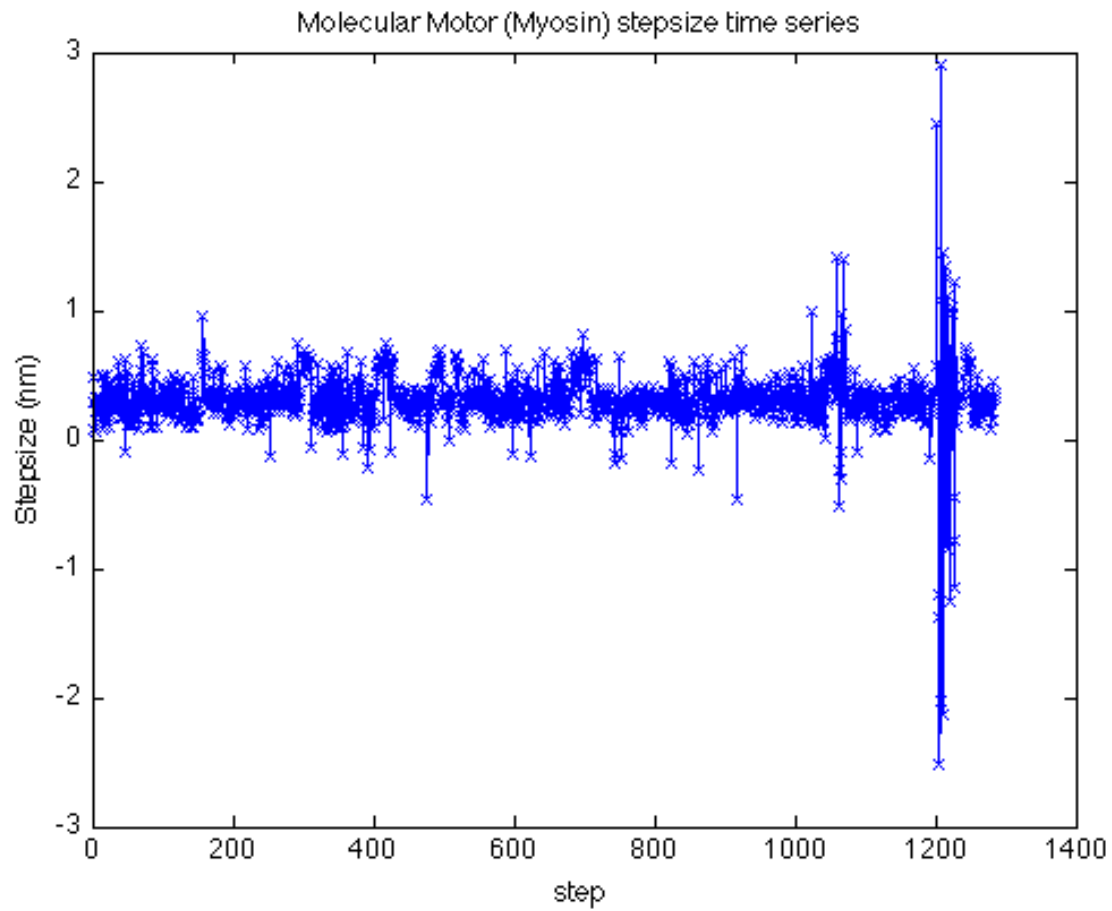


A Preliminary Markov Model  
Analysis for  
Myosin Stepsize

```
data: ./data/motor_stepsize.txt  
matlab:./matlab/motor.m
```

# Motor Stepsize



Note: we ignore the real lagtime for each step!

# Gaussian Mixture Model on Motor\_stepsize

Matlab Gaussian Mixture model fitting gives the following:

Gaussian mixture distribution with 2 components in 1 dimensions

Component 1:

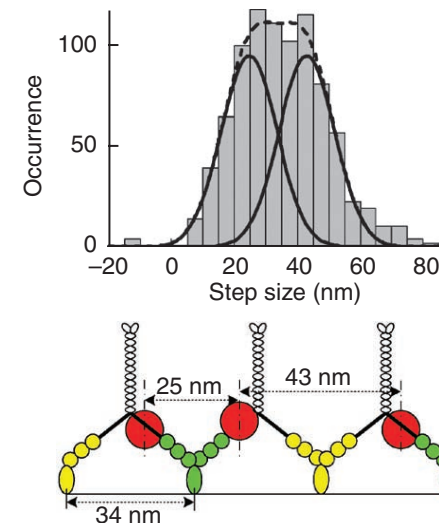
Mixing proportion: 0.049663

Mean: .1905

Component 2:

