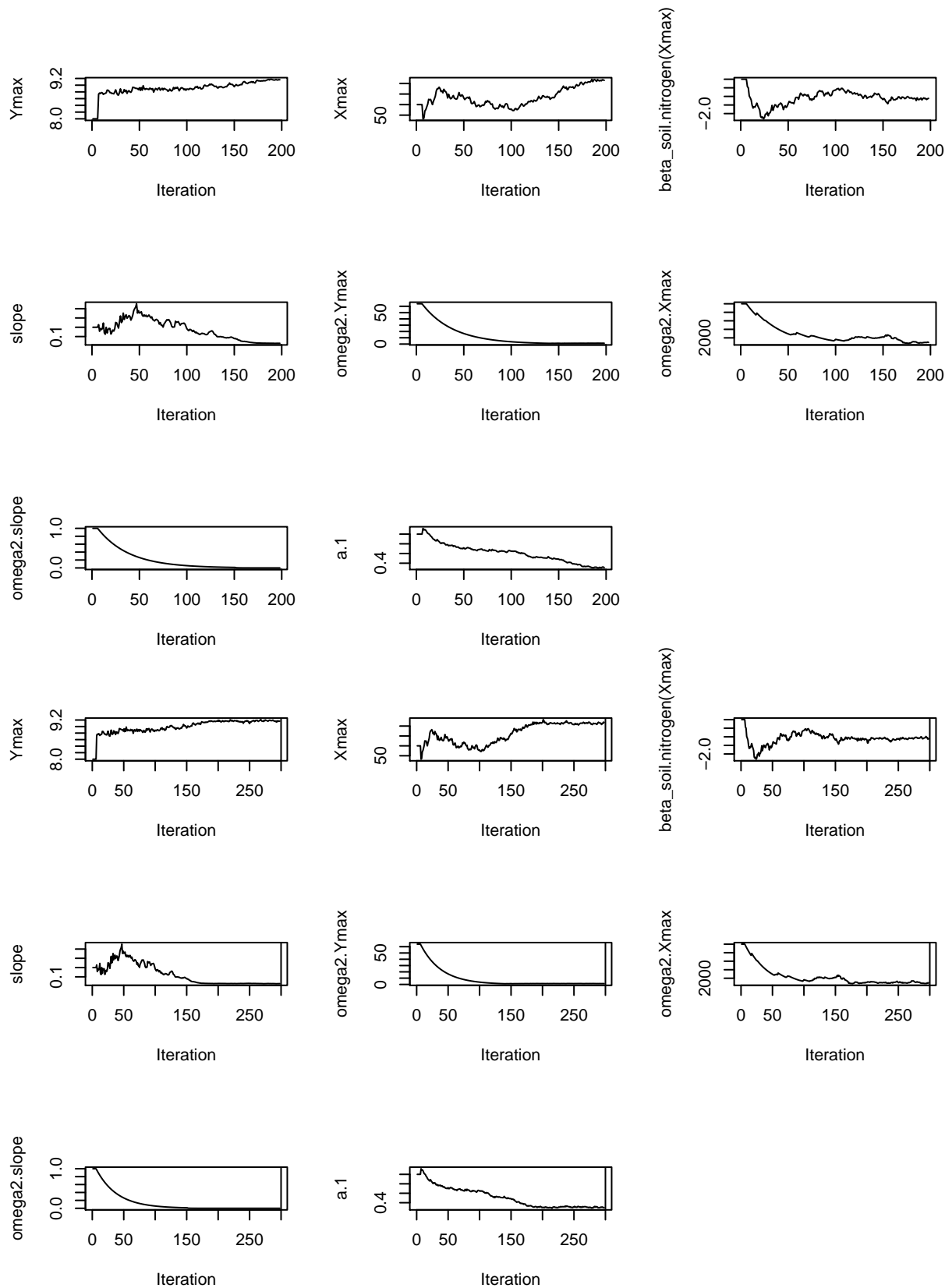
##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
## Model function: Linear plus plateau model Model type: structural
## function(psi,id,xidep) {
##   x<-xidep[,1]
##   ymax<-psi[id,1]
##   xmax<-psi[id,2]
##   slope<-psi[id,3]
##   f<-ymax+slope*(x-xmax)
##   #' cat(length(f)," ",length(ymax),"\n")
##   f[x>xmax]<-ymax[x>xmax]
##   return(f)
## }
## <bytecode: 0x564ed7e8b568>
## Nb of parameters: 3
## parameter names: Ymax Xmax slope
## distribution:
## Parameter Distribution Estimated
## [1,] Ymax normal Estimated
## [2,] Xmax normal Estimated
## [3,] slope normal Estimated
## Variance-covariance matrix:
## Ymax Xmax slope
## Ymax 1 0 0
## Xmax 0 1 0
## slope 0 0 1
## Error model: constant , initial values: a.1=1
## Covariate model:
## Ymax Xmax slope
## [1,] 0 1 0
## Initial values
## Ymax Xmax slope
## Pop.CondInit 8 100 0.2
## Cov.CondInit 0 0 0.0

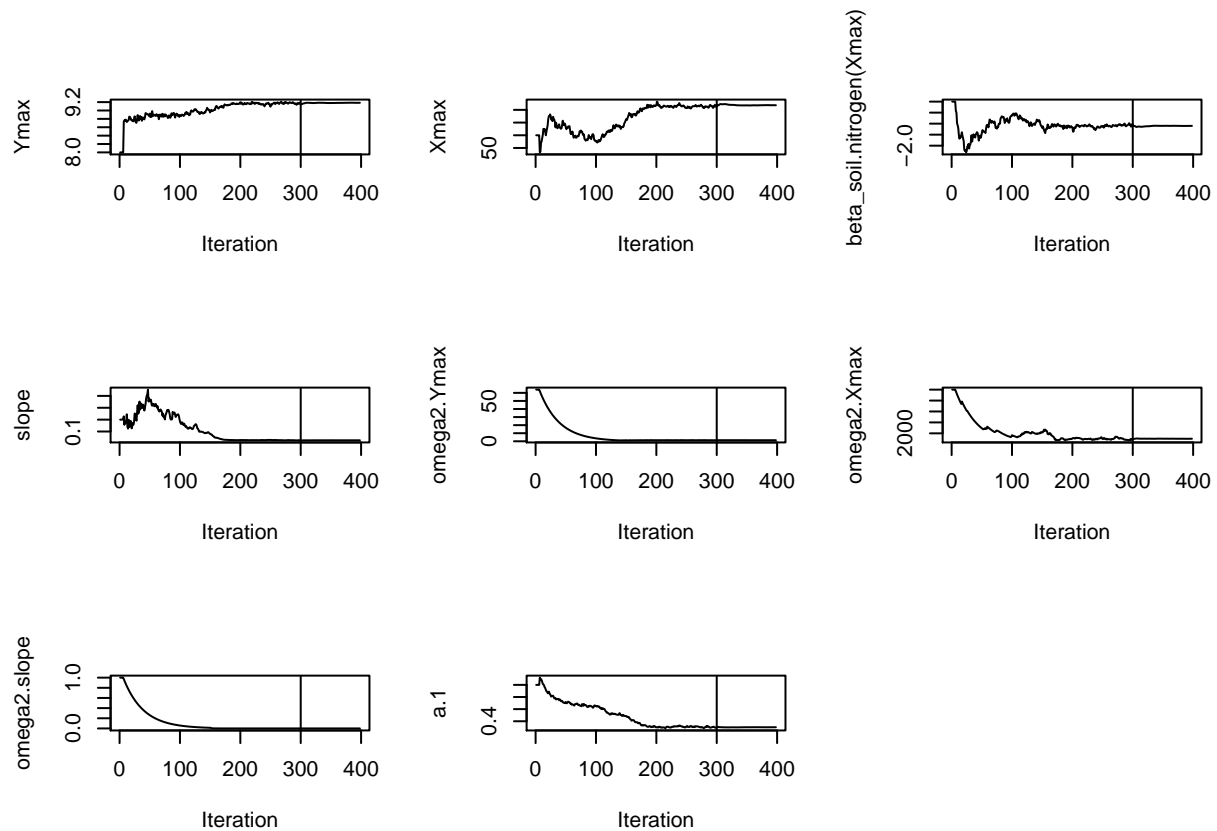
```

```
saemix.fit2<-saemix(saemix.model2,saemix.data,saemix.options)
```

```
## The number of subjects is small, increasing the number of chains to 2 to improve convergence
```







```
## Nonlinear mixed-effects model fit by the SAEM algorithm
```

```
## -----
## ----          Data          ----
## -----
```

```
## Object of class SaemixData
```

```
##   longitudinal data for use with the SAEM algorithm
```

```
## Dataset yield.saemix
```

```
##   Structured data: yield ~ dose | site
```

```
##   Predictor: dose (kg/ha)
```

```
##   covariates: soil.nitrogen (kg/ha)
```

```
## Dataset characteristics:
```

```
##   number of subjects:    37
```

```
##   number of observations: 224
```

```
##   average/min/max nb obs: 6.05 / 5 / 8
```

```
## First 10 lines of data:
```

```
##   site dose yield soil.nitrogen mdv cens occ ytype
## 1  1901   0  6.70           70  0   0   1   1
## 2  1901  70  8.58           70  0   0   1   1
## 3  1901 120 10.56           70  0   0   1   1
## 4  1901 170 11.54           70  0   0   1   1
## 5  1901 220 10.63           70  0   0   1   1
## 6  1901 270 11.54           70  0   0   1   1
## 7  1902   0  6.98           80  0   0   1   1
## 8  1902  70  9.94           80  0   0   1   1
## 9  1902 120 10.56           80  0   0   1   1
## 10 1902 170 11.07           80  0   0   1   1
```

```
## -----
## ----          Model          ----
```



```

## -----
## Nonlinear mixed-effects model
## Model function: Linear plus plateau model Model type: structural
## function(psi,id,xidep) {
##   x<-xidep[,1]
##   ymax<-psi[id,1]
##   xmax<-psi[id,2]
##   slope<-psi[id,3]
##   f<-ymax+slope*(x-xmax)
##   #' cat(length(f)," ",length(ymax),"\\n")
##   f[x>xmax]<-ymax[x>xmax]
##   return(f)
## }
## <bytecode: 0x564ed7e8b568>
## Nb of parameters: 3
##   parameter names: Ymax Xmax slope
##   distribution:
##   Parameter Distribution Estimated
## [1,] Ymax      normal      Estimated
## [2,] Xmax      normal      Estimated
## [3,] slope     normal      Estimated
## Variance-covariance matrix:
##   Ymax Xmax slope
## Ymax    1    0    0
## Xmax    0    1    0
## slope   0    0    1
## Error model: constant , initial values: a.1=1
## Covariate model:
##           [,1] [,2] [,3]
## soil.nitrogen  0   1   0
## Initial values
##           Ymax Xmax slope
## Pop.CondInit   8 100  0.2
## Cov.CondInit   0   0  0.0
## -----
## ---- Key algorithm options ----
## -----
## Estimation of individual parameters (MAP)
## Estimation of standard errors and linearised log-likelihood
## Estimation of log-likelihood by importance sampling
## Number of iterations: K1=300, K2=100
## Number of chains: 2
## Seed: 666
## Number of MCMC iterations for IS: 5000
## Simulations:
##   nb of simulated datasets used for npde: 1000
##   nb of simulated datasets used for VPC: 100
## Input/output
##   save the results to a file: FALSE
##   save the graphs to files: FALSE
## -----
## ---- Results ----
## -----
## ----- Fixed effects -----

```

```
## -----
##      Parameter          Estimate SE      CV(%) p-value
## [1,] Ymax                9.184  0.1919  2.1  -
## [2,] Xmax               218.403 15.7188  7.2  -
## [3,] beta_soil.nitrogen(Xmax) -1.106  0.1715 15.5 5.8e-11
## [4,] slope                0.026  0.0012  4.7  -
## [5,] a.1                  0.302  0.0192  6.4  -
## -----
## ----- Variance of random effects -----
## -----
##      Parameter      Estimate SE      CV(%)
## Ymax  omega2.Ymax  1.3e+00 3.2e-01 24
## Xmax  omega2.Xmax  1.0e+03 2.9e+02 28
## slope omega2.slope 2.9e-05 1.1e-05 38
## -----
## ----- Correlation matrix of random effects -----
## -----
##      omega2.Ymax omega2.Xmax omega2.slope
## omega2.Ymax  1          0          0
## omega2.Xmax  0          1          0
## omega2.slope 0          0          1
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
##      -2LL= 389.099
##      AIC = 405.099
##      BIC = 417.9863
##
## Likelihood computed by importance sampling
##      -2LL= 380.8696
##      AIC = 396.8696
##      BIC = 409.7569
## -----
```

```
# BIC for the two models
{
  cat("Model without covariate, BIC=",saemix.fit["results"]["bic.is"],"\n")
  cat("Model with covariate, BIC=",saemix.fit2["results"]["bic.is"],"\n")
  pval<-1-pchisq(-2*saemix.fit["results"]["ll.is"]+2*saemix.fit2["results"]["ll.is"],1)
  cat("      LRT: p=",pval,"\n")
}
```

```
## Model without covariate, BIC= 641.7812
## Model with covariate, BIC= 409.7569
##      LRT: p= 0
```

Discrete data model

Binary response model

Toenail data

- TODO

– add diagnostics (npd-categorical ?)

