Package: phenoCDM (via r-universe)

October 13, 2026

Title Continuous Development Models for Incremental Time-Series Analysis

Version 0.1.3

Date 2018-05-01

Author Bijan Seyednasrollah, Jennifer J. Swenson, Jean-Christophe Domec, James S. Clark

Maintainer Bijan Seyednasrollah <bijan.s.nasr@gmail.com>

Description Using the Bayesian state-space approach, we developed a continuous development model to quantify dynamic incremental changes in the response variable. While the model was originally developed for daily changes in forest green-up, the model can be used to predict any similar process. The CDM can capture both timing and rate of nonlinear processes. Unlike statics methods, which aggregate variations into a single metric, our dynamic model tracks the changing impacts over time. The CDM accommodates nonlinear responses to variation in predictors, which changes throughout development.

Depends R (>= 3.3.0)

Imports rjags

License MIT + file LICENSE

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1.9000

BugReports https://github.com/bnasr/phenoCDM/issues

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Repository https://cran.r-universe.dev

Date/Publication 2018-05-02 02:45:15 UTC

RemoteUrl https://github.com/cran/phenoCDM

RemoteRef HEAD

RemoteSha bb6ad3eba4afd33623b2091f3d256bdc98784ebf

Contents

fitCDM 2
getGibbsSummary 3
phenoSim 4
phenoSimPlot 5
plotPOGibbs 6
plotPost 8

Index **10**

`fitCDM` *Fit a CDM Model*

Description

This function fits a CDM model on the input data as it is described by the phenoSim function.

Usage

```
fitCDM(x, z, connect = NULL, nGibbs = 1000, nBurnin = 1, n.adapt = 100,
  n.chains = 4, quiet = FALSE, calcLatentGibbs = FALSE, trend = +1)
```

Arguments

`x`	Matrix of predictors [N x p].
`z`	Vector of response values [N x 1].
`connect`	The connectivity matrix for the z vector [n x 2]. Each row contains the last and next elements of the time-series. NA values indicate not connected.
`nGibbs`	Number of MCMC itterations
`nBurnin`	Number of burn-in itterations.
`n.adapt`	Number of itterations for adaptive sampling
`n.chains`	Number of MCMC chains
`quiet`	logical value indicating whether to report the progress
`calcLatentGibbs`	logical value indicating whether to calculate the latent states
`trend`	time-series expected trend as -1:decreasing, +1:increasing, 0: not constrained

Examples

```
#Summarize CDM Model Ouput

ssSim <- phenoSim(nSites = 2, #number of sites
                  nTSet = 30, #number of Time steps
                  beta = c(1, 2), #beta coefficients
                  sig = .01, #process error
                  tau = .1, #observation error
                  plotFlag = TRUE, #whether plot the data or not
                  miss = 0.05, #fraction of missing data
                  ymax = c(6, 3) #maximum of saturation trajectory
)

ssOut <- fitCDM(x = ssSim$x, #predictors
                nGibbs = 200,
                nBurnin = 100,
                z = ssSim$z,#response
                connect = ssSim$connect, #connectivity of time data
                quiet=TRUE)

summ <- getGibbsSummary(ssOut, burnin = 100, sigmaPerSeason = FALSE)

colMeans(summ$ymax)
colMeans(summ$betas)
colMeans(summ$tau)
colMeans(summ$sigma)
```

`getGibbsSummary` *Summarize Output of the CDM Model*

Description

This function return a summary of the output from the Gibbs-Sampling of the CDM model.

Usage

```
getGibbsSummary(ssOut, burnin = NULL, colNames = NULL,
  sigmaPerSeason = TRUE)
```

Arguments

`ssOut`	CDM output list.
`burnin`	Number of burnin itterations .
`colNames`	vector of charachters includes names of each variable in the output.
`sigmaPerSeason`	logical value indicating whether each site/season has a separate process error

Examples

```
#Summarize CDM Model Ouput

ssSim <- phenoSim(nSites = 2, #number of sites
                  nTSet = 30, #number of Time steps
                  beta = c(1, 2), #beta coefficients
                  sig = .01, #process error
                  tau = .1, #observation error
                  plotFlag = TRUE, #whether plot the data or not
                  miss = 0.05, #fraction of missing data
                  ymax = c(6, 3) #maximum of saturation trajectory
)

ssOut <- fitCDM(x = ssSim$x, #predictors
                nGibbs = 200,
                nBurnin = 100,
                z = ssSim$z,#response
                connect = ssSim$connect, #connectivity of time data
                quiet=TRUE)

summ <- getGibbsSummary(ssOut, burnin = 100, sigmaPerSeason = FALSE)

colMeans(summ$ymax)
colMeans(summ$betas)
colMeans(summ$tau)
colMeans(summ$sigma)
```

---

phenoSim *Simulate Green-up Phenology Data*

Description

This function return a set of simulated data for multiple green-up phenology time-series.

