simulation & inference of transients

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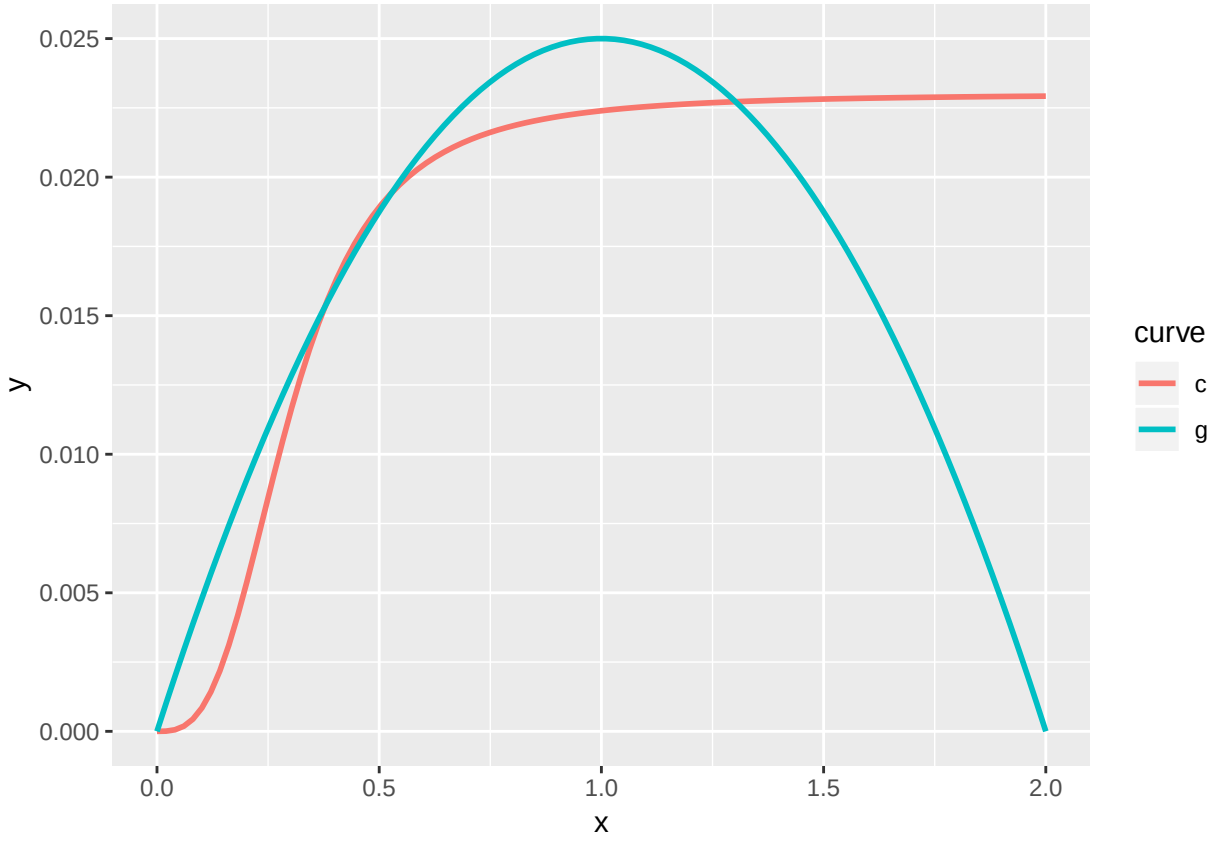
```
library(tidyverse)
```