```
if(testMode)
  data(toenail.saemix) else
    toenail.saemix<-read.table(file.path(datDir, "toenail.saemix.tab"), header=TRUE)

saemix.data<-saemixData(name.data=toenail.saemix,name.group=c("id"),name.predictors=c("time","y"), name
                        name.covariates=c("treatment"),name.X=c("time"))

## [1] "treatment"
##
##
## The following SaemixData object was successfully created:
##
## Object of class SaemixData
##   longitudinal data for use with the SAEM algorithm
## Dataset toenail.saemix
##   Structured data: y ~ time + y | id
##   X variable for graphs: time ()
##   covariates: treatment (-)
##   reference class for covariate treatment : 0

binary.model<-function(psi,id,xidep) {
  tim<-xidep[,1]
  y<-xidep[,2]
  inter<-psi[id,1]
  slope<-psi[id,2]
  logit<-inter+slope*tim
  pevent<-exp(logit)/(1+exp(logit))
  logpdf<-rep(0,length(tim))
  P.obs = (y==0)*(1-pevent)+(y==1)*pevent
  logpdf <- log(P.obs)
  return(logpdf)
}

saemix.model<-saemixModel(model=binary.model,description="Binary model",
                          modeltype="likelihood",
                          psi0=matrix(c(0,-.5,0,0.5),ncol=2,byrow=TRUE,dimnames=list(NULL,c("theta1","treatment"),
                          transform.par=c(0,0), covariate.model=c(0,1),covariance.model=matrix(c(1,0,0,1),ncol=2,byrow=TRUE)))

##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
##   Model function: Binary model   Model type: likelihood
## function(psi,id,xidep) {
##   tim<-xidep[,1]
##   y<-xidep[,2]
##   inter<-psi[id,1]
##   slope<-psi[id,2]
##   logit<-inter+slope*tim
##   pevent<-exp(logit)/(1+exp(logit))
##   logpdf<-rep(0,length(tim))
##   P.obs = (y==0)*(1-pevent)+(y==1)*pevent
```

```

## logpdf <- log(P.obs)
## return(logpdf)
## }
## Nb of parameters: 2
##     parameter names:  theta1 theta2
##     distribution:
##     Parameter Distribution Estimated
## [1,] theta1    normal      Estimated
## [2,] theta2    normal      Estimated
## Variance-covariance matrix:
##     theta1 theta2
## theta1     1     0
## theta2     0     1
## Covariate model:
##     theta1 theta2
## [1,]     0     1
## Initial values
##     theta1 theta2
## Pop.CondInit     0   -0.5
## Cov.CondInit     0    0.5

saemix.options<-list(seed=1234567,save=FALSE,save.graphs=FALSE, displayProgress=FALSE, nb.chains=10, fi

binary.fit<-saemix(saemix.model,saemix.data,saemix.options)

## Nonlinear mixed-effects model fit by the SAEM algorithm
## -----
## ----          Data          ----
## -----
## Object of class SaemixData
##     longitudinal data for use with the SAEM algorithm
## Dataset toenail.saemix
##     Structured data: y ~ time + y | id
##     X variable for graphs: time ()
##     covariates: treatment (-)
##     reference class for covariate treatment : 0
## Dataset characteristics:
##     number of subjects:      294
##     number of observations: 1908
##     average/min/max nb obs: 6.49 / 1 / 7
## First 10 lines of data:
##     id      time y y.1 treatment mdv cens occ ytype
## 1  1  0.0000000 1   1         1   0   0   1   1
## 2  1  0.8571429 1   1         1   0   0   1   1
## 3  1  3.5357143 1   1         1   0   0   1   1
## 4  1  4.5357143 0   0         1   0   0   1   1
## 5  1  7.5357143 0   0         1   0   0   1   1
## 6  1 10.0357143 0   0         1   0   0   1   1
## 7  1 13.0714286 0   0         1   0   0   1   1
## 8  2  0.0000000 0   0         0   0   0   1   1
## 9  2  0.9642857 0   0         0   0   0   1   1
## 10 2  2.0000000 1   1         0   0   0   1   1
## -----
## ----          Model          ----
## -----

```

```

## Nonlinear mixed-effects model
## Model function: Binary model Model type: likelihood
## function(psi,id,xidep) {
##   tim<-xidep[,1]
##   y<-xidep[,2]
##   inter<-psi[id,1]
##   slope<-psi[id,2]
##   logit<-inter+slope*tim
##   pevent<-exp(logit)/(1+exp(logit))
##   logpdf<-rep(0,length(tim))
##   P.obs = (y==0)*(1-pevent)+(y==1)*pevent
##   logpdf <- log(P.obs)
##   return(logpdf)
## }
## <bytecode: 0x564eda431678>
## Nb of parameters: 2
##   parameter names: theta1 theta2
##   distribution:
##   Parameter Distribution Estimated
## [1,] theta1    normal      Estimated
## [2,] theta2    normal      Estimated
## Variance-covariance matrix:
##   theta1 theta2
## theta1    1    0
## theta2    0    1
## Covariate model:
##   [,1] [,2]
## treatment  0  1
## Initial values
##   theta1 theta2
## Pop.CondInit    0 -0.5
## Cov.CondInit    0  0.5
## -----
## ---- Key algorithm options ----
## -----
## Estimation of individual parameters (MAP)
## Estimation of log-likelihood by importance sampling
## Number of iterations: K1=300, K2=100
## Number of chains: 10
## Seed: 1234567
## Number of MCMC iterations for IS: 5000
## Simulations:
##   nb of simulated datasets used for npde: 1000
##   nb of simulated datasets used for VPC: 100
## Input/output
##   save the results to a file: FALSE
##   save the graphs to files: FALSE
## -----
## ---- Results ----
## -----
## ----- Fixed effects -----
## -----
## Parameter Estimate
## [1,] theta1 -2.20

```

```
## [2,] theta2 -1.25
## [3,] beta_treatment(theta2) -0.47
## -----
## ----- Variance of random effects -----
## -----
## Parameter Estimate
## theta1 omega2.theta1 59.3
## theta2 omega2.theta2 1.1
## -----
## ----- Correlation matrix of random effects -----
## -----
## omega2.theta1 omega2.theta2
## omega2.theta1 1 0
## omega2.theta2 0 1
## -----
## ----- Statistical criteria -----
## -----
##
## Likelihood computed by importance sampling
## -2LL= 1116.755
## AIC = 1128.755
## BIC = 1150.856
## -----
```

Categorical response model

- Knee pain after 3, 7 and 10 days of treatment compared to baseline (time=0)
 - longitudinal ordinal model with 5 categories
 - similar results to Monolix in terms of parameter estimates
 - SE don't seem so off, but still higher than Monolix (but computed with linearisation anyway)
- Comparing the 3 covariate models - model with Age on alp1 and treatment on beta best

```
if(testMode)
  data(knee.saemix) else
    knee.saemix<-read.table(file.path(datDir, "knee.saemix.tab"), header=TRUE)

saemix.data<-saemixData(name.data=knee.saemix,name.group=c("id"),
                        name.predictors=c("y", "time"), name.X=c("time"),
                        name.covariates = c("Age","Sex","treatment"))

## Column name(s) do(es) not exist in the dataset, please check
## Remove columns 1 ( )
## No valid name given, attempting automatic recognition
## Automatic recognition of columns y successful
## [1] "Age" "Sex" "treatment"
##
##
## The following SaemixData object was successfully created:
##
## Object of class SaemixData
## longitudinal data for use with the SAEM algorithm
## Dataset knee.saemix
## Structured data: y ~ y + time | id
## X variable for graphs: time ()
```

```

##      covariates: Age (-), Sex (-), treatment (-)
##      reference class for covariate Sex : 0
##      reference class for covariate treatment : 0

ordinal.model<-function(psi,id,xidep) {
  y<-xidep[,1]
  time<-xidep[,2]
  alp1<-psi[id,1]
  alp2<-psi[id,2]
  alp3<-psi[id,3]
  alp4<-psi[id,4]
  beta<-psi[id,5]

  logit1<-alp1 + beta*time
  logit2<-logit1+alp2
  logit3<-logit2+alp3
  logit4<-logit3+alp4
  pge1<-exp(logit1)/(1+exp(logit1))
  pge2<-exp(logit2)/(1+exp(logit2))
  pge3<-exp(logit3)/(1+exp(logit3))
  pge4<-exp(logit4)/(1+exp(logit4))
  logpdf<-rep(0,length(y))
  P.obs = (y==1)*pge1+(y==2)*(pge2 - pge1)+(y==3)*(pge3 - pge2)+(y==4)*(pge4 - pge3)+(y==5)*(1 - pge4)
  logpdf <- log(P.obs)

  return(logpdf)
}

covmodel3<-covmodel2<-covmodel1<-matrix(data=0,ncol=5,nrow=3)
covmodel1[1:2,1]<-1
covmodel1[,5]<-1
covmodel2[1,1]<-covmodel2[3,5]<-1
covmodel2<-covmodel1<-matrix(data=0,ncol=5,nrow=3)
covmodel3[1,1]<-1

saemix.model<-saemixModel(model=ordinal.model,description="Ordinal categorical model",modeltype="likelihood",
  psi0=matrix(c(0,0.2, 0.6, 3, 0.2),ncol=5,byrow=TRUE,dimnames=list(NULL,c("alp1","alp2","alp3","alp4","beta")),
  transform.par=c(0,1,1,1,1),omega.init=diag(rep(1,5)), covariance.model = diag(5,1))

##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
## Model function: Ordinal categorical model Model type: likelihood
## function(psi,id,xidep) {
##   y<-xidep[,1]
##   time<-xidep[,2]
##   alp1<-psi[id,1]
##   alp2<-psi[id,2]
##   alp3<-psi[id,3]
##   alp4<-psi[id,4]
##   beta<-psi[id,5]
##
##   logit1<-alp1 + beta*time
##   logit2<-logit1+alp2

```

```

## logit3<-logit2+alp3
## logit4<-logit3+alp4
## pge1<-exp(logit1)/(1+exp(logit1))
## pge2<-exp(logit2)/(1+exp(logit2))
## pge3<-exp(logit3)/(1+exp(logit3))
## pge4<-exp(logit4)/(1+exp(logit4))
## logpdf<-rep(0,length(y))
## P.obs = (y==1)*pge1+(y==2)*(pge2 - pge1)+(y==3)*(pge3 - pge2)+(y==4)*(pge4 - pge3)+(y==5)*(1 - pge4)
## logpdf <- log(P.obs)
##
## return(logpdf)
## }
## Nb of parameters: 5
## parameter names: alp1 alp2 alp3 alp4 beta
## distribution:
## Parameter Distribution Estimated
## [1,] alp1 normal Estimated
## [2,] alp2 log-normal Estimated
## [3,] alp3 log-normal Estimated
## [4,] alp4 log-normal Estimated
## [5,] beta log-normal Estimated
## Variance-covariance matrix:
## alp1 alp2 alp3 alp4 beta
## alp1 1 0 0 0 0
## alp2 0 0 0 0 0
## alp3 0 0 0 0 0
## alp4 0 0 0 0 0
## beta 0 0 0 0 1
## No covariate in the model.
## Initial values
## alp1 alp2 alp3 alp4 beta
## Pop.CondInit 0 0.2 0.6 3 0.2

saemix.model.cov1<-saemixModel(model=ordinal.model,description="Ordinal categorical model",modeltype="1",
                                psi0=matrix(c(0,0.2, 0.6, 3, 0.2),ncol=5,byrow=TRUE,dimnames=list(NULL,c("alp1", "alp2", "alp3", "alp4", "beta")),
                                transform.par=c(0,1,1,1,1),omega.init=diag(rep(1,5)), covariance.model = diag(5),
                                covariate.model = covmodel)

##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
## Model function: Ordinal categorical model Model type: likelihood
## function(psi,id,xidep) {
## y<-xidep[,1]
## time<-xidep[,2]
## alp1<-psi[id,1]
## alp2<-psi[id,2]
## alp3<-psi[id,3]
## alp4<-psi[id,4]
## beta<-psi[id,5]
##
## logit1<-alp1 + beta*time
## logit2<-logit1+alp2

```



```

## logit3<-logit2+alp3
## logit4<-logit3+alp4
## pge1<-exp(logit1)/(1+exp(logit1))
## pge2<-exp(logit2)/(1+exp(logit2))
## pge3<-exp(logit3)/(1+exp(logit3))
## pge4<-exp(logit4)/(1+exp(logit4))
## logpdf<-rep(0,length(y))
## P.obs = (y==1)*pge1+(y==2)*(pge2 - pge1)+(y==3)*(pge3 - pge2)+(y==4)*(pge4 - pge3)+(y==5)*(1 - pge4)
## logpdf <- log(P.obs)
##
## return(logpdf)
## }
## Nb of parameters: 5
##      parameter names:  alp1 alp2 alp3 alp4 beta
##      distribution:
##      Parameter Distribution Estimated
## [1,] alp1      normal      Estimated
## [2,] alp2      log-normal   Estimated
## [3,] alp3      log-normal   Estimated
## [4,] alp4      log-normal   Estimated
## [5,] beta      log-normal   Estimated
## Variance-covariance matrix:
##      alp1 alp2 alp3 alp4 beta
## alp1    1    0    0    0    0
## alp2    0    0    0    0    0
## alp3    0    0    0    0    0
## alp4    0    0    0    0    0
## beta    0    0    0    0    1
##      No covariate in the model.
##      Initial values
##      alp1 alp2 alp3 alp4 beta
## Pop.CondInit    0 0.2 0.6    3 0.2

saemix.model.cov2<-saemixModel(model=ordinal.model,description="Ordinal categorical model",modeltype="1",
                                psi0=matrix(c(0,0.2, 0.6, 3, 0.2),ncol=5,byrow=TRUE,dimnames=list(NULL,c("alp1","alp2","alp3","alp4","beta")),
                                transform.par=c(0,1,1,1,1),omega.init=diag(rep(1,5)), covariance.model = covmodel2,
                                covariate.model = covmodel2)

