# VectorBiTE Methods Training
# Bayesian State Space Modeling for Time Series Data

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- We will discuss fitting non-linear SSMs in `JAGS`

# Fitting State Space Models

- We have discussed how to fit NDLMs, but what happens when we have models that are non-linear or non-Gaussian?
- This brings us into a much broader topic - non-linear SSMs
- We will discuss fitting non-linear SSMs in `JAGS`
- Motivate the use of other packages, like `nimbleSMC`

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- There are (usually) no analytic full conditional distributions
- This means that `JAGS` will just do a brute force MCMC-MH to estimate all the parameters and latent states
- Brute force with `JAGS` works sometimes, but we will cover some alternative methods

# Non-linear SSM in JAGS

Recall the SSM from the first presentation,

$$
\begin{aligned}
x_t &= \frac{x_{t-1}}{2} + 25\frac{x_{t-1}}{1+x_{t-1}^2} + 8\cos(1.2t) + \epsilon_{proc} \\
y_t &= \frac{x_t^2}{20} + \epsilon_{obs} \\
\epsilon_{proc} &\sim N(0,\phi), \epsilon_{obs} \sim N(0,\tau)
\end{aligned}
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This is a common test function in SSM literature (see *Andrieu, Doucet, and Holenstein* for example) because it is a bit of a nightmare to fit.

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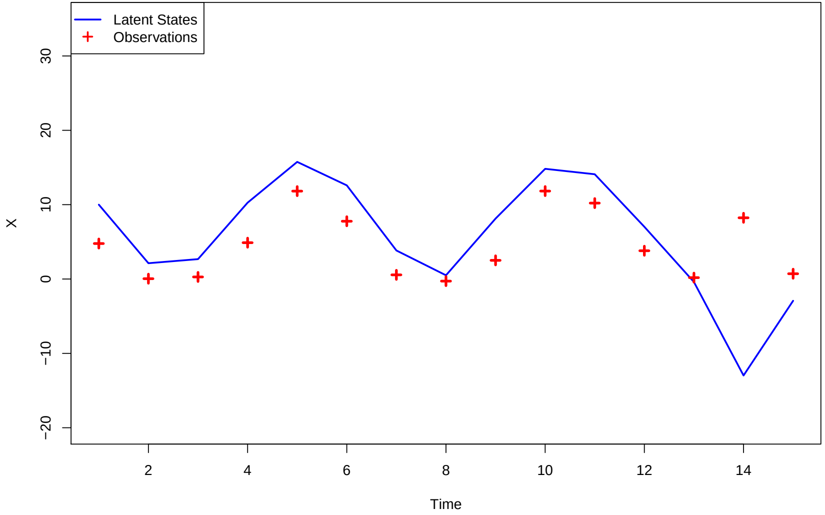
Let's fit this model in `JAGS`

# Non-linear SSM in JAGS

```
library(rjags)
> Loading required package: coda
> Linked to JAGS 4.3.0
> Loaded modules: basemod,bugs
library(coda)
set.seed(50)
## set parameters
t <- 15
x <- rep(NA, t)
phi <- 1
tau <- 4
x[1] <- 10
## generate data
for (i in 2:t){
  x[i] <- rnorm(1, .5*x[i-1] + 25*(x[i-1]) / (1 + x[i-1]^2)
              + 8*cos(1.2*i), sd = 1/sqrt(phi))
}
y <- .05*x^2 + rnorm(t, 0, 1/sqrt(tau))
```