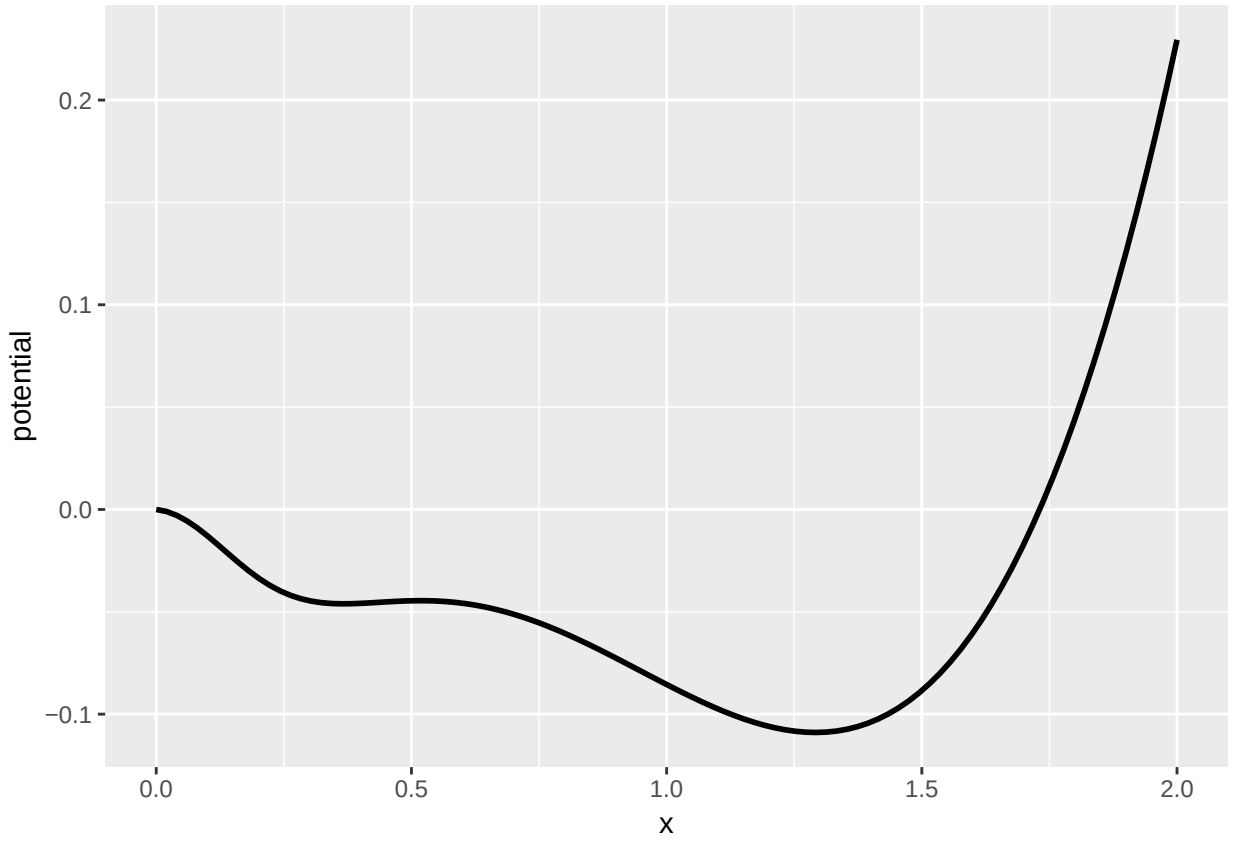
```
N <- 1e4
r <- 0.05; K <- 2
a <- 0.023; H <- 0.3; Q <- 3
x0 <- 0.2; sigma <- 0.02
growth <- function(x, r, K) x * r * (1 - x / K)
consumption <- function(x, a, H, Q) a * x^Q / (x^Q + H^Q)
```

```
theory <-
  tibble(x = seq(0,K, length.out = 100)) %>%
  mutate(g = growth(x, r, K),
         c = consumption(x, a, H, Q)) %>%
  mutate(potential = - cumsum(g - c)) %>%
  gather(curve, y, -x, -potential)
```

```
theory %>%
  ggplot(aes(x, y, col = curve)) +
  geom_line(lwd = 1)
```



```
theory %>%
  ggplot(aes(x, potential)) +
  geom_line(lwd = 1)
```




```
library(nimble)
```

```
## nimble version 0.8.0 is loaded.
## For more information on NIMBLE and a User Manual,
## please visit http://R-nimble.org.
```

```
##
## Attaching package: 'nimble'
```

```
## The following object is masked from 'package:stats':
##
##     simulate
```

```
## define truncated normal distribution ----
dtruncnorm <- nimbleFunction(
  run = function(x = double(0), mean = double(0),
                 sd = double(0), log = integer(0, default = 0)) {
    returnType(double(0))
    log_prob <- dnorm(x = x, mean = mean, sd = sd, log = 1) -
      pnorm(q = 0, mean = -mean, sd = sd, log = 1)
    if(log) return(log_prob)
    else return(exp(log_prob))
  })
rtruncnorm <- nimbleFunction(
  run = function(n = integer(0, default = 1), mean = double(0),
```

```
                sd = double(0)) {
    returnType(double(0))
    if(n != 1) print("rtruncnorm only allows n = 1; using n = 1.")
    draw <- rnorm(n = 1, mean = mean, sd = sd)
    while(draw < 0)
      draw <- rnorm(n = 1, mean = mean, sd = sd)
    return(draw)
  })
# Define stochastic model in BUGS notation ----
may <- nimble::nimbleCode({
  log(r) ~ dnorm(mu_r, sd_r)
  log(K) ~ dnorm(mu_K, sd_K)
  log(a) ~ dnorm(mu_a, sd_a)
  log(H) ~ dnorm(mu_H, sd_H)
  log(Q) ~ dnorm(mu_Q, sd_Q)
  x0 ~ dtruncnorm(mu_x0, sd_x0)
  log(sigma) ~ dnorm(mu_sigma, sd_sigma)
  x[1] <- x0
  for(t in 1:(N - 1)){
    mu[t] <- x[t] + x[t] * r * (1 - x[t] / K) - a * x[t]^Q / (x[t]^Q + H^Q)
    x[t + 1] ~ dtruncnorm(mean = mu[t], sd = sigma)
  }
})
# constants ----
constants <- list(
  mu_r = log(r), sd_r = 1,
  mu_K = log(K), sd_K = 1,
  mu_a = log(a), sd_a = 1,
  mu_H = log(H), sd_H = 1,
  mu_Q = log(Q), sd_Q = 1,
  mu_x0 = x0, sd_x0 = 1,
  mu_sigma = log(sigma), sd_sigma = 1
)
## inits ----
inits <- list("log_r" = log(r), "log_K" = log(K),
              "log_a" = log(a), "log_H" = log(H), "log_Q" = log(Q),
              "log_sigma" = log(sigma), "x0" = x0)
# define and compile model ----
model <- nimbleModel(code = may, constants = constants, inits = inits)
```

```
## defining model...
```

```
## Registering the following user-provided distributions: dtruncnorm .
## NIMBLE has registered dtruncnorm as a distribution based on its use in BUGS code. Note that if you ma
```

```
## building model...
```

```
## setting data and initial values...
```

```
## running calculate on model (any error reports that follow may simply reflect missing values in model
## checking model sizes and dimensions... This model is not fully initialized. This is not an error. To
## model building finished.
```

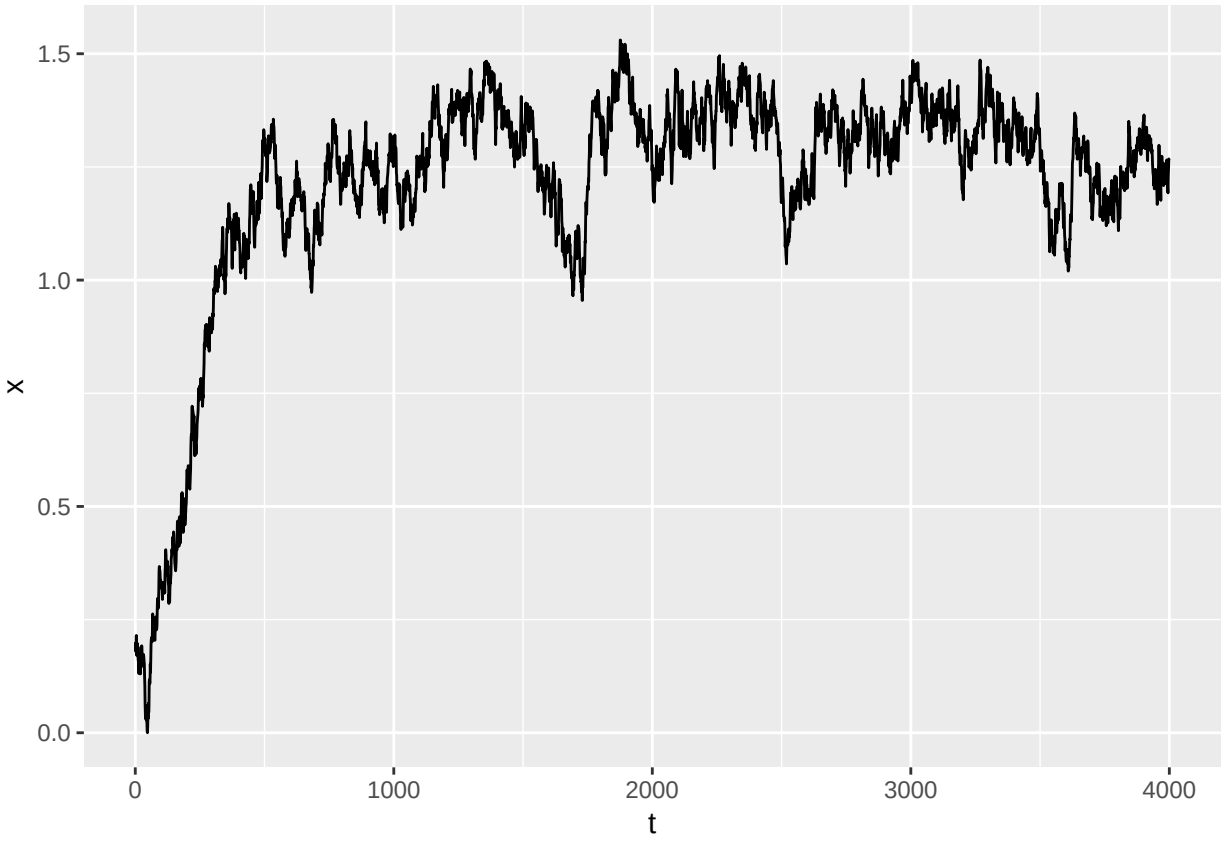
```
cmodel <- compileNimble(model)
```

```
## compiling... this may take a minute. Use 'showCompilerOutput = TRUE' to see C++ compilation details.
```

```
## compilation finished.
```