##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
## Model function: Ordinal categorical model Model type: likelihood
## function(psi,id,xidep) {
##   y<-xidep[,1]
##   time<-xidep[,2]
##   alp1<-psi[id,1]
##   alp2<-psi[id,2]
##   alp3<-psi[id,3]
##   alp4<-psi[id,4]
##   beta<-psi[id,5]
##
##   logit1<-alp1 + beta*time
##   logit2<-logit1+alp2

```

```

## logit3<-logit2+alp3
## logit4<-logit3+alp4
## pge1<-exp(logit1)/(1+exp(logit1))
## pge2<-exp(logit2)/(1+exp(logit2))
## pge3<-exp(logit3)/(1+exp(logit3))
## pge4<-exp(logit4)/(1+exp(logit4))
## logpdf<-rep(0,length(y))
## P.obs = (y==1)*pge1+(y==2)*(pge2 - pge1)+(y==3)*(pge3 - pge2)+(y==4)*(pge4 - pge3)+(y==5)*(1 - pge4)
## logpdf <- log(P.obs)
##
## return(logpdf)
## }
## Nb of parameters: 5
## parameter names: alp1 alp2 alp3 alp4 beta
## distribution:
## Parameter Distribution Estimated
## [1,] alp1 normal Estimated
## [2,] alp2 log-normal Estimated
## [3,] alp3 log-normal Estimated
## [4,] alp4 log-normal Estimated
## [5,] beta log-normal Estimated
## Variance-covariance matrix:
## alp1 alp2 alp3 alp4 beta
## alp1 1 0 0 0 0
## alp2 0 0 0 0 0
## alp3 0 0 0 0 0
## alp4 0 0 0 0 0
## beta 0 0 0 0 1
## No covariate in the model.
## Initial values
## alp1 alp2 alp3 alp4 beta
## Pop.CondInit 0 0.2 0.6 3 0.2

saemix.model.cov3<-saemixModel(model=ordinal.model,description="Ordinal categorical model",modeltype="1",
                                psi0=matrix(c(0,0.2, 0.6, 3, 0.2),ncol=5,byrow=TRUE,dimnames=list(NULL,c("alp1","alp2","alp3","alp4","beta")),
                                transform.par=c(0,1,1,1,1),omega.init=diag(rep(1,5)), covariance.model = covmodel3,
                                covariate.model = covmodel3)

##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
## Model function: Ordinal categorical model Model type: likelihood
## function(psi,id,xidep) {
## y<-xidep[,1]
## time<-xidep[,2]
## alp1<-psi[id,1]
## alp2<-psi[id,2]
## alp3<-psi[id,3]
## alp4<-psi[id,4]
## beta<-psi[id,5]
##
## logit1<-alp1 + beta*time
## logit2<-logit1+alp2

```

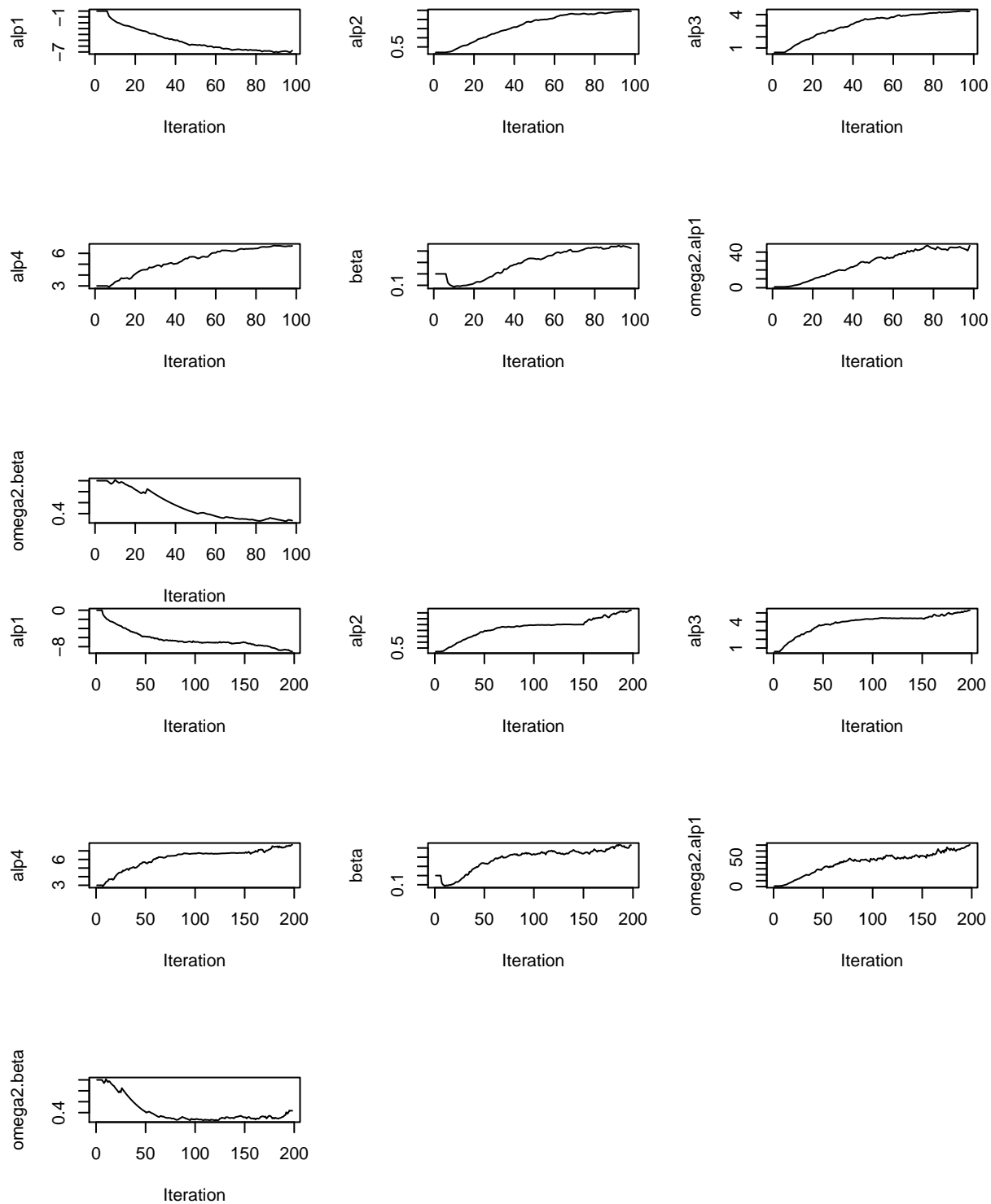
```

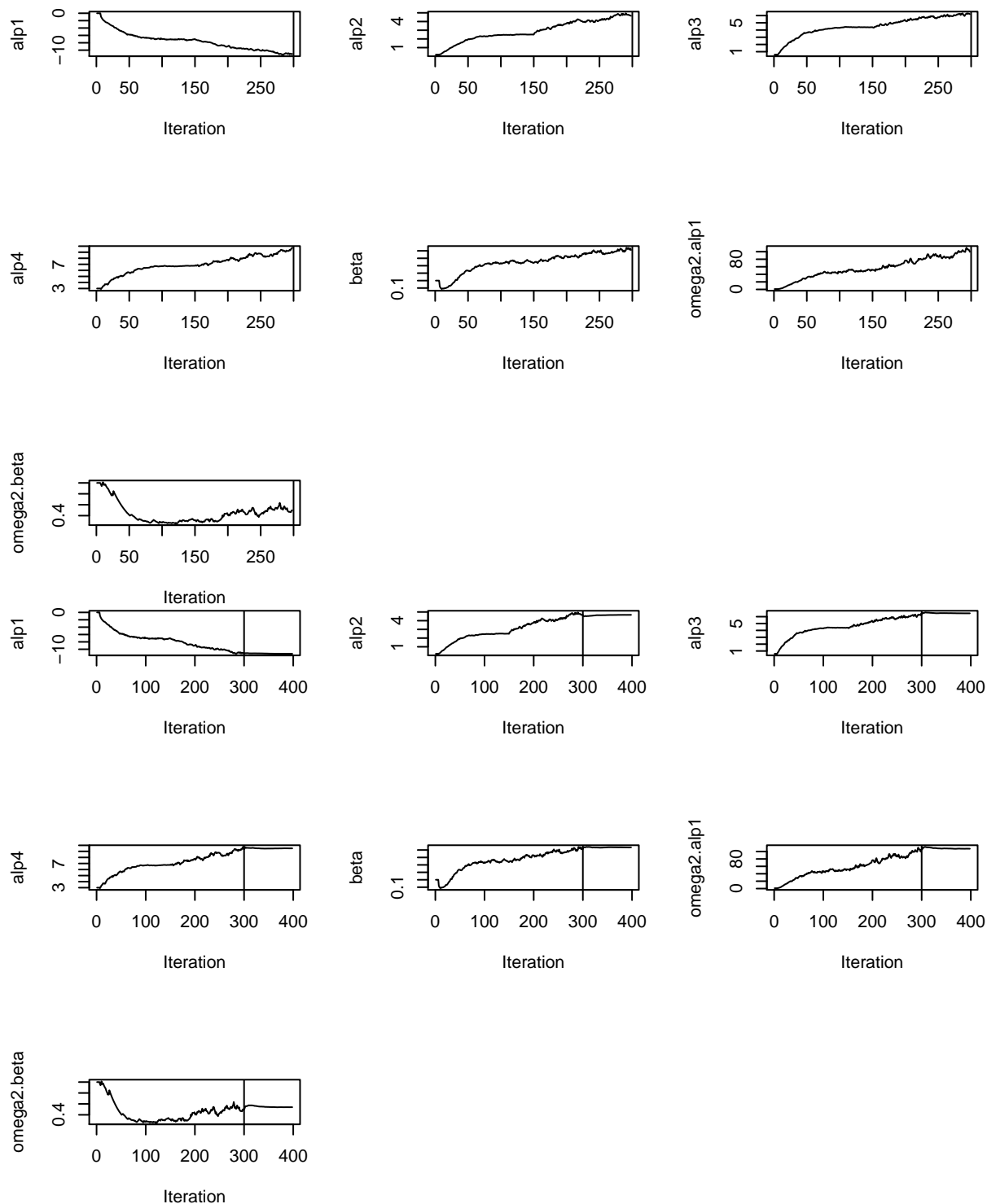
## logit3<-logit2+alp3
## logit4<-logit3+alp4
## pge1<-exp(logit1)/(1+exp(logit1))
## pge2<-exp(logit2)/(1+exp(logit2))
## pge3<-exp(logit3)/(1+exp(logit3))
## pge4<-exp(logit4)/(1+exp(logit4))
## logpdf<-rep(0,length(y))
## P.obs = (y==1)*pge1+(y==2)*(pge2 - pge1)+(y==3)*(pge3 - pge2)+(y==4)*(pge4 - pge3)+(y==5)*(1 - pge4)
## logpdf <- log(P.obs)
##
## return(logpdf)
## }
## Nb of parameters: 5
##      parameter names:  alp1 alp2 alp3 alp4 beta
##      distribution:
##      Parameter Distribution Estimated
## [1,] alp1      normal      Estimated
## [2,] alp2      log-normal   Estimated
## [3,] alp3      log-normal   Estimated
## [4,] alp4      log-normal   Estimated
## [5,] beta      log-normal   Estimated
## Variance-covariance matrix:
##      alp1 alp2 alp3 alp4 beta
## alp1    1    0    0    0    0
## alp2    0    0    0    0    0
## alp3    0    0    0    0    0
## alp4    0    0    0    0    0
## beta    0    0    0    0    1
## Covariate model:
##      alp1 alp2 alp3 alp4 beta
## [1,]    1    0    0    0    0
## [2,]    0    0    0    0    0
## [3,]    0    0    0    0    0
## Initial values
##      alp1 alp2 alp3 alp4 beta
## Pop.CondInit    0 0.2 0.6  3 0.2
## Cov.CondInit    0 0.0 0.0  0 0.0

saemix.options<-list(seed=632545,save=FALSE,save.graphs=FALSE, nb.chains=5)

ord.fit<-saemix(saemix.model,saemix.data,saemix.options)

```





```
## Error in solve.default(F0) :
##   routine Lapack dgesv : le système est exactement singulier : U[2,2] = 0
## Nonlinear mixed-effects model fit by the SAEM algorithm
## -----
##      Data
## -----
## Object of class SaemixData
```