Mixing proportion: 0.950337

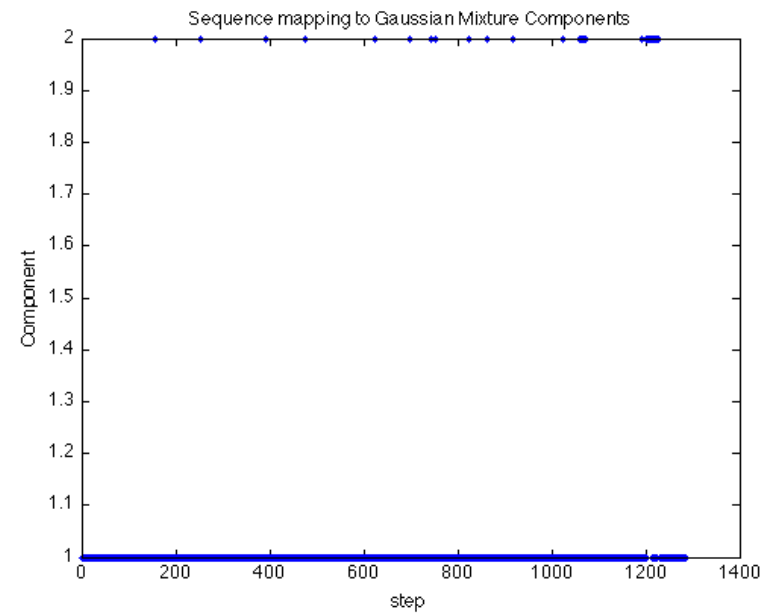
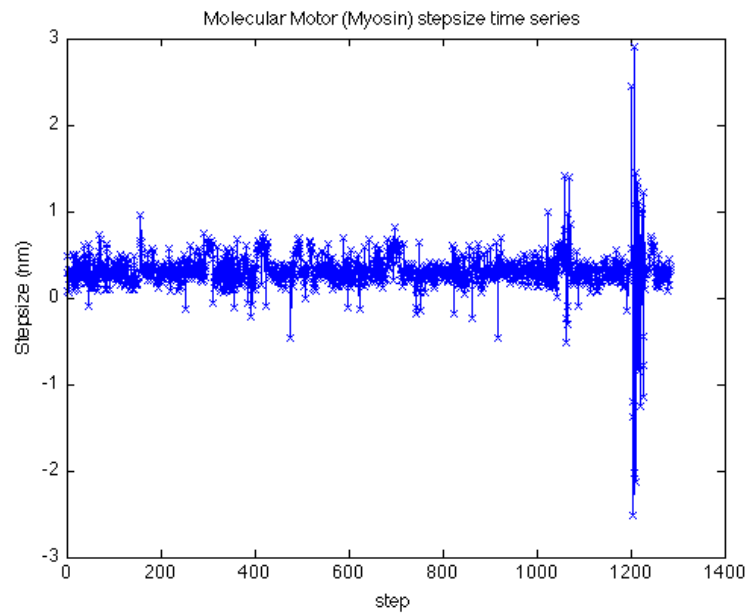
Mean: .3195