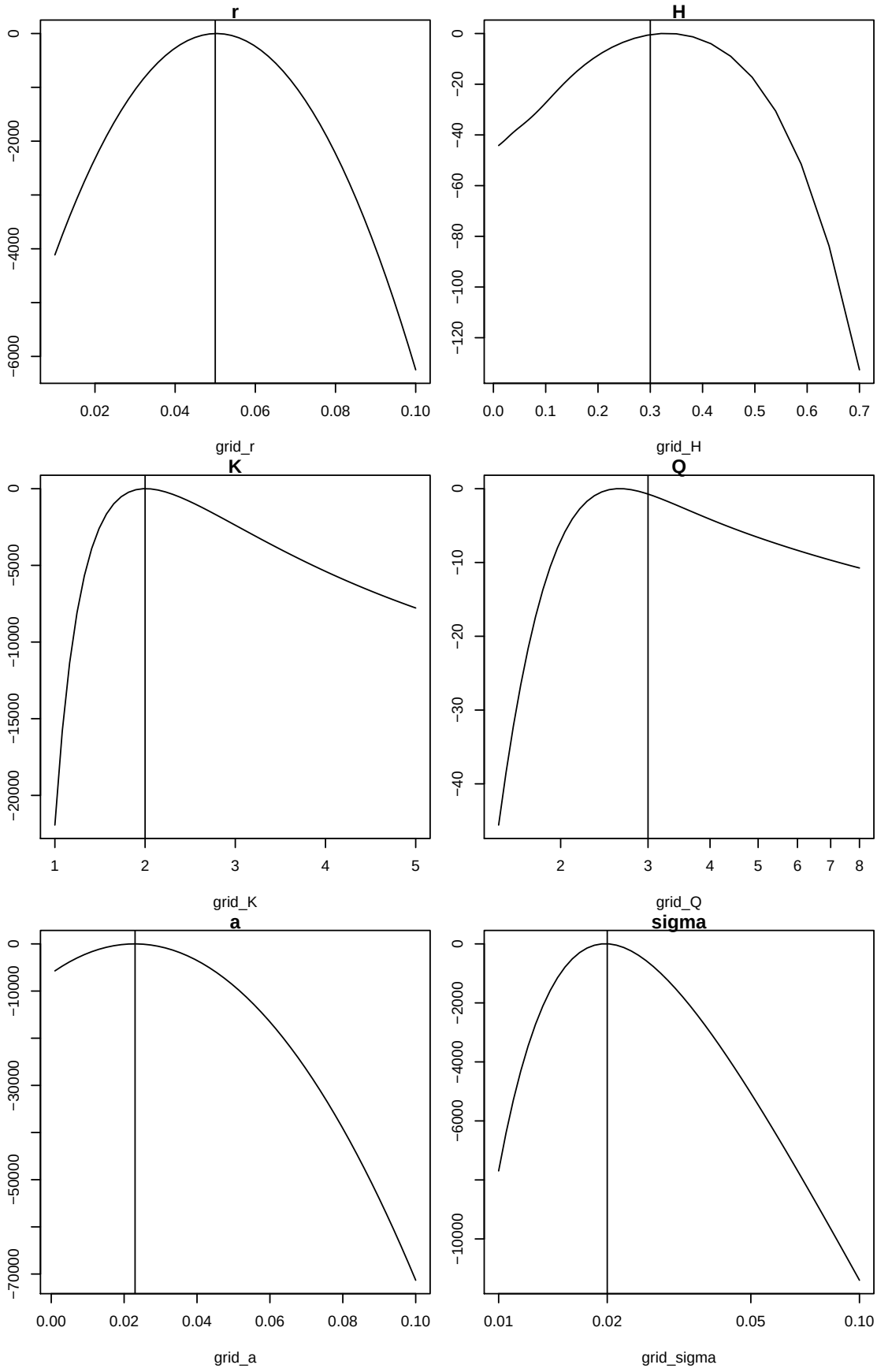
```
set.seed(1234)
simulate(cmodel, nodes = c('x', 'mu'))
df <- tibble(t = seq_along(cmodel$x), x = cmodel$x)
```

```
df %>% filter(t < 4000) %>% ggplot(aes(t, x)) + geom_line()
```