```

##      longitudinal data for use with the SAEM algorithm
## Dataset knee.saemix
##      Structured data: y ~ y + time | id
##      X variable for graphs: time ()
##      covariates: Age (-), Sex (-), treatment (-)
##      reference class for covariate Sex : 0
##      reference class for covariate treatment : 0
## Dataset characteristics:
##      number of subjects:      127
##      number of observations: 508
##      average/min/max nb obs: 4.00 / 4 / 4
## First 10 lines of data:
##      id y time y.1 Age Sex treatment mdv cens occ ytype
## 1  1 4 0 4 -2 1 0 0 0 1 1
## 2  1 4 3 4 -2 1 0 0 0 1 1
## 3  1 4 7 4 -2 1 0 0 0 1 1
## 4  1 4 10 4 -2 1 0 0 0 1 1
## 5  2 4 0 4 2 1 0 0 0 1 1
## 6  2 4 3 4 2 1 0 0 0 1 1
## 7  2 4 7 4 2 1 0 0 0 1 1
## 8  2 4 10 4 2 1 0 0 0 1 1
## 9  3 3 0 3 11 1 0 0 0 1 1
## 10 3 3 3 3 11 1 0 0 0 1 1
## -----
## ----          Model          ----
## -----
## Nonlinear mixed-effects model
## Model function: Ordinal categorical model Model type: likelihood
## function(psi,id,xidep) {
##   y<-xidep[,1]
##   time<-xidep[,2]
##   alp1<-psi[id,1]
##   alp2<-psi[id,2]
##   alp3<-psi[id,3]
##   alp4<-psi[id,4]
##   beta<-psi[id,5]
##
##   logit1<-alp1 + beta*time
##   logit2<-logit1+alp2
##   logit3<-logit2+alp3
##   logit4<-logit3+alp4
##   pge1<-exp(logit1)/(1+exp(logit1))
##   pge2<-exp(logit2)/(1+exp(logit2))
##   pge3<-exp(logit3)/(1+exp(logit3))
##   pge4<-exp(logit4)/(1+exp(logit4))
##   logpdf<-rep(0,length(y))
##   P.obs = (y==1)*pge1+(y==2)*(pge2 - pge1)+(y==3)*(pge3 - pge2)+(y==4)*(pge4 - pge3)+(y==5)*(1 - pge4)
##   logpdf <- log(P.obs)
##
##   return(logpdf)
## }
## <bytecode: 0x564edbb5ef80>
## Nb of parameters: 5
##      parameter names: alp1 alp2 alp3 alp4 beta

```

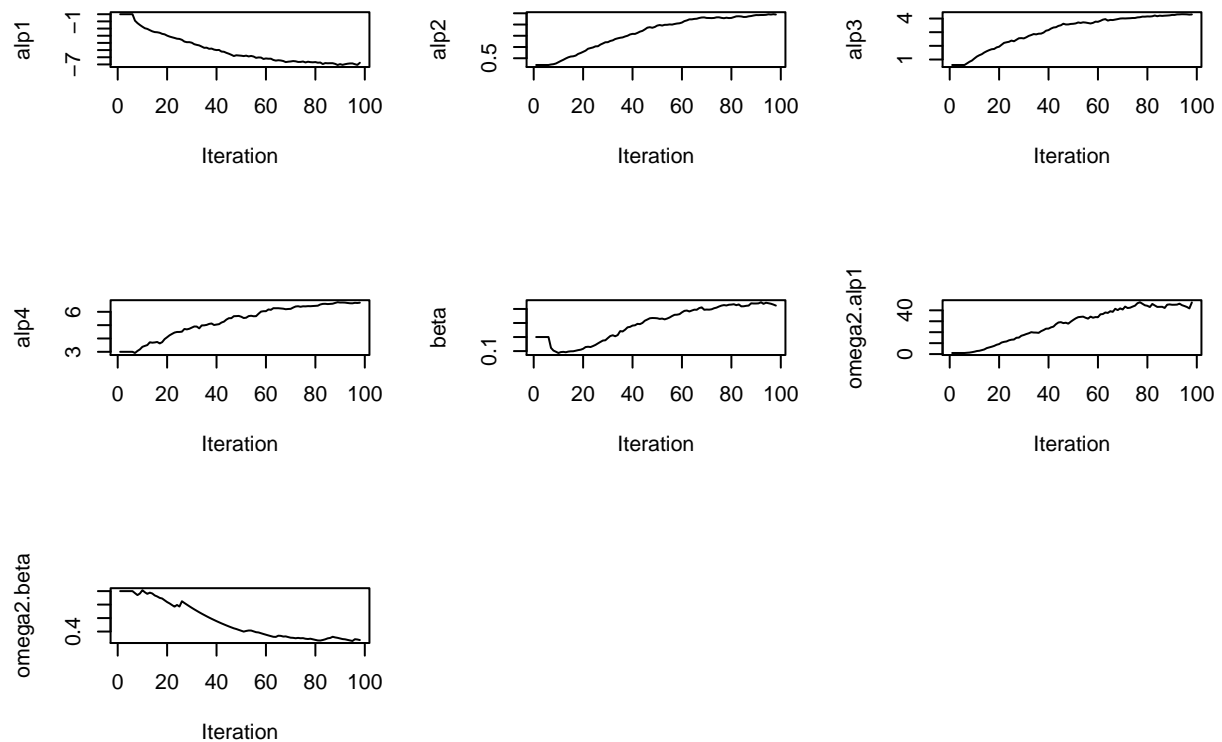
```

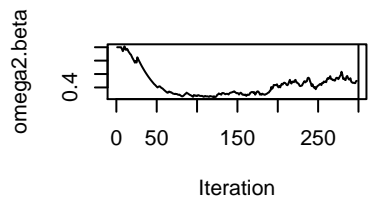
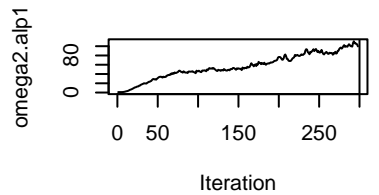
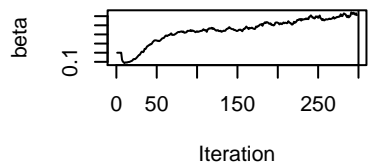
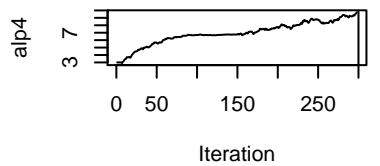
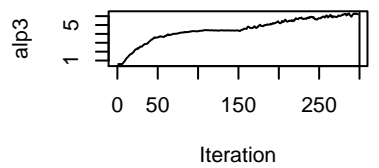
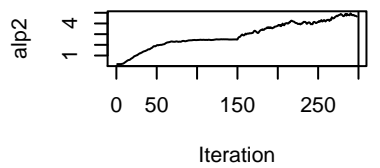
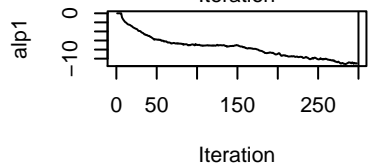
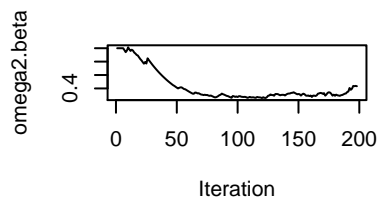
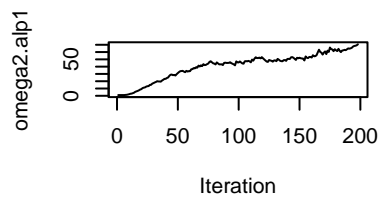
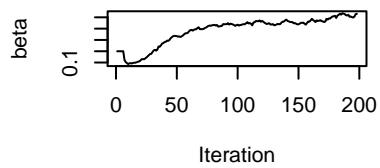
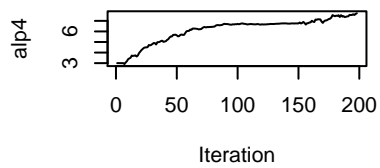
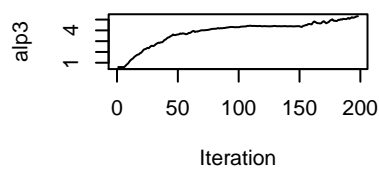
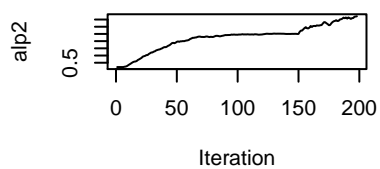
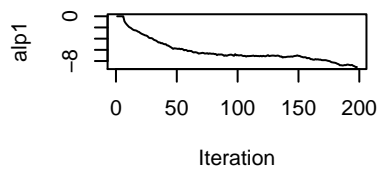
##      distribution:
##      Parameter Distribution Estimated
## [1,] alp1      normal      Estimated
## [2,] alp2      log-normal   Estimated
## [3,] alp3      log-normal   Estimated
## [4,] alp4      log-normal   Estimated
## [5,] beta      log-normal   Estimated
##      Variance-covariance matrix:
##      alp1 alp2 alp3 alp4 beta
## alp1    1    0    0    0    0
## alp2    0    0    0    0    0
## alp3    0    0    0    0    0
## alp4    0    0    0    0    0
## beta    0    0    0    0    1
##      No covariate in the model.
##      Initial values
##      alp1 alp2 alp3 alp4 beta
## Pop.CondInit    0 0.2 0.6   3 0.2
## -----
## ----      Key algorithm options      ----
## -----
##      Estimation of individual parameters (MAP)
##      Estimation of standard errors and linearised log-likelihood
##      Estimation of log-likelihood by importance sampling
##      Number of iterations:  K1=300, K2=100
##      Number of chains:  5
##      Seed:  632545
##      Number of MCMC iterations for IS:  5000
##      Simulations:
##      nb of simulated datasets used for npde:  1000
##      nb of simulated datasets used for VPC:  100
##      Input/output
##      save the results to a file:  FALSE
##      save the graphs to files:  FALSE
## -----
## ----                        Results                        ----
## -----
## -----      Fixed effects      -----
## -----
##      Parameter Estimate SE   CV(%)
## [1,] alp1      -11.22   1.64 15
## [2,] alp2       4.67   1.57 34
## [3,] alp3       6.49   1.39 21
## [4,] alp4       9.49   2.71 29
## [5,] beta       0.64   0.14 22
## -----
## -----      Variance of random effects      -----
## -----
##      Parameter   Estimate SE CV(%)
## alp1 omega2.alp1 107.58  NA  NA
## beta omega2.beta   0.54  NA  NA
## -----
## -----      Correlation matrix of random effects      -----
## -----

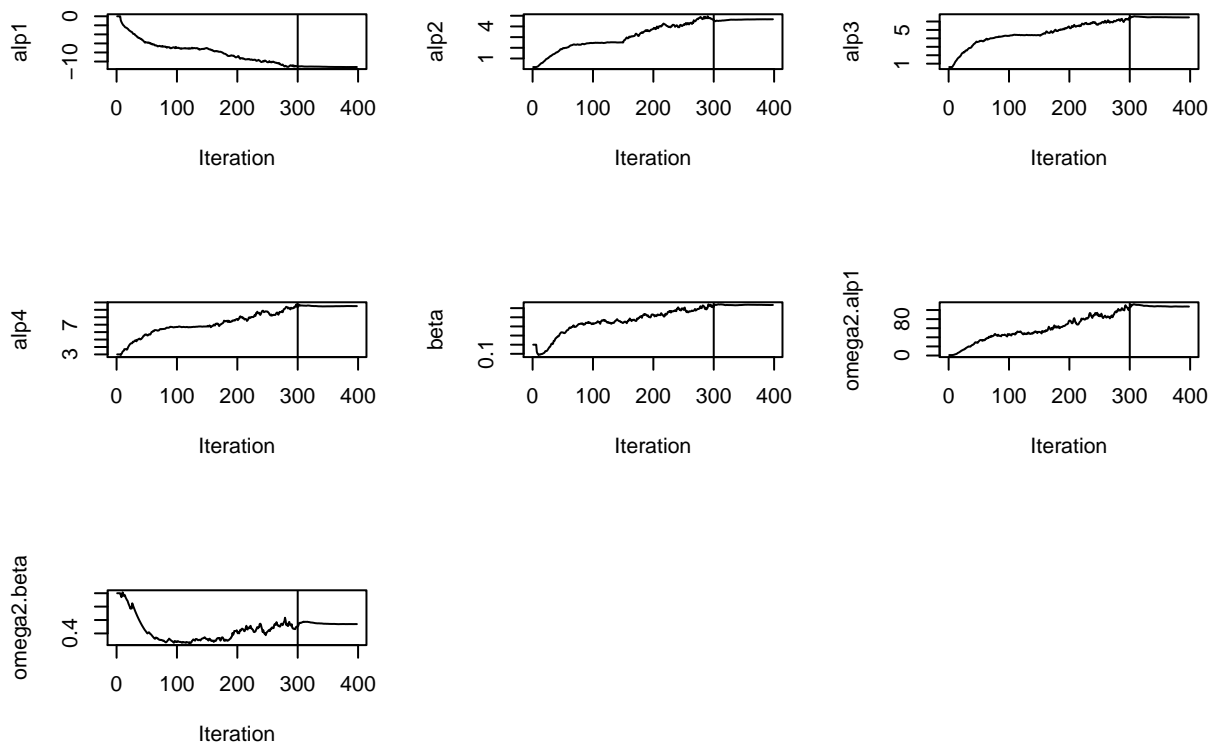
```

```
##          omega2.alp1 omega2.beta
## omega2.alp1 1          0
## omega2.beta 0          1
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
##      -2LL= 5968.801
##      AIC = 5984.801
##      BIC = 6007.554
##
## Likelihood computed by importance sampling
##      -2LL= 869.1684
##      AIC = 885.1684
##      BIC = 907.9219
## -----
```