Usage

```
phenoSim(nSites = 1000, nTSet = c(3:6), p = 2, beta = NULL, sig = 0.1,
  tau = 0.01, miss = 0, plotFlag = FALSE, ymax = 1, trend = +1)
```

Arguments

nSites	Number of sites/seasons
nTSet	A vector of integer values. Length of each time-series will be randomly sampled from this vector.
p	Number of predictors in the model.
beta	Beta coefficients
sig	Process error.

tau	Observation error.
miss	Fraction of missing data.
plotFlag	logical value indicating whether to plot the resulted time-series.
ymax	Asymptotic maximum values.
trend	time-series expected trend as -1:decreasing, +1:increasing, 0: not constrained

Examples

```
#Simulate Phenology Data
ssSim <- phenoSim(nSites = 2, #number of sites
                  nTSet = 30, #number of time steps
                  beta = c(1, 2), #beta coefficients
                  sig = .01, #process error
                  tau = .1, #observation error
                  plotFlag = TRUE, #whether plot the data or not
                  miss = 0.05, #fraction of missing data
                  ymax = c(6, 3) #maximum of saturation trajectory
)
```

---

phenoSimPlot *Plot Simulated Phenology Data*

Description

This function plots the time-series data described with a connectivity matrix.

Usage

```
phenoSimPlot(z, connect, add = FALSE, col = "blue", ylim = range(z, na.rm
  = TRUE), pch = 1, lwd = 1)
```

Arguments

z	A vector of time-series data [n x 1]
connect	The connectivity matrix for the z vector [n x 2]. Each row contains the last and next elements of the time-series. NA values means not connected.
add	logical value indicating whether the plot should be overlaid on the current panel.
col	The color variable as charachter
ylim	Range of the y axis
pch	pch value for the symbols
lwd	lwd value for line tickness

Examples

```
#Simulate Phenology Data
ssSim <- phenoSim(nSites = 2, #number of sites
                  nTSet = 30, #number of time steps
                  beta = c(1, 2), #beta coefficients
                  sig = .01, #process error
                  tau = .1, #observation error
                  plotFlag = TRUE, #whether plot the data or not
                  miss = 0.05, #fraction of missing data
                  ymax = c(6, 3) #maximum of saturation trajectory
)

#Plot Simulated Data
phenoSimPlot(ssSim$z, ssSim$connect)
```

`plotPOGibbs` *Plot Observed vs Predicted*

Description

This function plot posterior distributions of the parameters.

Usage

```
plotPOGibbs(o, p, nburnin = NULL, xlim = range(o, na.rm = TRUE),
  ylim = range(p, na.rm = TRUE), xlab = "Observed", ylab = "Predicted",
  colSet = c("#fb8072", "#80b1d3", "black"), cex = 1, lwd = 2, pch = 19)
```

Arguments

`o`	Observed vector
`p`	Predicted Gibbs samples
`nburnin`	numbe of burn-in itterations
`xlim`	x-axis range
`ylim`	y-axis range
`xlab`	x-axis label
`ylab`	y-axis label
`colSet`	vector of colors for points, bars and the 1:1 line
`cex`	cex value for size
`lwd`	line width
`pch`	pch value for symbols