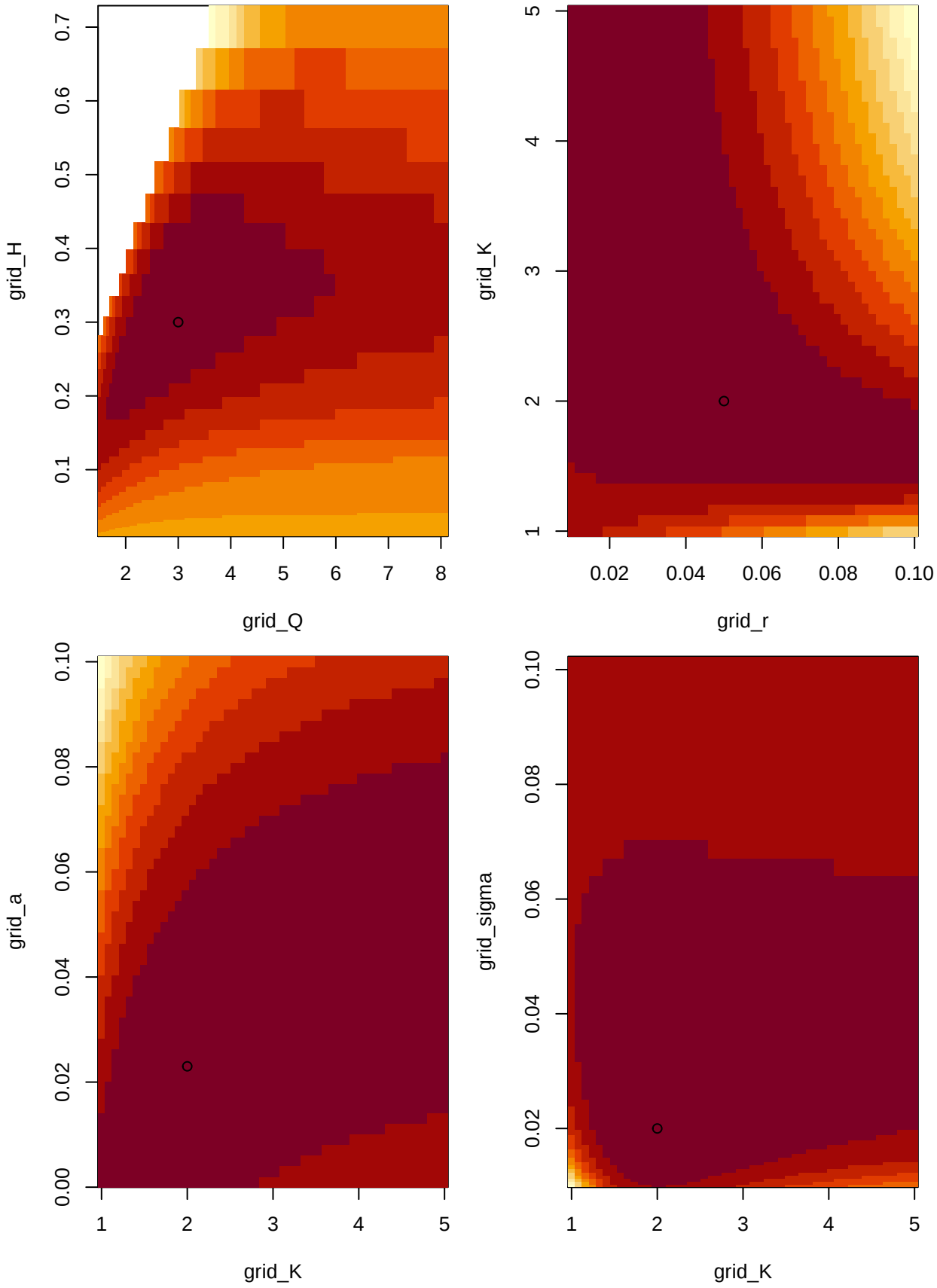

```
dnorm_mod <- function(x, mean, sd, log = T){
  dnorm(x = x, mean = mean, sd = sd, log = log) -
    log(1 - pnorm(q = 0, mean = mean, sd = sd))
}
get_ll <- function(x, r, K, a, H, Q, sigma){
  TIME <- length(x)
  mu <- x + x * r * (1 - x / K) - a * x^Q / (x^Q + H^Q)
  sum(dnorm_mod(x = x[-1], mean = mu[-TIME], sd = sigma, log = T))
}
##
grid_r <- seq(1e-2, 1e-1, l=5e1)
ll_r <- sapply(grid_r, function(r) get_ll(a = cmodel$a, x = cmodel$x, r = r, K = cmodel$K,
                                          H = cmodel$H, Q = cmodel$Q, sigma = cmodel$sigma))
##
grid_K <- seq(1, 5, l=5e1)
ll_K <- sapply(grid_K, function(K) get_ll(a = cmodel$a, x = cmodel$x, r = cmodel$r, K = K,
                                          H = cmodel$H, Q = cmodel$Q, sigma = cmodel$sigma))
##
grid_a <- seq(1e-3, 1e-1, l=5e1)
ll_a <- sapply(grid_a, function(a) get_ll(a = a, x = cmodel$x, r = cmodel$r, K = cmodel$K,
```

```
                                          H = cmodel$H, Q = cmodel$Q, sigma = cmodel$sigma))
##
grid_H <- exp(seq(log(1e-2), log(0.7), l=5e1))
ll_H <- sapply(grid_H, function(H) get_ll(a = cmodel$a, x = cmodel$x, r = cmodel$r, K = cmodel$K,
                                          H = H, Q = cmodel$Q, sigma = cmodel$sigma))
##
grid_Q <- exp(seq(log(1.5), log(8), l=5e1))
ll_Q <- sapply(grid_Q, function(Q) get_ll(a = cmodel$a, x = cmodel$x, r = cmodel$r, K = cmodel$K,
                                          H = cmodel$H, Q = Q, sigma = cmodel$sigma))
##
grid_sigma <- exp(seq(log(1e-2), log(1e-1), l=5e1))
ll_sigma <- sapply(grid_sigma, function(sigma)
  get_ll(a = cmodel$a, x = cmodel$x, r = cmodel$r, K = cmodel$K,
         H = cmodel$H, Q = cmodel$Q, sigma = sigma))
##
layout(matrix(1:6, 3, 2)); par(mar = c(4.1, 2, 1, 1))
plot(grid_r, (ll_r - max(ll_r)), type = "l", main = "r")
abline(v = cmodel$r)
plot(grid_K, (ll_K - max(ll_K)), type = "l", main = "K")
abline(v = cmodel$K)
plot(grid_a, (ll_a - max(ll_a)), type = "l", main = "a")
abline(v = cmodel$a)
plot(grid_H, (ll_H - max(ll_H)), type = "l", main = "H")
abline(v = cmodel$H)
plot(grid_Q, (ll_Q - max(ll_Q)), type = "l", main = "Q", log = "x")
abline(v = cmodel$Q)
plot(grid_sigma, (ll_sigma - max(ll_sigma)), log = "x", type = "l", main = "sigma")
abline(v = cmodel$sigma)
```