```
ord.fit.cov1<-saemix(saemix.model.cov1,saemix.data,saemix.options)
```







```
## Error in solve.default(F0) :
## routine Lapack dgesv : le système est exactement singulier : U[2,2] = 0
## Nonlinear mixed-effects model fit by the SAEM algorithm
## -----
## Data
## -----
## Object of class SaemixData
## longitudinal data for use with the SAEM algorithm
## Dataset knee.saemix
## Structured data: y ~ y + time | id
## X variable for graphs: time ()
## covariates: Age (-), Sex (-), treatment (-)
## reference class for covariate Sex : 0
## reference class for covariate treatment : 0
## Dataset characteristics:
## number of subjects: 127
## number of observations: 508
## average/min/max nb obs: 4.00 / 4 / 4
## First 10 lines of data:
## id y time y.1 Age Sex treatment mdv cens occ ytype
## 1 1 4 0 4 -2 1 0 0 0 1 1
## 2 1 4 3 4 -2 1 0 0 0 1 1
## 3 1 4 7 4 -2 1 0 0 0 1 1
## 4 1 4 10 4 -2 1 0 0 0 1 1
## 5 2 4 0 4 2 1 0 0 0 1 1
## 6 2 4 3 4 2 1 0 0 0 1 1
## 7 2 4 7 4 2 1 0 0 0 1 1
## 8 2 4 10 4 2 1 0 0 0 1 1
## 9 3 3 0 3 11 1 0 0 0 1 1
## 10 3 3 3 3 11 1 0 0 0 1 1
```

```

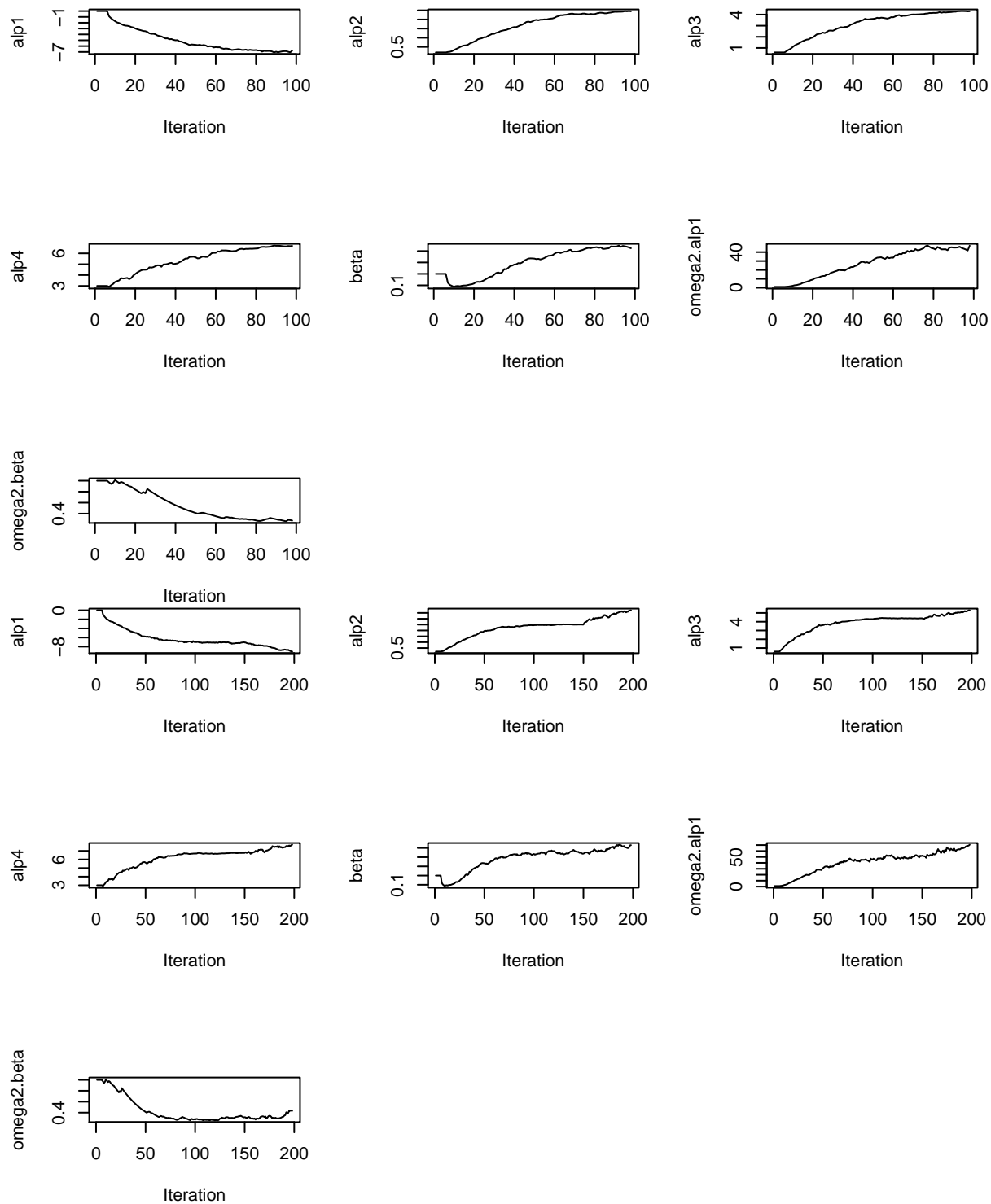
## -----
## -----          Model          -----
## -----
## Nonlinear mixed-effects model
## Model function: Ordinal categorical model Model type: likelihood
## function(psi,id,xidep) {
##   y<-xidep[,1]
##   time<-xidep[,2]
##   alp1<-psi[id,1]
##   alp2<-psi[id,2]
##   alp3<-psi[id,3]
##   alp4<-psi[id,4]
##   beta<-psi[id,5]
##
##   logit1<-alp1 + beta*time
##   logit2<-logit1+alp2
##   logit3<-logit2+alp3
##   logit4<-logit3+alp4
##   pge1<-exp(logit1)/(1+exp(logit1))
##   pge2<-exp(logit2)/(1+exp(logit2))
##   pge3<-exp(logit3)/(1+exp(logit3))
##   pge4<-exp(logit4)/(1+exp(logit4))
##   logpdf<-rep(0,length(y))
##   P.obs = (y==1)*pge1+(y==2)*(pge2 - pge1)+(y==3)*(pge3 - pge2)+(y==4)*(pge4 - pge3)+(y==5)*(1 - pge4)
##   logpdf <- log(P.obs)
##
##   return(logpdf)
## }
## <bytecode: 0x564edbb5ef80>
## Nb of parameters: 5
##   parameter names: alp1 alp2 alp3 alp4 beta
##   distribution:
##   Parameter Distribution Estimated
## [1,] alp1      normal      Estimated
## [2,] alp2      log-normal   Estimated
## [3,] alp3      log-normal   Estimated
## [4,] alp4      log-normal   Estimated
## [5,] beta      log-normal   Estimated
## Variance-covariance matrix:
##   alp1 alp2 alp3 alp4 beta
## alp1   1   0   0   0   0
## alp2   0   0   0   0   0
## alp3   0   0   0   0   0
## alp4   0   0   0   0   0
## beta   0   0   0   0   1
## No covariate in the model.
## Initial values
##   alp1 alp2 alp3 alp4 beta
## Pop.CondInit   0 0.2 0.6   3 0.2
## -----
## ----- Key algorithm options -----
## -----
## Estimation of individual parameters (MAP)
## Estimation of standard errors and linearised log-likelihood

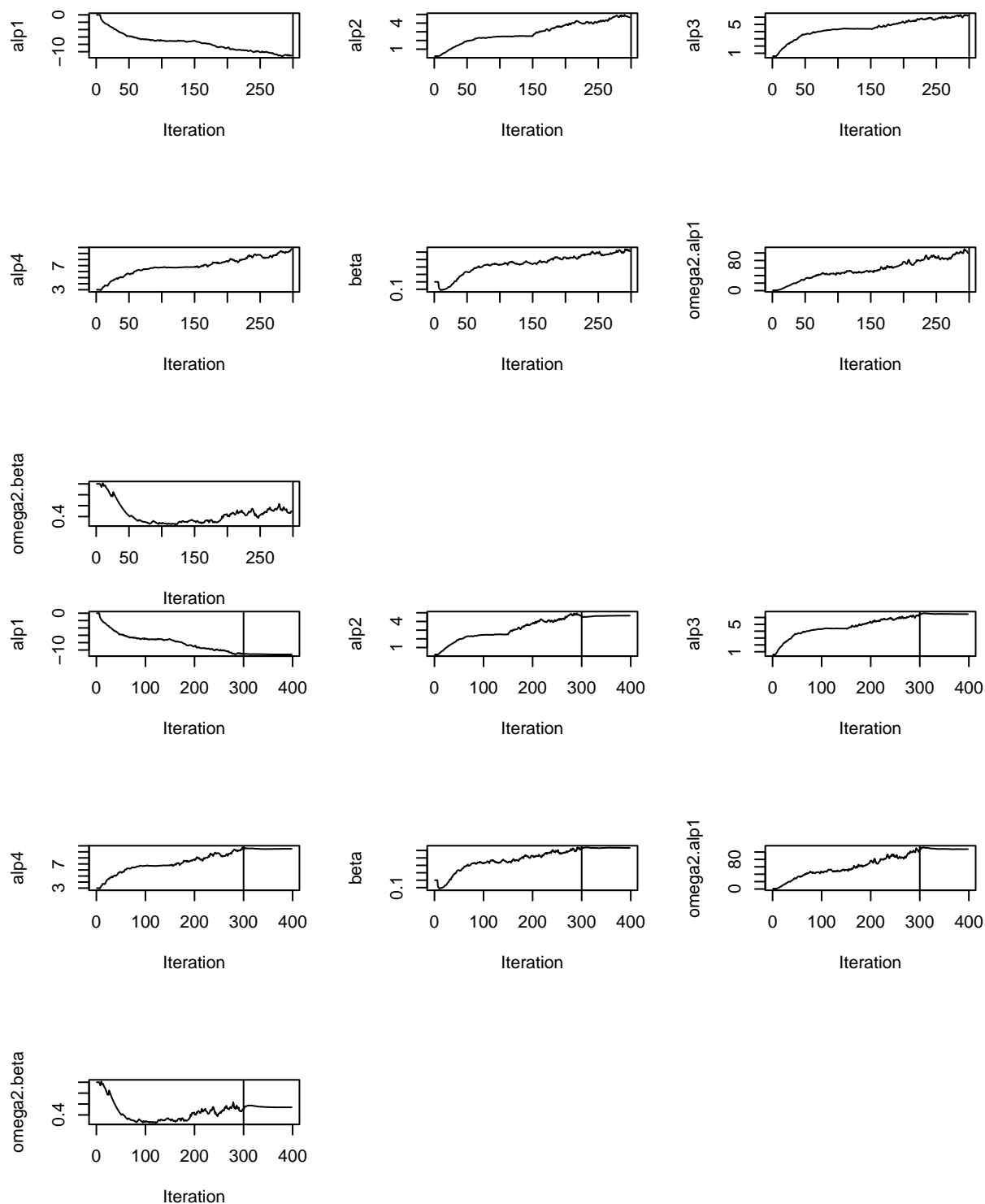
```

```

## Estimation of log-likelihood by importance sampling
## Number of iterations: K1=300, K2=100
## Number of chains: 5
## Seed: 632545
## Number of MCMC iterations for IS: 5000
## Simulations:
##     nb of simulated datasets used for npde: 1000
##     nb of simulated datasets used for VPC: 100
## Input/output
##     save the results to a file: FALSE
##     save the graphs to files: FALSE
## -----
## ----                      Results                      ----
## -----
## ----- Fixed effects -----
## -----
##      Parameter Estimate SE   CV(%)
## [1,] alp1      -11.22  1.64 15
## [2,] alp2       4.67  1.57 34
## [3,] alp3       6.49  1.39 21
## [4,] alp4       9.49  2.71 29
## [5,] beta       0.64  0.14 22
## -----
## ----- Variance of random effects -----
## -----
##      Parameter   Estimate SE CV(%)
## alp1 omega2.alp1 107.58  NA NA
## beta omega2.beta  0.54  NA NA
## -----
## ----- Correlation matrix of random effects -----
## -----
##      omega2.alp1 omega2.beta
## omega2.alp1 1      0
## omega2.beta 0      1
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
##      -2LL= 5968.801
##      AIC = 5984.801
##      BIC = 6007.554
##
## Likelihood computed by importance sampling
##      -2LL= 869.1684
##      AIC = 885.1684
##      BIC = 907.9219
## -----
ord.fit.cov2<-saemix(saemix.model.cov2,saemix.data,saemix.options)

```