# Non-linear SSM in JAGS



# Non-linear SSM in JAGS

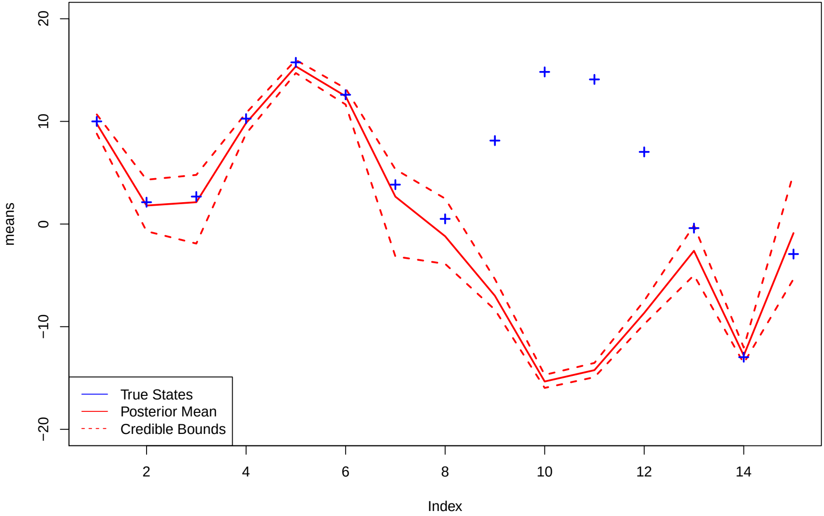
```
## sink the JAGS model
sink('jags_test_ex2.bug')
cat('model {
  for(i in 2:nday){
    x.pred[i] = .5*x[i-1] + 25*(x[i-1]) / (1 + x[i-1]^2)
      + 8*cos(1.2*i)
    x[i] ~ dnorm(x.pred[i], phi)
  }
  for(i in 1:nday){
    y[i] ~ dnorm(.05*x[i]^2, tau)
  }
  ## Initial conditions
  x[1] ~ dnorm(10, .5)

  ## Priors on process errors
  phi ~ dnorm(0, .01)T(0,100)
}'
)
sink()
```

# Non-linear SSMs in JAGS

```r
## make list of model data
model_data <- list('nday' = t,
                   'y' = y,
                   'tau' = tau)
## compile model
jags_ex2 <- jags.model('jags_test_ex2.bug',
                       data = model_data,
                       n.chains=1,
                       n.adapt=1000)
## generate samples
samples_ex1 = coda.samples(model = jags_ex2,
                           variable.names =
                           c('phi', paste0(paste0('x[', 1:t), ']')),
                           n.iter = 20000)
```

# Non-linear SSMs in JAGS



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- The MCMC is having difficulty determining the sign of the latent states
- MCMC-MH can have trouble exploring the entire parameter space for the latent states
- One method of more efficiently generating samples for SSMs is a *particle filter*

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- When observations are available, these particles get weights assigned and are resampled
- This generates approximations to the latent states

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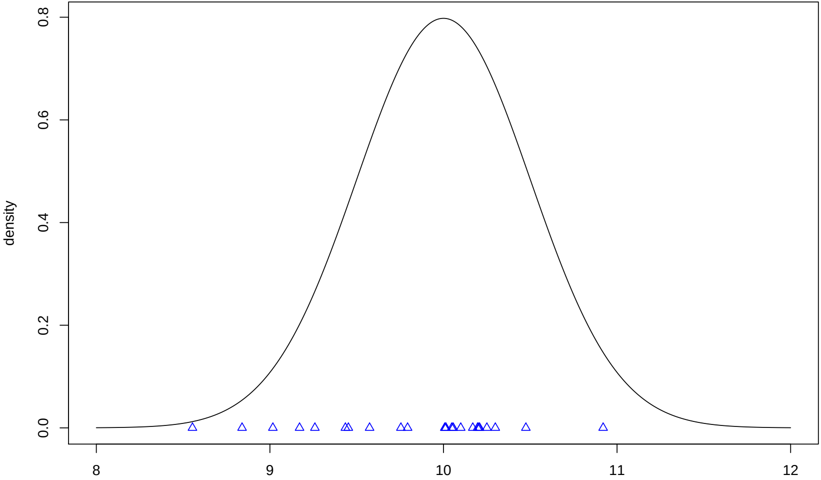
- Relatively easy to implement