r
0
−2000
−4000
−6000
0.02
0.04
0.06
0.08
0.10
grid_r
H
0
−20
−40
−60
−80
−100
−120
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
grid_H
K
0
−5000
−10000
−15000
−20000
1
2
3
4
5
grid_K
Q
0
−10
−20
−30
−40
2
3
4
5
6
7
8
grid_Q
a
0
−10000
−30000
−50000
−70000
0.00
0.02
0.04
0.06
0.08
0.10
grid_a
sigma
0
−2000
−4000
−6000
−10000
0.01
0.02
0.05
0.10
grid_sigma

```
ll_QH <- apply(expand.grid(grid_Q, grid_H), 1, function(pair)
  if(pair[2] > (0.6 / 3) * pair[1] + 0.18 - (0.6 / 3)) NA else
  get_ll(a = cmodel$a, x = cmodel$x, r = cmodel$r, K = cmodel$K,
         H = pair[2], Q = pair[1], sigma = cmodel$sigma))
ll_Ka <- apply(expand.grid(grid_K, grid_a), 1, function(pair)
  get_ll(a = pair[2], x = cmodel$x, r = cmodel$r, K = pair[1],
         H = cmodel$H, Q = cmodel$Q, sigma = cmodel$sigma))
ll_rK <- apply(expand.grid(grid_r, grid_K), 1, function(pair)
  get_ll(x = cmodel$x, r = pair[1], K = pair[2], a = cmodel$a,
         H = cmodel$H, Q = cmodel$Q, sigma = cmodel$sigma))
ll_Ksigma <- apply(expand.grid(grid_K, grid_sigma), 1, function(pair)
  get_ll(x = cmodel$x, r = cmodel$r, K = pair[1], a = cmodel$a,
         H = cmodel$H, Q = cmodel$Q, sigma = pair[2]))
```

```
layout(matrix(1:4, 2, 2)); par(mar = c(4, 4, 1, 1))
image(grid_Q, grid_H, matrix((ll_QH - max(ll_QH, na.rm = T)), length(grid_Q), length(grid_H)))
points(cmodel$Q, cmodel$H)
##
image(grid_K, grid_a, matrix((ll_Ka - max(ll_Ka)), length(grid_K), length(grid_a)))
points(cmodel$K, cmodel$a)
##
image(grid_r, grid_K, matrix((ll_rK - max(ll_rK)), length(grid_r), length(grid_K)))
points(cmodel$r, cmodel$K)
##
image(grid_K, grid_sigma, matrix((ll_Ksigma - max(ll_Ksigma)), length(grid_a), length(grid_sigma)))
points(cmodel$K, cmodel$sigma)
```


grid_H
0.1
0.2
0.3
0.4
0.5
0.6
0.7
2
3
4
5
6
7
8
grid_Q
grid_K
1
2
3
4
5
0.02
0.04
0.06
0.08
0.10
grid_r
grid_a
0.00
0.02
0.04
0.06
0.08
0.10
1
2
3
4
5
grid_K
grid_sigma
0.02
0.04
0.06
0.08
0.10
1
2
3
4
5
grid_K

```
model$setData(x = cmodel$x)
cmodel <- compileNimble(model)
```

```
## compiling... this may take a minute. Use 'showCompilerOutput = TRUE' to see C++ compilation details.
```

```
## compilation finished.
```

```
## block sampler
system.time({
  mcmcConf <- configureMCMC(model)
  mcmcConf$getSamplers()
  mcmcConf$removeSamplers(c("x0"))
  mcmcConf$addSampler(target = c("log_r", "log_K", "log_a",
                                 "log_H", "log_Q", "log_sigma"),
                      type = 'RW_block')
  mcmcConf$getSamplers()
})
```

```
## Note: Assigning an RW_block sampler to nodes with very different scales can result in low MCMC effic
```

```
##    user  system elapsed
##   9.735   0.175  10.645
```

```
system.time({
  mcmc <- buildMCMC(mcmcConf)
  Cmcmc <- compileNimble(mcmc, project = model)
})
```

```
## compiling... this may take a minute. Use 'showCompilerOutput = TRUE' to see C++ compilation details.
## compilation finished.
```

```
##    user  system elapsed
##  21.160   0.902  23.356
```

```
##
n_iterations <- 1e4
system.time({
  Cmcmc$run(n_iterations, nburnin = n_iterations / 2)
})
```

```
## |-------------|-------------|-------------|-------------|
## |-------------------------------------------------------|
```

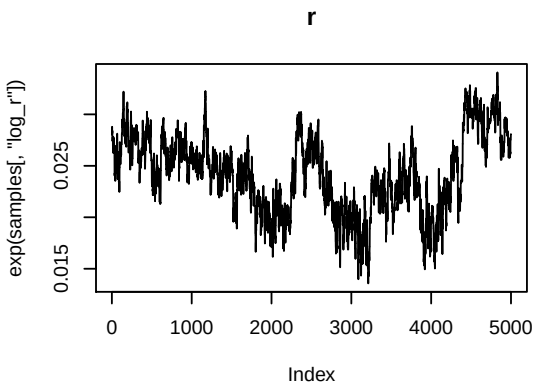
```
##    user  system elapsed
## 176.013   2.631 198.411
```

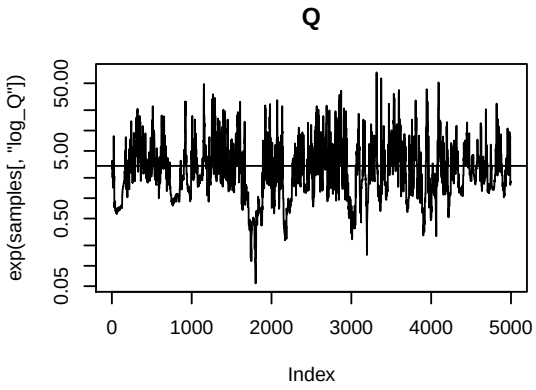
```
samples <- as.matrix(Cmcmc$mvSamples)
```