```
## Error in solve.default(F0) :
##   routine Lapack dgesv : le système est exactement singulier : U[2,2] = 0
## Nonlinear mixed-effects model fit by the SAEM algorithm
## -----
##      Data
## -----
## Object of class SaemixData
```

```

##      longitudinal data for use with the SAEM algorithm
## Dataset knee.saemix
##      Structured data: y ~ y + time | id
##      X variable for graphs: time ()
##      covariates: Age (-), Sex (-), treatment (-)
##      reference class for covariate Sex : 0
##      reference class for covariate treatment : 0
## Dataset characteristics:
##      number of subjects:      127
##      number of observations: 508
##      average/min/max nb obs: 4.00 / 4 / 4
## First 10 lines of data:
##      id y time y.1 Age Sex treatment mdv cens occ ytype
## 1  1 4 0 4 -2 1 0 0 0 1 1
## 2  1 4 3 4 -2 1 0 0 0 1 1
## 3  1 4 7 4 -2 1 0 0 0 1 1
## 4  1 4 10 4 -2 1 0 0 0 1 1
## 5  2 4 0 4 2 1 0 0 0 1 1
## 6  2 4 3 4 2 1 0 0 0 1 1
## 7  2 4 7 4 2 1 0 0 0 1 1
## 8  2 4 10 4 2 1 0 0 0 1 1
## 9  3 3 0 3 11 1 0 0 0 1 1
## 10 3 3 3 3 11 1 0 0 0 1 1
## -----
## ----          Model          ----
## -----
## Nonlinear mixed-effects model
## Model function: Ordinal categorical model Model type: likelihood
## function(psi,id,xidep) {
##   y<-xidep[,1]
##   time<-xidep[,2]
##   alp1<-psi[id,1]
##   alp2<-psi[id,2]
##   alp3<-psi[id,3]
##   alp4<-psi[id,4]
##   beta<-psi[id,5]
##
##   logit1<-alp1 + beta*time
##   logit2<-logit1+alp2
##   logit3<-logit2+alp3
##   logit4<-logit3+alp4
##   pge1<-exp(logit1)/(1+exp(logit1))
##   pge2<-exp(logit2)/(1+exp(logit2))
##   pge3<-exp(logit3)/(1+exp(logit3))
##   pge4<-exp(logit4)/(1+exp(logit4))
##   logpdf<-rep(0,length(y))
##   P.obs = (y==1)*pge1+(y==2)*(pge2 - pge1)+(y==3)*(pge3 - pge2)+(y==4)*(pge4 - pge3)+(y==5)*(1 - pge4)
##   logpdf <- log(P.obs)
##
##   return(logpdf)
## }
## <bytecode: 0x564edbb5ef80>
## Nb of parameters: 5
##      parameter names: alp1 alp2 alp3 alp4 beta

```

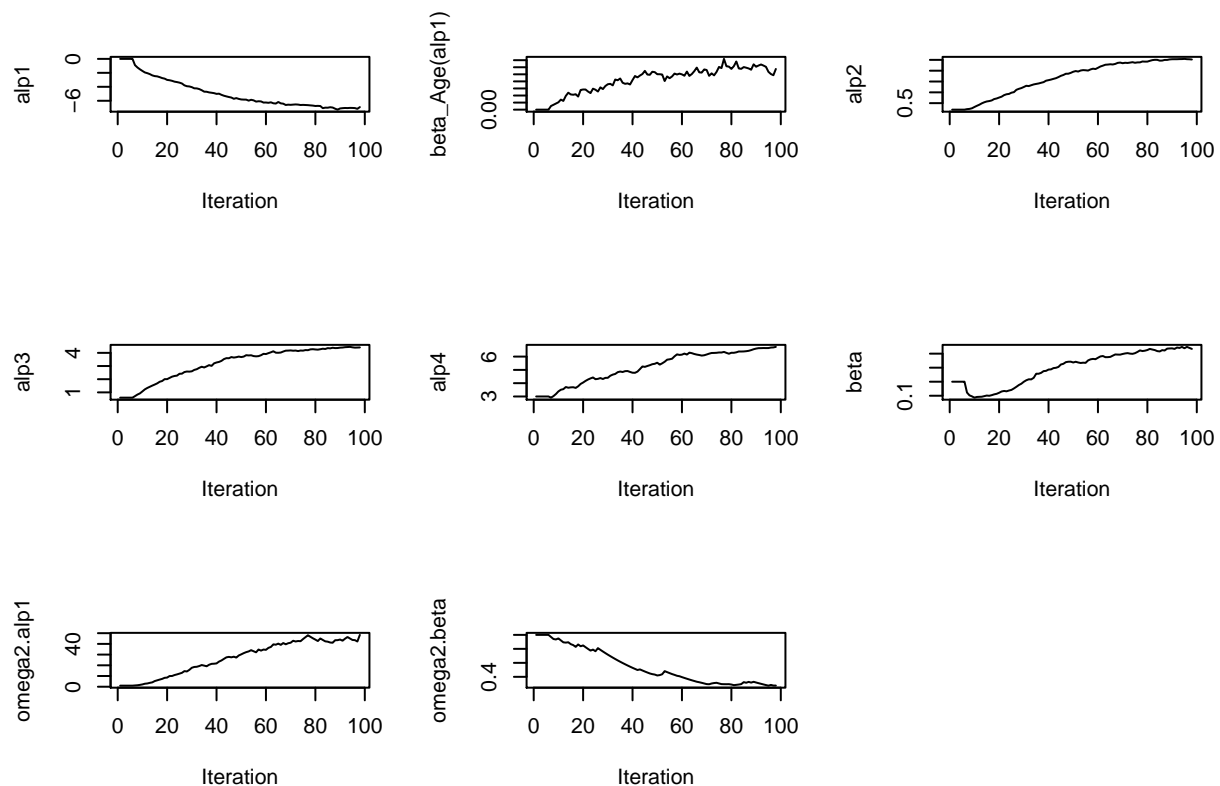
```

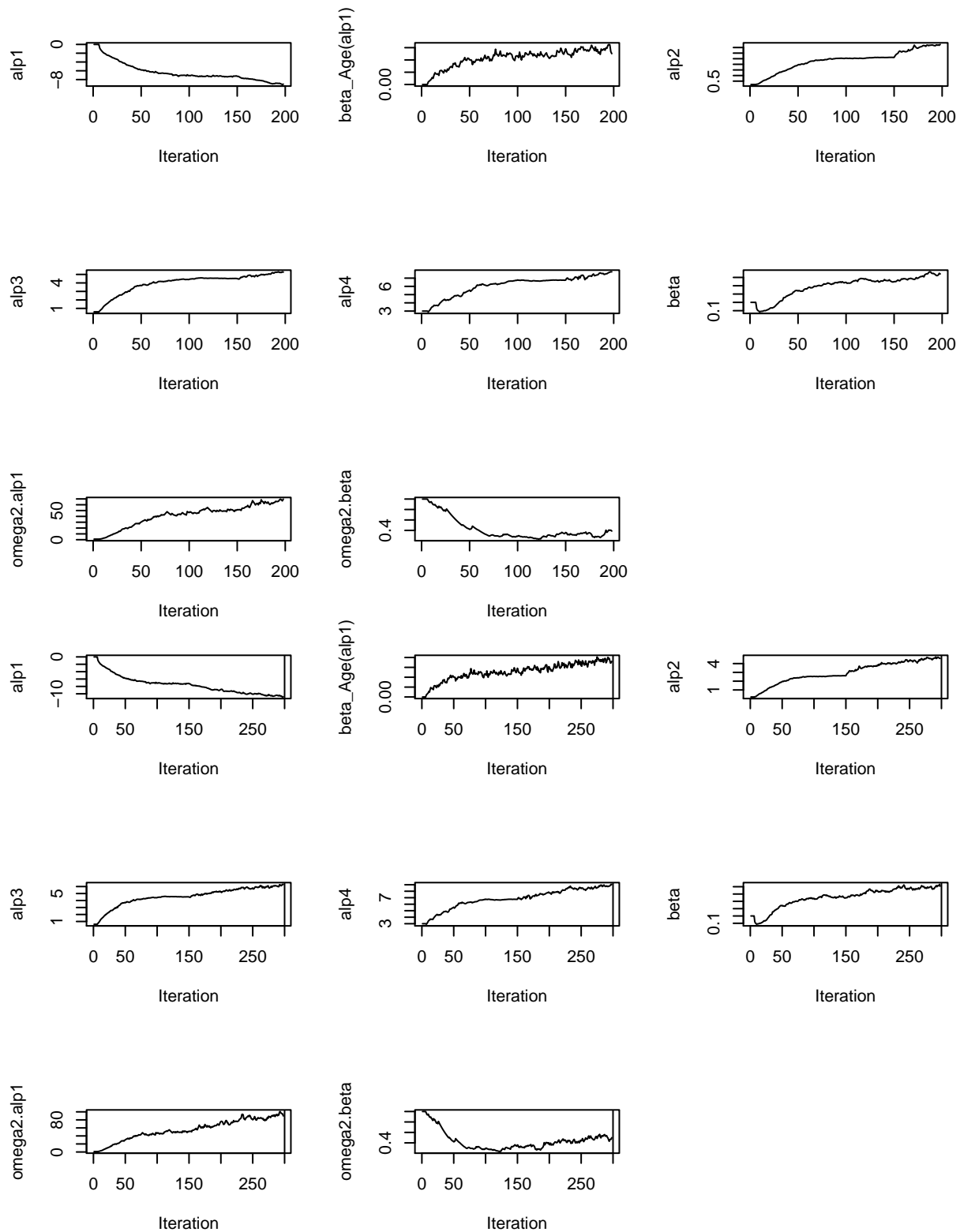
##      distribution:
##      Parameter Distribution Estimated
## [1,] alp1      normal      Estimated
## [2,] alp2      log-normal   Estimated
## [3,] alp3      log-normal   Estimated
## [4,] alp4      log-normal   Estimated
## [5,] beta      log-normal   Estimated
##      Variance-covariance matrix:
##      alp1 alp2 alp3 alp4 beta
## alp1    1    0    0    0    0
## alp2    0    0    0    0    0
## alp3    0    0    0    0    0
## alp4    0    0    0    0    0
## beta    0    0    0    0    1
##      No covariate in the model.
##      Initial values
##      alp1 alp2 alp3 alp4 beta
## Pop.CondInit    0 0.2 0.6   3 0.2
## -----
## ----      Key algorithm options      ----
## -----
##      Estimation of individual parameters (MAP)
##      Estimation of standard errors and linearised log-likelihood
##      Estimation of log-likelihood by importance sampling
##      Number of iterations:  K1=300, K2=100
##      Number of chains:  5
##      Seed:  632545
##      Number of MCMC iterations for IS:  5000
##      Simulations:
##      nb of simulated datasets used for npde:  1000
##      nb of simulated datasets used for VPC:  100
##      Input/output
##      save the results to a file:  FALSE
##      save the graphs to files:  FALSE
## -----
## ----                        Results                        ----
## -----
## -----      Fixed effects      -----
## -----
##      Parameter Estimate SE   CV(%)
## [1,] alp1      -11.22   1.64 15
## [2,] alp2       4.67   1.57 34
## [3,] alp3       6.49   1.39 21
## [4,] alp4       9.49   2.71 29
## [5,] beta       0.64   0.14 22
## -----
## -----      Variance of random effects      -----
## -----
##      Parameter   Estimate SE CV(%)
## alp1 omega2.alp1 107.58   NA  NA
## beta omega2.beta   0.54   NA  NA
## -----
## -----      Correlation matrix of random effects      -----
## -----