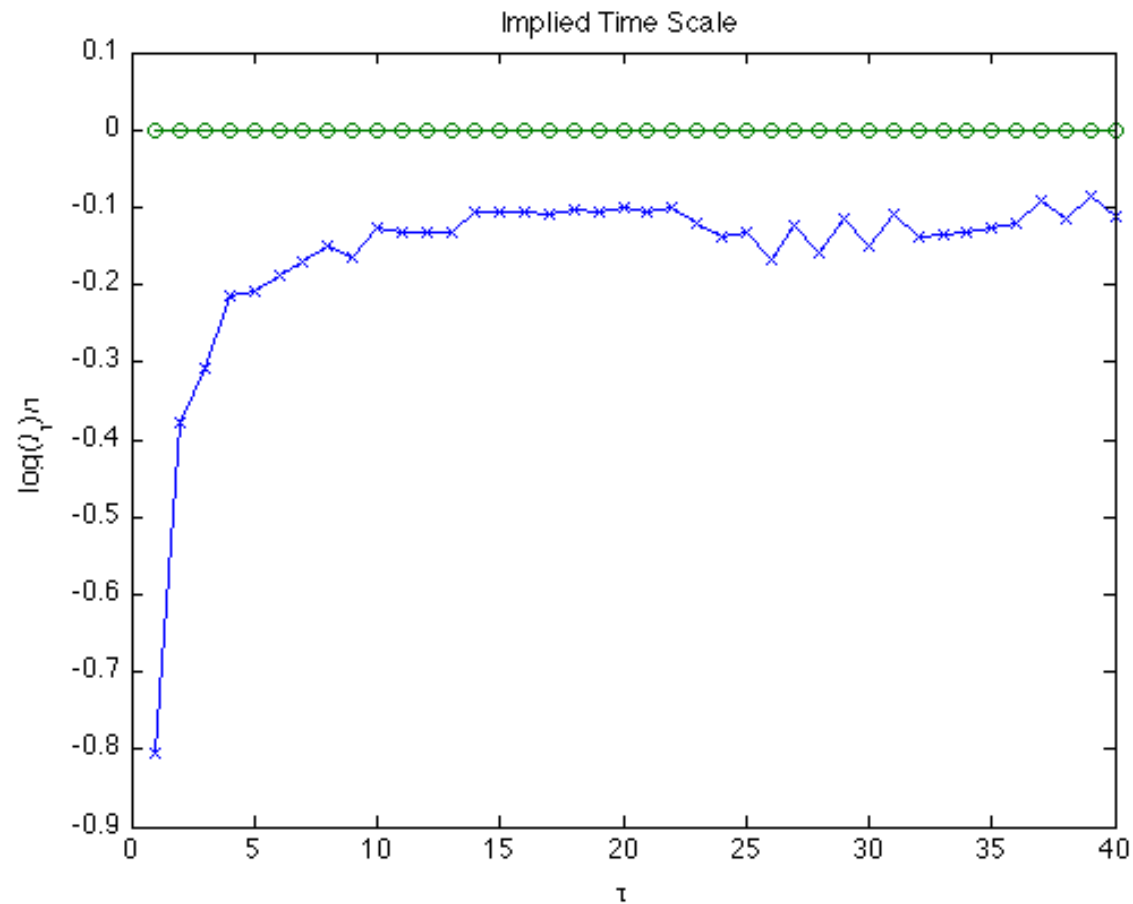
This is different to the paper with two modes centered at 25nm and 43nm

We get a sequence {1 2 1 1 1 2 2 1 2 ...} by mapping to the two components.