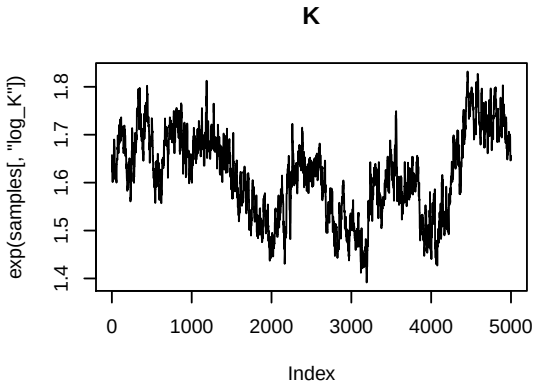
```
layout(matrix(1:8, 4, 2))
plot(exp(samples[, 'log_r']), type = "l", main = "r")
abline(h = r)
plot(exp(samples[, 'log_K']), type = "l", main = "K")
abline(h = K)
plot(exp(samples[, 'log_a']), type = "l", main = "a",
     ylim = range(exp(samples[, 'log_a']), a))
abline(h = a)
plot(exp(samples[, 'log_H']), type = "l", main = "H")
abline(h = H)
plot(exp(samples[, 'log_Q']), type = "l", main = "Q", log = "y")
```

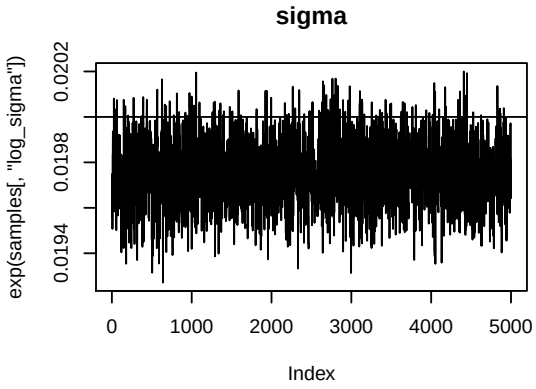
```
abline(h = Q)
plot(exp(samples[, 'log_sigma']), type = "l", main = "sigma")
abline(h = sigma)
plot(samples[, 'x0'], type = "l", main = "x0")
abline(h = x0)
corrplot::corrplot(cor(samples[, c("log_r", "log_K", "log_a", "log_H", "log_Q", "log_sigma", "x0")]))
```

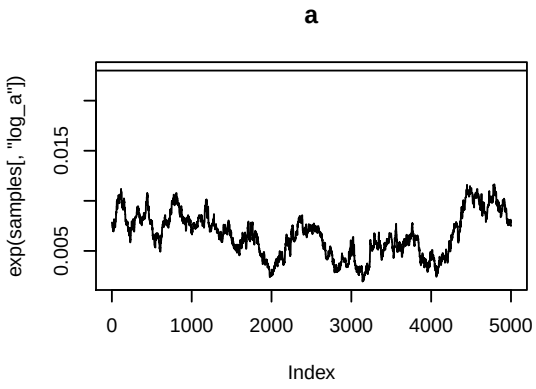
```
## Warning in cor(samples[, c("log_r", "log_K", "log_a", "log_H", "log_Q", :
## the standard deviation is zero
```

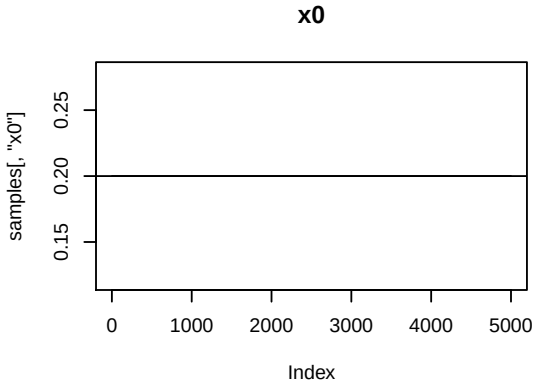

r
exp(samples[, "log_r"])
0.015
0.025
0
1000
2000
3000
4000
5000
Index

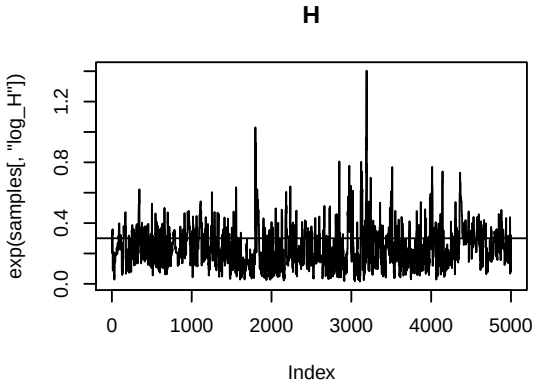

Q
exp(samples[, "log_Q"])
0.05
0.50
5.00
50.00
0
1000
2000
3000
4000
5000
Index

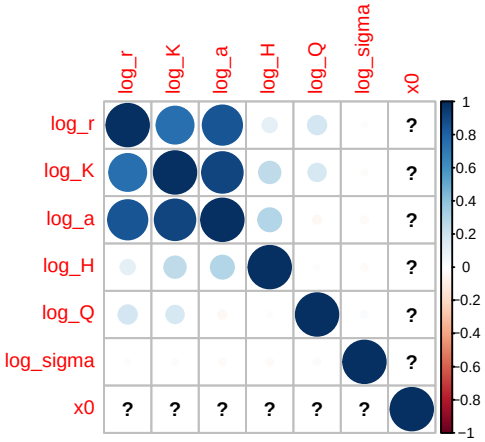

K
exp(samples[, "log_K"])
1.4
1.5
1.6
1.7
1.8
0
1000
2000
3000
4000
5000
Index


sigma
exp(samples[, "log_sigma"])
0.0194
0.0198
0.0202
0
1000
2000
3000
4000
5000
Index