Examples

```
ssSim <- phenoSim(nSites = 2, #number of sites
                  nTSet = 30, #number of Time steps
                  beta = c(1, 2), #beta coefficients
                  sig = .01, #process error
                  tau = .1, #observation error
                  plotFlag = TRUE, #whether plot the data or not
                  miss = 0.05, #fraction of missing data
                  ymax = c(6, 3) #maximum of saturation trajectory
)

ssOut <- fitCDM(x = ssSim$x, #predictors
                nGibbs = 200,
                nBurnin = 100,
                z = ssSim$z,#response
                connect = ssSim$connect, #connectivity of time data
                quiet=TRUE)

summ <- getGibbsSummary(ssOut, burnin = 100, sigmaPerSeason = FALSE)

colMeans(summ$ymax)
colMeans(summ$betas)
colMeans(summ$tau)
colMeans(summ$sigma)

par(mfrow = c(1,3), oma = c(1,1,3,1), mar=c(2,2,0,1), font.axis=2)

plotPost(chains = ssOut$chains[,c("beta.1", "beta.2")], trueValues = ssSim$beta)
plotPost(chains = ssOut$chains[,c("ymax.1", "ymax.2")], trueValues = ssSim$ymax)
plotPost(chains = ssOut$chains[,c("sigma", "tau")], trueValues = c(ssSim$sig, ssSim$tau))

mtext('Posterior distributions of the parameters', side = 3, outer = TRUE, line = 1, font = 2)
legend('topleft', legend = c('posterior', 'true value'),
     col = c('black', 'red'), lty = 1, bty = 'n', cex=1.5, lwd =2)


yGibbs <- ssOut$latentGibbs
zGibbs <- ssOut$zpred
o <- ssOut$data$z
p <- apply(ssOut$rawsamples$y, 1, mean)
R2 <- cor(na.omit(cbind(o, p)))[1,2]^2
#Plot Observed vs Predicted
par( mar=c(4,4,1,1), font.axis=2)
plotPOGibbs(o = o , p = zGibbs,
            xlim = c(0,10), ylim=c(0,10),
            cex = .7, nburnin = 1000)
            points(o, p, pch = 3)

mtext(paste0('R² = ', signif(R2, 3)), line = -1, cex = 2, font = 2, side = 1, adj = .9)
legend('topleft', legend = c('mean', '95th percentile', '1:1 line', 'latent states'),
      col = c('#fb8072','#80b1d3','black', 'black'),
      bty = 'n', cex=1.5,
```

```
        lty = c(NA, 1, 2, NA), lwd =c(NA, 2, 2, 2), pch = c(16, NA, NA, 3))
```

---

plotPost *Plot Posterior Distributions*

Description

This function plot posterior distributions of the parameters.

Usage

```
plotPost(chains, trueValues = NULL, outline = FALSE)
```

Arguments

chains	Gibbs sampling chains
trueValues	numeric vector of true values
outline	logical value whether showing outliers

Examples

```
ssSim <- phenoSim(nSites = 2, #number of sites
                  nTSet = 30, #number of Time steps
                  beta = c(1, 2), #beta coefficients
                  sig = .01, #process error
                  tau = .1, #observation error
                  plotFlag = TRUE, #whether plot the data or not
                  miss = 0.05, #fraction of missing data
                  ymax = c(6, 3) #maximum of saturation trajectory
)

ssOut <- fitCDM(x = ssSim$x, #predictors
                nGibbs = 200,
                nBurnin = 100,
                z = ssSim$z,#response
                connect = ssSim$connect, #connectivity of time data
                quiet=TRUE)

summ <- getGibbsSummary(ssOut, burnin = 100, sigmaPerSeason = FALSE)

colMeans(summ$ymax)
colMeans(summ$betas)
colMeans(summ$tau)
colMeans(summ$sigma)

par(mfrow = c(1,3), oma = c(1,1,3,1), mar=c(2,2,0,1), font.axis=2)

plotPost(chains = ssOut$chains[,c("beta.1", "beta.2")], trueValues = ssSim$beta)
```

```
plotPost(chains = ssOut$chains[,c("ymax.1", "ymax.2")], trueValues = ssSim$ymax)
plotPost(chains = ssOut$chains[,c("sigma", "tau")], trueValues = c(ssSim$sig, ssSim$tau))

mtext('Posterior distributions of the parameters', side = 3, outer = TRUE, line = 1, font = 2)
legend('topleft', legend = c('posterior', 'true value'), col = c('black', 'red'),
         lty = 1, bty = 'n', cex=1.5, lwd =2)
```

Index

∗ **CDM**
fitCDM, 2
∗ **Data**
phenoSim, 4
phenoSimPlot, 5
∗ **Distributions**
plotPost, 8
∗ **Fit**
fitCDM, 2
∗ **Gibbs**
getGibbsSummary, 3
∗ **Model**
fitCDM, 2
∗ **Observed**
plotPOGibbs, 6
∗ **Output**
getGibbsSummary, 3
∗ **Phenology**
phenoSim, 4
phenoSimPlot, 5
∗ **Plot**
phenoSimPlot, 5
plotPOGibbs, 6
plotPost, 8
∗ **Posterior**
plotPost, 8
∗ **Predicted**
plotPOGibbs, 6
∗ **Sammary**
getGibbsSummary, 3
∗ **Sampling**
getGibbsSummary, 3
∗ **Simulated**
phenoSimPlot, 5
∗ **Simulate**
phenoSim, 4
∗ **vs**
plotPOGibbs, 6

fitCDM, 2

getGibbsSummary, 3

phenoSim, 4
phenoSimPlot, 5
plotPOGibbs, 6
plotPost, 8