# Motor Stepsize Discretization

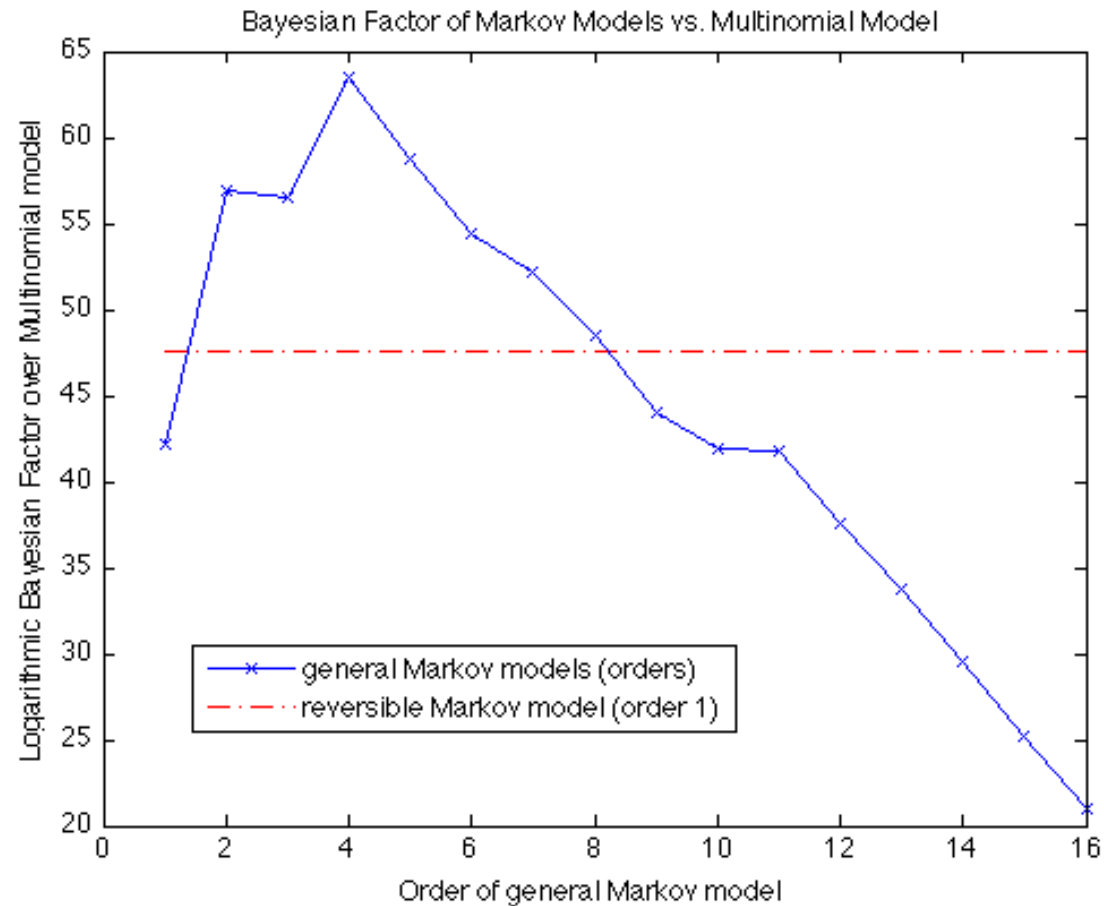


# Implied Time Scale



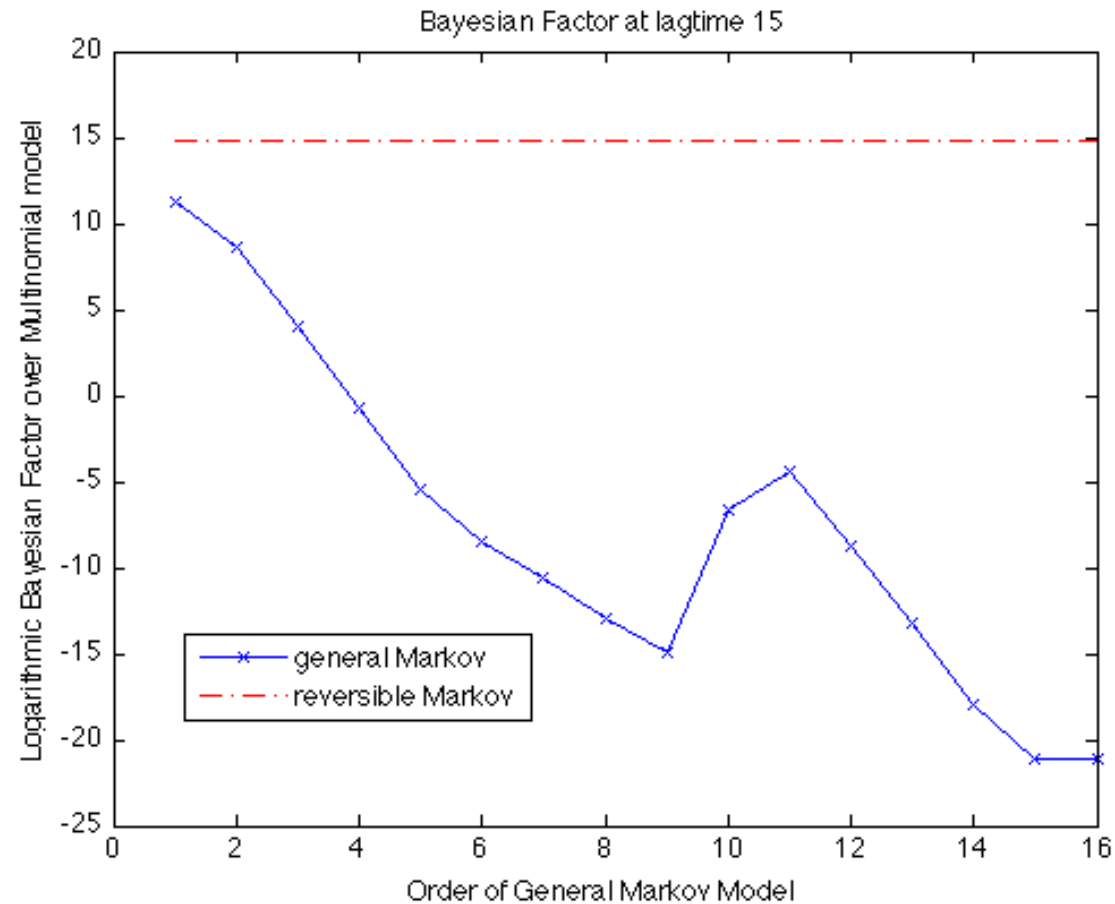
This says when the sequence jumps at lagtime in [14,22], the dynamics is like a Markov model

# Bayesian Factor when lagtime=1



When lagtime is 1, the sequence is best described by a 4-th order general Markov Chain, better than reversible Markov chain (order 1) and multinomial model.

# Bayesian Factor with lagtime=15



However when lagtime=15, the sequence is best described by a reversible Markov Chain (order 1), then a general Markov Chain (order 1). Higher orders are worse.