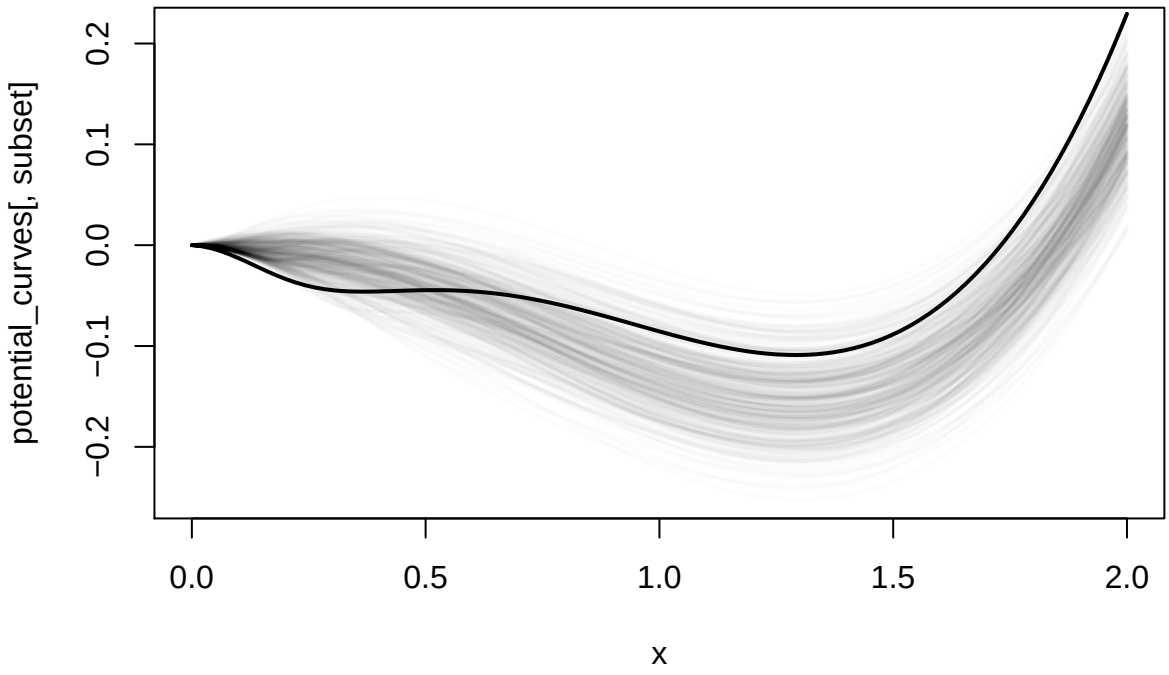

a
exp(samples[, "log_a"])
0.005
0.015
0
1000
2000
3000
4000
5000
Index


x0
samples[, "x0"]
0.15
0.20
0.25
0
1000
2000
3000
4000
5000
Index


H
exp(samples[, "log_H"])
0.0
0.4
0.8
1.2
0
1000
2000
3000
4000
5000
Index


log_r
log_K
log_a
log_H
log_Q
log_sigma
x0
?
1
0.8
0.6
0.4
0.2
0
−0.2
−0.4
−0.6
−0.8
−1

```
x <- seq(0, 2, l=1e2)
potential <- function(x = seq(0, 2, l = 1e2), a, r, H, Q, K){
  - cumsum(growth(x = x, r = r, K = K) -
           consumption(x = x, a = a, H = H, Q = Q))
}
potential_curves <- apply(samples, 1, function(row){
  potential(x = x, a = exp(row['log_a']), r = exp(row['log_r']),
            H = exp(row['log_H']), Q = exp(row['log_Q']), K = exp(row['log_K']))
})
subset <- sample(1:nrow(samples), min(400, nrow(samples)))
matplot(x, potential_curves[, subset], type = "l", lty = 1,
        col = scales::alpha(1, 1e-2), lwd = 2)
lines(x, potential(x = x, a = a, r = r, H = H, Q = Q, K = K), lwd = 2)
```



Notice a, r, and K are highly correlated. Taking out two of them stablizes somewhat, but dependence in the posterior distributions arises between other variables.

```
## block sampler
system.time({
  mcmcConf <- configureMCMC(model)
  mcmcConf$getSamplers()
  mcmcConf$removeSamplers(c("log_a", "log_K", "x0"))
  mcmcConf$addSampler(target = c("log_r", "log_H", "log_Q", "log_sigma"),
                      type = 'RW_block')
  mcmcConf$getSamplers()
})
```

```
## Note: Assigning an RW_block sampler to nodes with very different scales can result in low MCMC effici
```

```
##    user  system elapsed
##   9.095   0.143   9.487
```

```
system.time({
  mcmc <- buildMCMC(mcmcConf)
```

```
  Cmcmc <- compileNimble(mcmc, project = model, resetFunctions = T)
})
```

```
## compiling... this may take a minute. Use 'showCompilerOutput = TRUE' to see C++ compilation details.
```

```
## compilation finished.
```

```
##    user  system elapsed
##  20.335   0.855  21.855
```

```
##
n_iterations <- 1e4
system.time({
  Cmcmc$run(n_iterations, nburnin = n_iterations / 2)
})
```

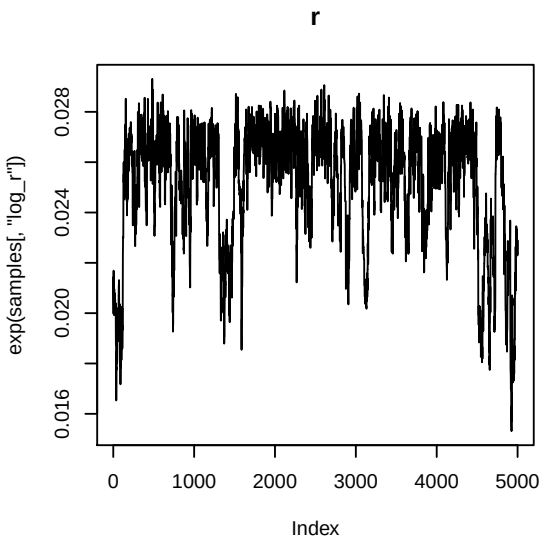
```
## |-------------|-------------|-------------|-------------|
## |-------------------------------------------------------|
```

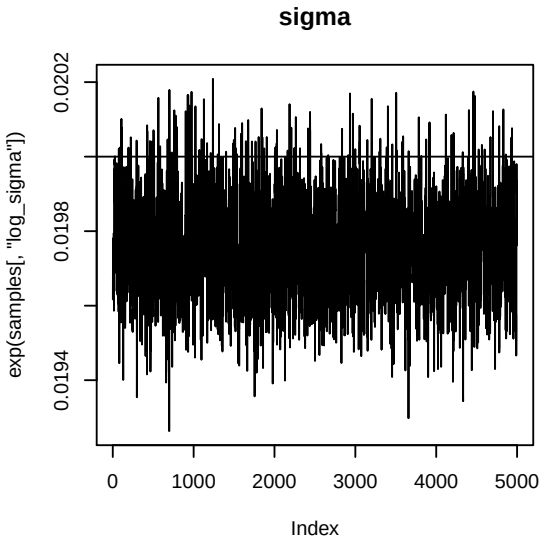
```
##    user  system elapsed
## 115.383   1.124 118.517
```