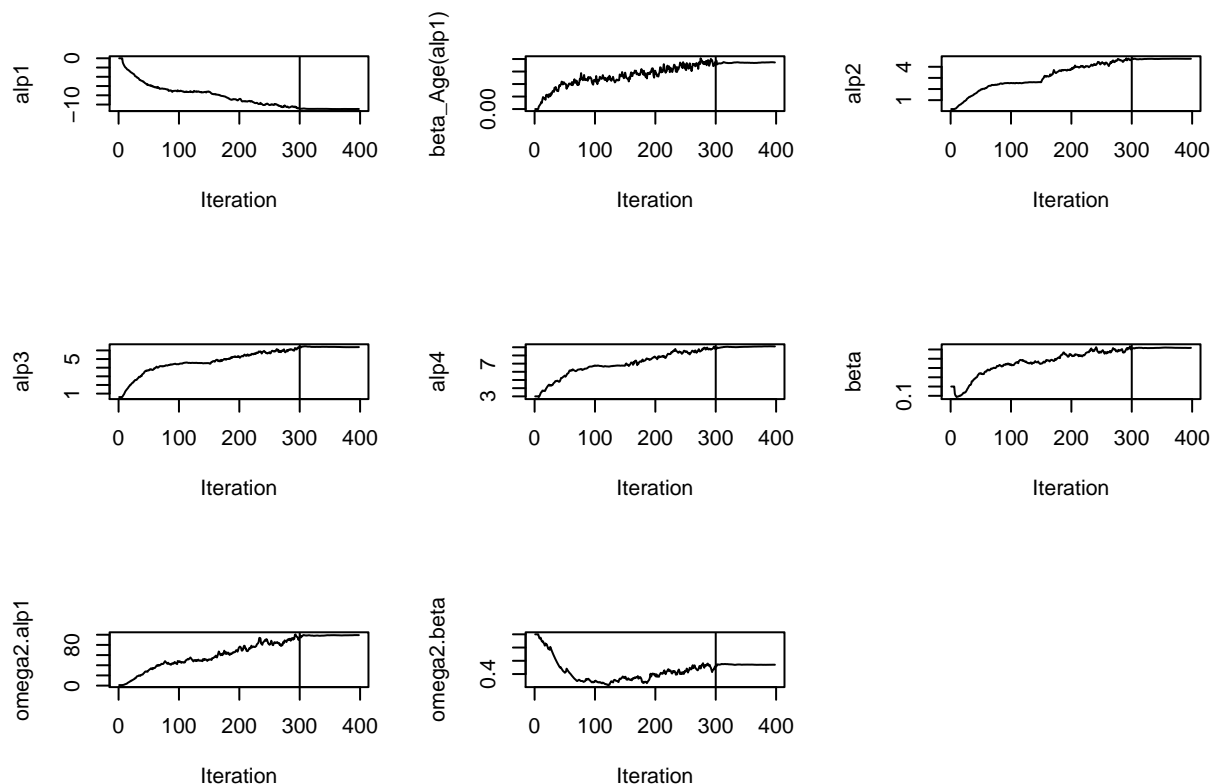
```



```
##          omega2.alp1 omega2.beta
## omega2.alp1 1          0
## omega2.beta 0          1
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
##      -2LL= 5968.801
##      AIC = 5984.801
##      BIC = 6007.554
##
## Likelihood computed by importance sampling
##      -2LL= 869.1684
##      AIC = 885.1684
##      BIC = 907.9219
## -----
ord.fit.cov3<-saemix(saemix.model.cov3,saemix.data,saemix.options)
```







```
## Error in solve.default(F0) :
##   routine Lapack dgesv : le système est exactement singulier : U[2,2] = 0
## Nonlinear mixed-effects model fit by the SAEM algorithm
## -----
##      Data
## -----
## Object of class SaemixData
##   longitudinal data for use with the SAEM algorithm
## Dataset knee.saemix
##   Structured data: y ~ y + time | id
##   X variable for graphs: time ()
##   covariates: Age (-), Sex (-), treatment (-)
##   reference class for covariate Sex : 0
##   reference class for covariate treatment : 0
## Dataset characteristics:
##   number of subjects: 127
##   number of observations: 508
##   average/min/max nb obs: 4.00 / 4 / 4
## First 10 lines of data:
##   id y time y.1 Age Sex treatment mdv cens occ ytype
## 1  1 4  0  4 -2  1      0  0  0  1  1
## 2  1 4  3  4 -2  1      0  0  0  1  1
## 3  1 4  7  4 -2  1      0  0  0  1  1
## 4  1 4 10  4 -2  1      0  0  0  1  1
## 5  2 4  0  4  2  1      0  0  0  1  1
## 6  2 4  3  4  2  1      0  0  0  1  1
## 7  2 4  7  4  2  1      0  0  0  1  1
## 8  2 4 10  4  2  1      0  0  0  1  1
## 9  3 3  0  3 11  1      0  0  0  1  1
```

```

## 10 3 3 3 3 11 1 0 0 0 1 1
## -----
## ---- Model ----
## -----
## Nonlinear mixed-effects model
## Model function: Ordinal categorical model Model type: likelihood
## function(psi,id,xidep) {
##   y<-xidep[,1]
##   time<-xidep[,2]
##   alp1<-psi[id,1]
##   alp2<-psi[id,2]
##   alp3<-psi[id,3]
##   alp4<-psi[id,4]
##   beta<-psi[id,5]
##
##   logit1<-alp1 + beta*time
##   logit2<-logit1+alp2
##   logit3<-logit2+alp3
##   logit4<-logit3+alp4
##   pge1<-exp(logit1)/(1+exp(logit1))
##   pge2<-exp(logit2)/(1+exp(logit2))
##   pge3<-exp(logit3)/(1+exp(logit3))
##   pge4<-exp(logit4)/(1+exp(logit4))
##   logpdf<-rep(0,length(y))
##   P.obs = (y==1)*pge1+(y==2)*(pge2 - pge1)+(y==3)*(pge3 - pge2)+(y==4)*(pge4 - pge3)+(y==5)*(1 - pge4)
##   logpdf <- log(P.obs)
##
##   return(logpdf)
## }
## <bytecode: 0x564edbb5ef80>
## Nb of parameters: 5
## parameter names: alp1 alp2 alp3 alp4 beta
## distribution:
## Parameter Distribution Estimated
## [1,] alp1 normal Estimated
## [2,] alp2 log-normal Estimated
## [3,] alp3 log-normal Estimated
## [4,] alp4 log-normal Estimated
## [5,] beta log-normal Estimated
## Variance-covariance matrix:
## alp1 alp2 alp3 alp4 beta
## alp1 1 0 0 0 0
## alp2 0 0 0 0 0
## alp3 0 0 0 0 0
## alp4 0 0 0 0 0
## beta 0 0 0 0 1
## Covariate model:
## [,1] [,2] [,3] [,4] [,5]
## Age 1 0 0 0 0
## Initial values
## alp1 alp2 alp3 alp4 beta
## Pop.CondInit 0 0.2 0.6 3 0.2
## Cov.CondInit 0 0.0 0.0 0 0.0
## -----

```

```

## ---- Key algorithm options ----
## -----
## Estimation of individual parameters (MAP)
## Estimation of standard errors and linearised log-likelihood
## Estimation of log-likelihood by importance sampling
## Number of iterations: K1=300, K2=100
## Number of chains: 5
## Seed: 632545
## Number of MCMC iterations for IS: 5000
## Simulations:
##     nb of simulated datasets used for npde: 1000
##     nb of simulated datasets used for VPC: 100
## Input/output
##     save the results to a file: FALSE
##     save the graphs to files: FALSE
## -----
## ---- Results ----
## -----
## ----- Fixed effects -----
## -----
## Parameter      Estimate SE    CV(%) p-value
## [1,] alp1      -10.96  1.698 15    -
## [2,] beta_Age(alp1) 0.19  0.084 45    0.013
## [3,] alp2       4.72  1.622 34    -
## [4,] alp3       6.39  1.372 21    -
## [5,] alp4       9.10  2.585 28    -
## [6,] beta       0.62  0.135 22    -
## -----
## ----- Variance of random effects -----
## -----
## Parameter      Estimate SE CV(%)
## alp1 omega2.alp1 99.28    NA NA
## beta omega2.beta  0.54    NA NA
## -----
## ----- Correlation matrix of random effects -----
## -----
##           omega2.alp1 omega2.beta
## omega2.alp1 1          0
## omega2.beta 0          1
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
##     -2LL= 5955.436
##     AIC = 5973.436
##     BIC = 5999.034
##
## Likelihood computed by importance sampling
##     -2LL= 866.072
##     AIC = 884.072
##     BIC = 909.6697
## -----

```

```
## Likelihoods calculated by importance sampling
##           AIC           BIC   BIC.cov
## 1 885.1684 907.9219 897.5482
## 2 885.1684 907.9219 897.5482
## 3 884.0720 909.6697 899.2960
```

Vraies données **TODO** ??? (difficile à trouver :-/)

TTE model

```

if(FALSE) {
  library(survival)
  data(cancer)
  cancer$cens<-as.integer(cancer$status==1) # censored=1, non-censored=0
  cancer$status<-cancer$status-1 # dead=1, alive=0
  cancer<-cbind(id=1:dim(cancer)[1],cancer)
  cancer2<-cancer
  cancer2$time<-0
  cancer2$status<-0
  cancer2$cens<-0
  lung.saemix<-rbind(cancer2, cancer)
  lung.saemix<-lung.saemix[order(lung.saemix$id, lung.saemix$time),]
  lung.saemix$sex<-lung.saemix$sex-1
  lung.saemix<-lung.saemix[,c("id","time","status","cens","inst","age", "sex", "ph.ecog", "ph.karno", "ph.pat")]
  hasnoNA<-function(xmat)
    apply(xmat,1,function(x) sum(is.na(x))==0)
  lung.saemix<-lung.saemix[hasnoNA(lung.saemix[,5:9]),]
  write.table(lung.saemix, file.path(datDir, "lung.saemix.tab"), quote=F, row.names=F)
}

```

- The `Surv` function from the `survival` package creates a survival object for use as the response in a model formula.
 - one entry for each subject that is the survival time, which is followed by a `+` if the subject was censored
 - transform `lung.saemix` in the `Surv` format to check the survival function w/r `saemix` fit
- Weibull model
 - parametric survival function

$$S(t) = e^{-(\frac{t}{\lambda})^\beta}$$

- Also tried computing a SE for $S(t)$ using the delta-method where the vector of derivatives for the survival function of Weibull model are:

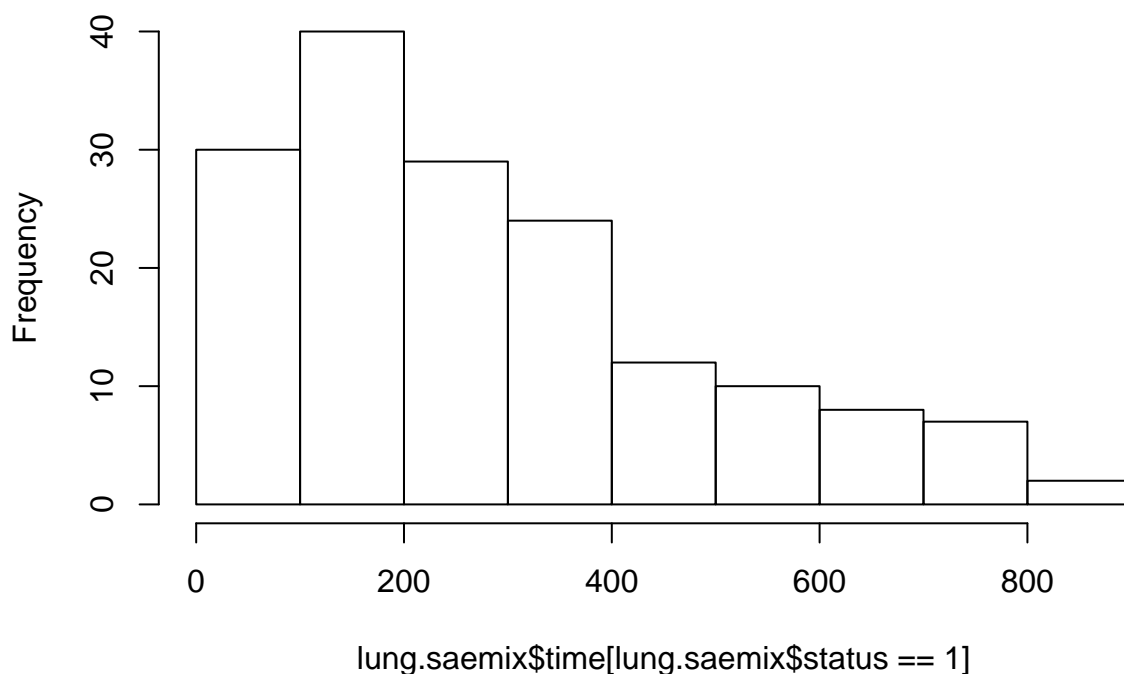
$$\begin{pmatrix} \frac{\partial S}{\partial \lambda} \\ \frac{\partial S}{\partial \beta} \end{pmatrix} = \begin{pmatrix} \frac{\beta}{\lambda} \left(\frac{t}{\lambda}\right)^{\beta} e^{-\left(\frac{t}{\lambda}\right)^{\beta}} \\ -\ln\left(\frac{t}{\lambda}\right) \left(\frac{t}{\lambda}\right)^{\beta} e^{-\left(\frac{t}{\lambda}\right)^{\beta}} \end{pmatrix}$$

- works pretty well compared to the non-parametric KM estimate

```
if(testMode)
  data(lung.saemix) else
    lung.saemix<-read.table(file.path(datDir, "lung.saemix.tab"), header=TRUE)

hist(lung.saemix$time[lung.saemix$status==1])
```

Histogram of lung.saemix\$time[lung.saemix\$status == 1]



```
# Note: missing data in pat.karno, wt.loss and meal.cal
if(FALSE)
  print(summary(lung.saemix))

saemix.data<-saemixData(name.data=lung.saemix,header=TRUE,name.group=c("id"),
  name.predictors=c("time","status","cens"),name.response=c("status"),
  name.covariates=c("age","sex","ph.ecog","ph.karno","pat.karno","wt.loss","meal.cal"),
  units=list(x="days",y="",covariates=c("yr","","-","%", "%","cal","pounds")))

## [1] "age"      "sex"      "ph.ecog"  "ph.karno" "pat.karno" "wt.loss"
## [7] "meal.cal"
##
##
## The following SaemixData object was successfully created:
##
## Object of class SaemixData
```