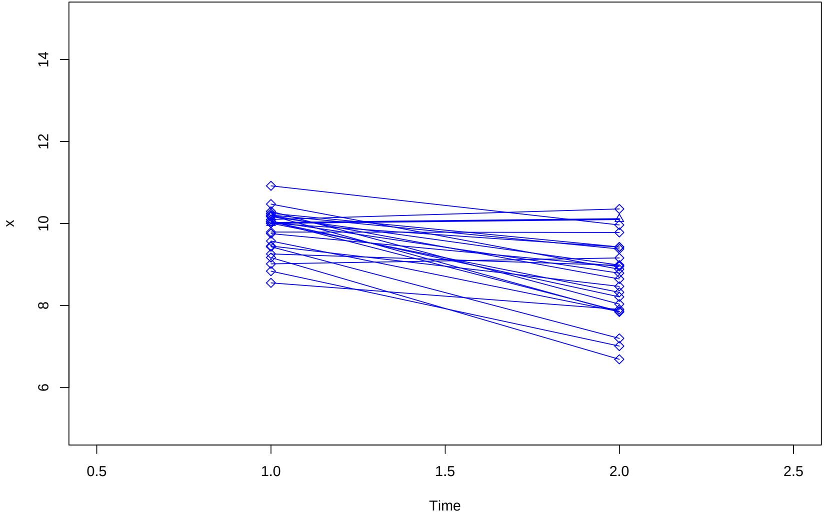
# The Bootstrap Filter Algorithm

Step 1: Generate a set of particles by sampling from the initial conditions



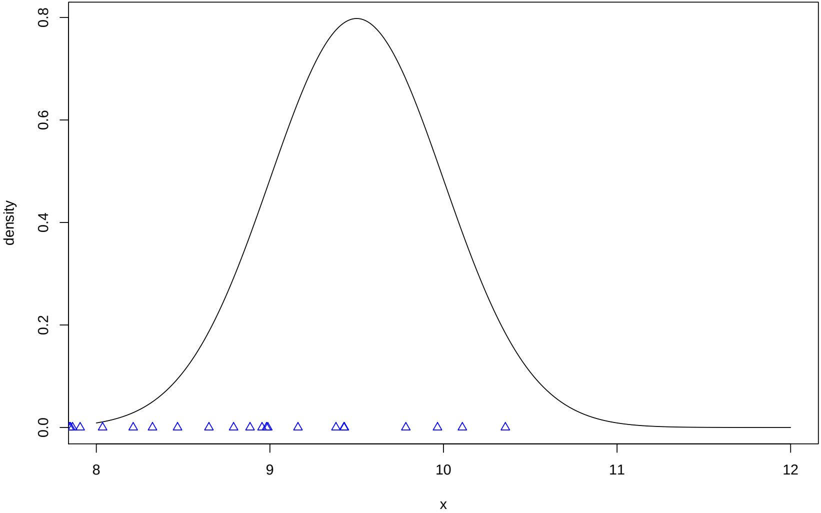
# The Bootstrap Filter Algorithm

Step 2: Evolve the particles to the next timestep using $f(x_t | x_{t-1}, \Theta)$



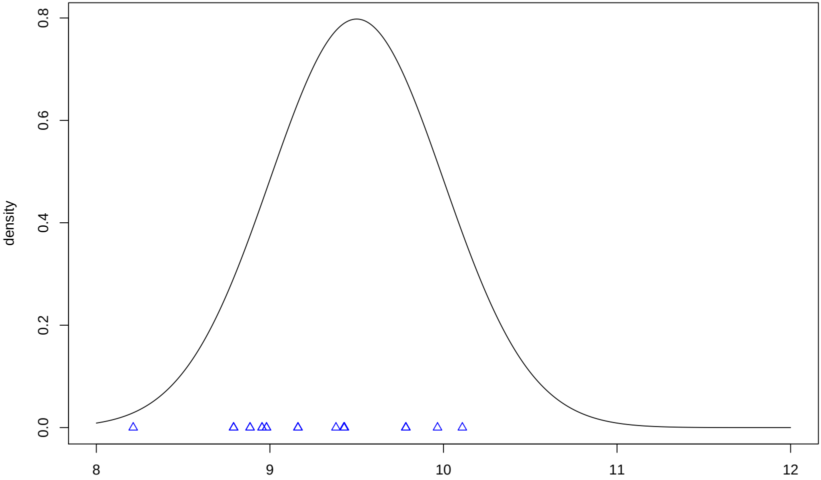
# The Bootstrap Filter Algorithm

Step 3: Generate weights for the particles using $g(y_t|x_t, \Theta)$



# The Bootstrap Filter Algorithm

Step 4: Resample the particles using the weights from Step 3 with replacement (a la Bootstrapping)



# The Bootstrap Filter Algorithm

Step 5: Repeat this process for the next timestep, using the bootstrap samples as the new set of particles

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- Generally, larger numbers of particles lead to better approximations
- Large numbers of particles lead to a large increase in computation time
- While the bootstrap filter is easy to implement, it can be difficult to implement effectively and quickly

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- NIMBLE is an R package that extends the JAGS/BUGS language
- NIMBLE also uses a symbolic language to make coding of models easier, and converts it to C++ code
- Can use methods other than MCMC-MH for sampling, including particle filters

# Non-linear SSMs in NIMBLE

NIMBLE models are generated similarly to how they are in JAGS

```
library(nimble, quietly = TRUE)
library(nimbleSMC, quietly = TRUE)
nimble_ssm <- nimbleCode({
  ## initial conditions
  x[1] ~ dnorm(10, tau = .5)
  ## phi prior
  phi ~ dexp(scale = 10)
  ## latent process
  for(i in 2:nday){
    x[i] ~ dnorm(.5*x[i-1] + 25* (x[i-1] / (1 + x[i-1]^2))
                 + 8*cos(1.2*i), tau = phi)
  }
  ## observation model
  for(i in 1:nday){
    y[i] ~ dnorm(.05*x[i]^2, tau = tau)
  }
})
```