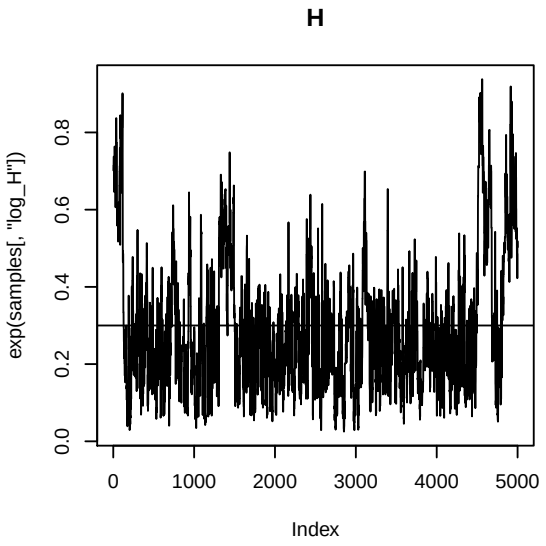
```
samples <- as.matrix(Cmcmc$mvSamples)
```

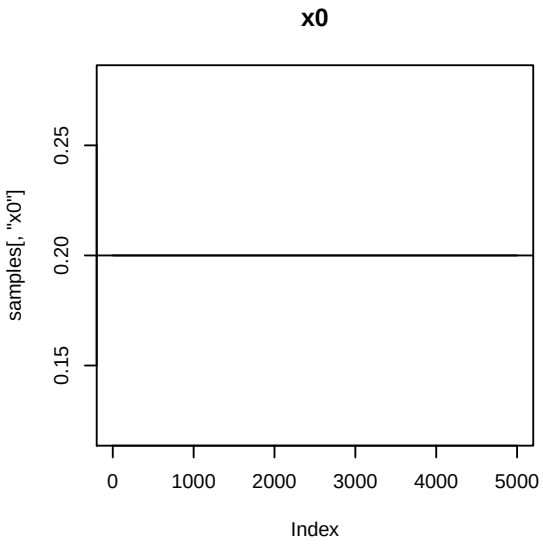
```
layout(matrix(1:6, 3, 2))
plot(exp(samples[, 'log_r']), type = "l", main = "r")
abline(h = r)
plot(exp(samples[, 'log_H']), type = "l", main = "H")
abline(h = H)
plot(exp(samples[, 'log_Q']), type = "l", main = "Q", log = "y")
abline(h = Q)
plot(exp(samples[, 'log_sigma']), type = "l", main = "sigma")
abline(h = sigma)
plot(samples[, 'x0'], type = "l", main = "x0")
abline(h = x0)
corrplot::corrplot(cor(samples[, c("log_r", "log_H", "log_Q", "log_sigma", "x0")]))
```

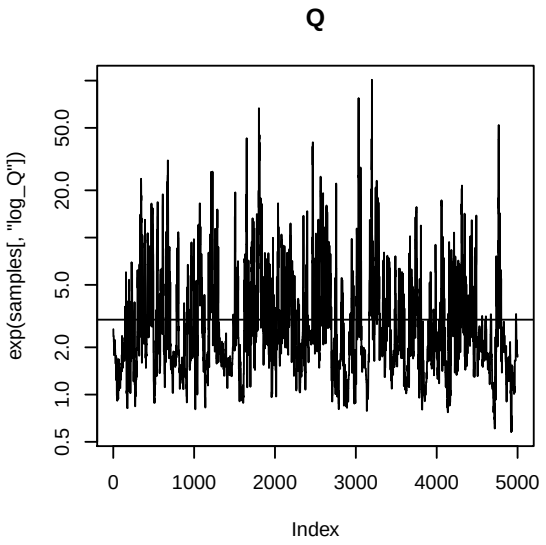
```
## Warning in cor(samples[, c("log_r", "log_H", "log_Q", "log_sigma", "x0")]):
## the standard deviation is zero
```

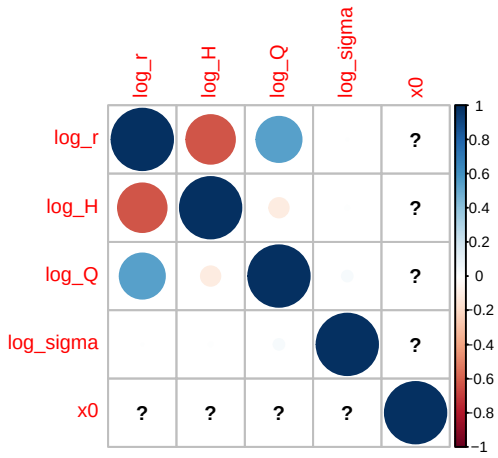

r
exp(samples[, "log_r"])
0.016
0.020
0.024
0.028
0
1000
2000
3000
4000
5000
Index


sigma
exp(samples[, "log_sigma"])
0.0194
0.0198
0.0202
0
1000
2000
3000
4000
5000
Index


H
exp(samples[, "log_H"])
0.0
0.2
0.4
0.6
0.8
0
1000
2000
3000
4000
5000
Index


x0
samples[, "x0"]
0.15
0.20
0.25
0
1000
2000
3000
4000
5000
Index


Q
exp(samples[, "log_Q"])
0.5
1.0
2.0
5.0
20.0
50.0
0
1000
2000
3000
4000
5000
Index


log_r
log_H
log_Q
log_sigma
x0
?
1
0.8
0.6
0.4
0.2
0
−0.2
−0.4
−0.6
−0.8
−1

```r
x <- seq(0, 2, l=1e2)
potential <- function(x = seq(0, 2, l = 1e2), a = a, r, H, Q, K = 2){
  - cumsum(growth(x = x, r = r, K = K) -
           consumption(x = x, a = a, H = H, Q = Q))
}
potential_curves <- apply(samples, 1, function(row){
  potential(x = x, a = a, r = exp(row['log_r']),
            H = exp(row['log_H']), Q = exp(row['log_Q']), K = K)
})
subset <- sample(1:nrow(samples), min(400, nrow(samples)))
matplot(x, potential_curves[, subset], type = "l", lty = 1,
        col = scales::alpha(1, 1e-2), lwd = 2)
lines(x, potential(x = x, a = a, r = r, H = H, Q = Q, K = K), lwd = 2)
```