```

##      longitudinal data for use with the SAEM algorithm
## Dataset lung.saemix
##      Structured data: status ~ time + status + cens | id
##      X variable for graphs: time (days)
##      covariates: age (yr), sex (), ph.ecog (-), ph.karno (%), pat.karno (%), wt.loss (cal), meal.cal
##      reference class for covariate sex : 0

weibulltte.model<-function(psi,id,xidep) {
  T<-xidep[,1]
  y<-xidep[,2] # events (1=event, 0=no event)
  cens<-which(xidep[,3]==1) # censoring times (subject specific)
  init <- which(T==0)
  lambda <- psi[id,1] # Parameters of the Weibull model
  beta <- psi[id,2]
  Nj <- length(T)

  ind <- setdiff(1:Nj, append(init,cens)) # indices of events
  hazard <- (beta/lambda)*(T/lambda)^(beta-1) # ln(H')
  H <- (T/lambda)^beta # ln(H)
  logpdf <- rep(0,Nj) # ln(l(T=0))=0
  logpdf[cens] <- -H[cens] + H[cens-1] # ln(l(T=censoring time))
  logpdf[ind] <- -H[ind] + H[ind-1] + log(hazard[ind]) # ln(l(T=event time))
  return(logpdf)
}

saemix.model<-saemixModel(model=weibulltte.model,description="time model",modeltype="likelihood",
  psi0=matrix(c(1,2),ncol=2,byrow=TRUE,dimnames=list(NULL, c("lambda","beta"))),
  transform.par=c(1,1),covariance.model=matrix(c(1,0,0,0),ncol=2, byrow=TRUE))

##
##
## The following SaemixModel object was successfully created:
##
## Nonlinear mixed-effects model
## Model function: time model Model type: likelihood
## function(psi,id,xidep) {
##   T<-xidep[,1]
##   y<-xidep[,2] # events (1=event, 0=no event)
##   cens<-which(xidep[,3]==1) # censoring times (subject specific)
##   init <- which(T==0)
##   lambda <- psi[id,1] # Parameters of the Weibull model
##   beta <- psi[id,2]
##   Nj <- length(T)
##
##   ind <- setdiff(1:Nj, append(init,cens)) # indices of events
##   hazard <- (beta/lambda)*(T/lambda)^(beta-1) # ln(H')
##   H <- (T/lambda)^beta # ln(H)
##   logpdf <- rep(0,Nj) # ln(l(T=0))=0
##   logpdf[cens] <- -H[cens] + H[cens-1] # ln(l(T=censoring time))
##   logpdf[ind] <- -H[ind] + H[ind-1] + log(hazard[ind]) # ln(l(T=event time))
##   return(logpdf)
## }
## Nb of parameters: 2
## parameter names: lambda beta
## distribution:

```



```

##      Parameter Distribution Estimated
## [1,] lambda    log-normal    Estimated
## [2,] beta      log-normal    Estimated
##      Variance-covariance matrix:
##          lambda beta
## lambda      1      0
## beta         0      0
##      No covariate in the model.
##      Initial values
##          lambda beta
## Pop.CondInit      1      2

saemix.options<-list(seed=632545,save=FALSE,save.graphs=FALSE, displayProgress=FALSE)
tte.fit<-saemix(saemix.model,saemix.data,saemix.options)

## Nonlinear mixed-effects model fit by the SAEM algorithm
## -----
## ----          Data          ----
## -----
## Object of class SaemixData
##      longitudinal data for use with the SAEM algorithm
## Dataset lung.saemix
##      Structured data: status ~ time + status + cens | id
##      X variable for graphs: time (days)
##      covariates: age (yr), sex (), ph.ecog (-), ph.karno (%), pat.karno (%), wt.loss (cal), meal.cal
##      reference class for covariate sex : 0
## Dataset characteristics:
##      number of subjects:      225
##      number of observations: 450
##      average/min/max nb obs: 2.00 / 2 / 2
## First 10 lines of data:
##      id time status cens status.1 age sex ph.ecog ph.karno pat.karno wt.loss
## 1  1  0  0  0  0  74  0  1  90  100  NA
## 2  1 306  1  0  1  74  0  1  90  100  NA
## 3  2  0  0  0  0  68  0  0  90  90  15
## 4  2 455  1  0  1  68  0  0  90  90  15
## 5  3  0  0  0  0  56  0  0  90  90  15
## 6  3 1010 0  1  0  56  0  0  90  90  15
## 7  4  0  0  0  0  57  0  1  90  60  11
## 8  4 210  1  0  1  57  0  1  90  60  11
## 9  5  0  0  0  0  60  0  0  100  90  0
## 10 5 883  1  0  1  60  0  0  100  90  0
##      meal.cal mdv cens.1 occ ytype
## 1  1175  0  0  1  1
## 2  1175  0  0  1  1
## 3  1225  0  0  1  1
## 4  1225  0  0  1  1
## 5  NA  0  0  1  1
## 6  NA  0  0  1  1
## 7  1150  0  0  1  1
## 8  1150  0  0  1  1
## 9  NA  0  0  1  1
## 10 NA  0  0  1  1
## -----
## ----          Model          ----

```

```

## -----
## Nonlinear mixed-effects model
## Model function: time model Model type: likelihood
## function(psi,id,xidep) {
##   T<-xidep[,1]
##   y<-xidep[,2] # events (1=event, 0=no event)
##   cens<-which(xidep[,3]==1) # censoring times (subject specific)
##   init <- which(T==0)
##   lambda <- psi[id,1] # Parameters of the Weibull model
##   beta <- psi[id,2]
##   Nj <- length(T)
##
##   ind <- setdiff(1:Nj, append(init,cens)) # indices of events
##   hazard <- (beta/lambda)*(T/lambda)^(beta-1) # ln(H')
##   H <- (T/lambda)^beta # ln(H)
##   logpdf <- rep(0,Nj) # ln(l(T=0))=0
##   logpdf[cens] <- -H[cens] + H[cens-1] # ln(l(T=censoring time))
##   logpdf[ind] <- -H[ind] + H[ind-1] + log(hazard[ind]) # ln(l(T=event time))
##   return(logpdf)
## }
## <bytecode: 0x564ed9a720c0>
## Nb of parameters: 2
##   parameter names: lambda beta
##   distribution:
##   Parameter Distribution Estimated
## [1,] lambda    log-normal Estimated
## [2,] beta      log-normal Estimated
## Variance-covariance matrix:
##   lambda beta
## lambda      1    0
## beta        0    0
## No covariate in the model.
## Initial values
##   lambda beta
## Pop.CondInit    1    2
## -----
## ---- Key algorithm options ----
## -----
## Estimation of individual parameters (MAP)
## Estimation of standard errors and linearised log-likelihood
## Estimation of log-likelihood by importance sampling
## Number of iterations: K1=300, K2=100
## Number of chains: 1
## Seed: 632545
## Number of MCMC iterations for IS: 5000
## Simulations:
##   nb of simulated datasets used for npde: 1000
##   nb of simulated datasets used for VPC: 100
## Input/output
##   save the results to a file: FALSE
##   save the graphs to files: FALSE
## -----
## ---- Results ----
## -----

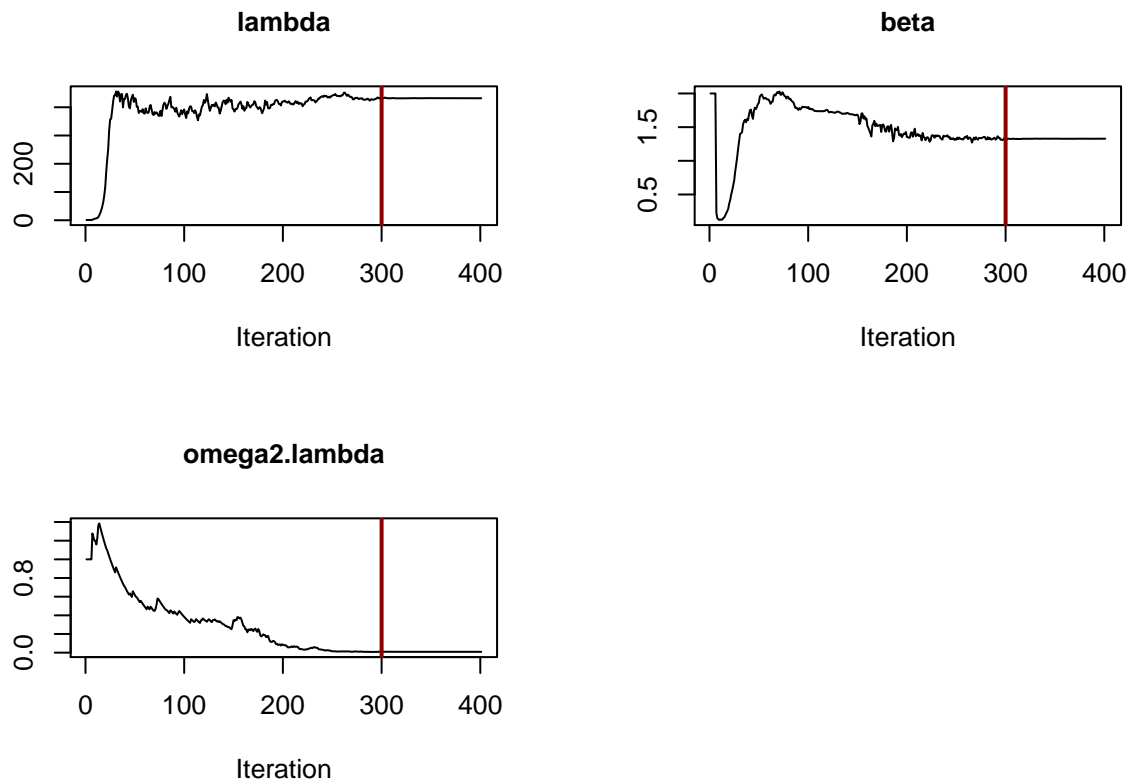
```

```

## ----- Fixed effects -----
## -----
##      Parameter Estimate SE    CV(%)
## [1,] lambda      431.8   51.60 12
## [2,] beta        1.3    0.19 14
## -----
## ----- Variance of random effects -----
## -----
##      Parameter      Estimate SE    CV(%)
## lambda omega2.lambda 0.009    0.17 1858
## -----
## ----- Correlation matrix of random effects -----
## -----
##              omega2.lambda
## omega2.lambda 1
## -----
## ----- Statistical criteria -----
## -----
## Likelihood computed by linearisation
##      -2LL= 5189.352
##      AIC = 5197.352
##      BIC = 5211.017
##
## Likelihood computed by importance sampling
##      -2LL= 2269.357
##      AIC = 2277.357
##      BIC = 2291.021
## -----
plot(tte.fit, plot.type="convergence")

## Plotting convergence plots

```



```
ypred<-predict(tte.fit)
```

```
## No fitted values of type ipred available
```

```
# Use survival package to assess Survival curve
```

```
if(FALSE) {
```

```
  library(survival)
```

```
  lung.surv<-lung.saemix[lung.saemix$time>0,]
```

```
  lung.surv$status<-lung.surv$status+1
```

```
  Surv(lung.surv$time, lung.surv$status) # 1=censored, 2=dead
```

```
  f1 <- survfit(Surv(time, status) ~ 1, data = lung.surv)
```

```
  xtim<-seq(0,max(lung.saemix$time), length.out=200)
```

```
  estpar<-tte.fit@results@fixed.effects
```

```
  estse<-tte.fit@results@se.fixed
```

```
  ypred<-exp(-(xtim/estpar[1])^(estpar[2]))
```

```
# Computing SE for the survival curve based on linearised FIM (probably not a good idea) through the de
```

```
  invfim<-solve(tte.fit@results@fim[1:2,1:2])
```

```
  xcal<- (xtim/estpar[1])^estpar[2]
```

```
  dsdbeta<- -log(xtim/estpar[1]) * xcal *exp(-xcal)
```

```
  dsdalpha<- estpar[2]/estpar[1] * xcal *exp(-xcal)
```

```
  xmat<-rbind(dsdalpha, dsdbeta)
```

```
  # x1<-t(xmat[,1:3]) %*% invfim %*% xmat[,1:3]
```

```
  sesurv<-rep(0,length(xcal))
```

```
  for(i in 1:length(xcal))
```

```
    sesurv[i]<-sqrt(t(xmat[,i]) %*% invfim %*% xmat[,i])
```

```
  plot(f1, xlab = "Days", ylab = "Overall survival probability")
```

```
  lines(xtim,ypred, col="red",lwd=2)
```

```
  lines(xtim,ypred+1.96*sesurv, col="red",lwd=1, lty=2)
```

```
  lines(xtim,ypred-1.96*sesurv, col="red",lwd=1, lty=2)
```

```
# ypred2<-exp(-(xtim/(estpar[1]-1.96*sqrt(invfim[1,1]))))^(estpar[2]+1.96*sqrt(invfim[2,2])))  
# ypred3<-exp(-(xtim/(estpar[1]+1.96*sqrt(invfim[1,1]))))^(estpar[2]+1.96*sqrt(invfim[2,2])))  
# lines(xtim,ypred2, col="blue",lwd=1, lty=2)  
# lines(xtim,ypred3, col="blue",lwd=1, lty=2)  
}
```

RTTE model

Exemple simulé de Belhal **TODO**