# Non-linear SSMs in NIMBLE

```
## make data list
data <- list(y = y)
## set model constants
constants <- list(nday = 15, tau = tau)
## set starting values
inits <- list(
  phi = 1,
  x = sqrt(20*abs(y))
)
## compile model
stateSpaceModel <- nimbleModel(nimble_ssm,
                               data = data,
                               constants = constants,
                               inits = inits,
                               check = FALSE)
```

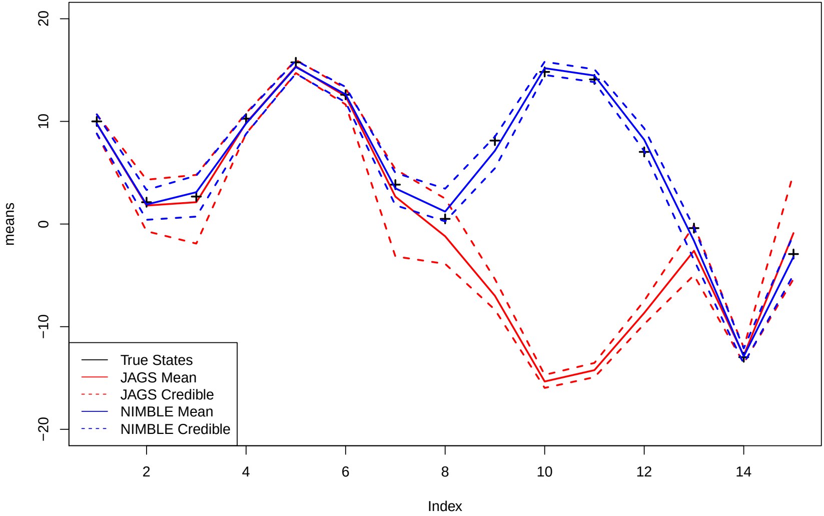
# Non-linear SSMs in NIMBLE

```r
## add bootstrap filter for latent states
bootstrapFilter <- buildBootstrapFilter(stateSpaceModel, nodes = 'x')
## compile model to add bootstrap filter
compiledList <- compileNimble(stateSpaceModel, bootstrapFilter)

stateSpaceMCMCconf <- configureMCMC(stateSpaceModel, nodes = NULL)

## add a random walk sampler for phi
stateSpaceMCMCconf$addSampler(target = 'phi',
                              type = 'RW_PF',
                              control = list(latents = 'x'))
## re-compile to add phi sampler
stateSpaceMCMC <- buildMCMC(stateSpaceMCMCconf)
compiledList <- compileNimble(stateSpaceModel,
                              stateSpaceMCMC,
                              resetFunctions = TRUE)
## generate samples
compiledList$stateSpaceMCMC$run(10000)
```

# Comparison



20
10
0
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means
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6
8
10
12
14
Index
True States
JAGS Mean
JAGS Credible
NIMBLE Mean
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# Review

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- NDLM estimation theory
- How to fit, assess, and forecast using `JAGS`
- Background for particle filters
- How to use particle methods in `NIMBLE`

# What Else?

There are still a lot of things we didn't have time to cover about SSMs. For those interested in learning more, I suggest reading *An introduction to state-space modeling of ecological time series* by Auger-Methe et al, 2020.

# Other Options for Fitting

Table 1: Comparison of the fitting methods discussed in Section 3.

| Method | Framework | Pros | Cons | R package |
|---|---|---|---|---|
| Kalman filter & MLE | Frequentist | Efficient & exact | Only applicable to linear Gaussian SSMs | dlm, MARSS |
| Laplace approximation | Frequentist | Efficient & flexible | States need to be approximatable with a continuous unimodal distribution (e.g., no discrete states) | TMB |
| Particle filter & iterative filtering | Frequentist | Flexible | Can be slow and sensitive to starting values | pomp |
| MCMC-MH | Bayesian | Flexible | Can be slow and sensitive to convergence problems | rjags, NIMBLE, R2WinBUGS, BRugs |
| MCMC-HMC | Bayesian | Efficient & flexible | Require continuous parameters and states or marginalization | rstan |
| Information reduction | Bayesian | Flexible & fewer estimation problems | Can be slow and imprecise | EasyABC |

# Thank You Everyone!