

DOBAD Package: Gibbs Sampling MCMC of Linear Birth-Death Chain with Partial Data

Charles Doss

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Part I

Estimating Rates for Linear Birth-Death chain via Gibbs Sampler MCMC by Exact Conditional Simulation

We are demonstrating the use of the `DOBAD` package's capability to do Bayesian estimation of the rate parameters for a linear Birth-Death chain, given partial observations, using the methods of Doss et al. (2010). Call the chain $\{X(t)\}_{t \in \mathbb{R}}$, and its birth rate λa and its death rate μ . We fix $\beta \in \mathbb{R}$ and constrain ν , the immigration rate, to be $\nu = \beta \lambda a$. We will denote $\theta = (\lambda a, \mu)$. The data is the value of the process at a finite number of discrete time points. That is, for some fixed times $0 = t_0, t_1, \dots, t_n$, we see the state of the process, $X(t_i)$. Thus the data, D , is 2 parts: a vector of the times t_i , $i = 0, \dots, n$ and a vector of states at each of those times, s_i , for $i = 0, \dots, n$ (where $X(t_i) = s_i$). The gamma prior is the conjugate prior if we observed the chain continuously instead of partially. The way we proceed, then, is to use independent Gamma priors on the λ and μ and augment the state space for our MCMC to include the entire chain $\{X_t\}_{t \in [0, t_n]}$ by conditionally sampling $\{X_t\}_{t \in [0, t_n]}; \theta | D$.

First we generate the underlying process and the “data”, set our prior parameters, and compute some summary statistics of the fully observed and partially observed processes.

```
> library(DOBAD)
> ##### Generate the "data"
> initstate=7;
> set.seed(112);
> T=5;  L <- .2; mu <- .4;
> beta.immig <- .987;
> trueParams <- c(L,mu,beta.immig); names(trueParams) <- c("lambda", "mu","beta") #for saving
```

```

> dr <- 0.0000000001; #Need |dr| < |L-mu| always o/w get sqrt(negative).
> n.fft <- 1024;
> delta <- 1;#play with. or make observation intervals distinct
> dat <- birth.death.simulant(t=T, lambda=L, mu=mu, nu=L*beta.immig, X0=initstate);
> fullSummary <- BDsummaryStats(dat); fullSummary

```

```

      Nplus      Nminus Holdtime
12.00000 14.00000 26.73947

```

```

> #fullSummary <- BDsummaryStats(dat[[1]]); fullSummary
> MLEs <- M.step.SC( EMSuffStats=fullSummary, T=T, beta.immig= beta.immig); MLEs

```

```

lambdahat      muhat
0.3788540 0.5235706

```

```

> partialData <- getPartialData( seq(0,T,delta), dat);
> observedSummary <- BDsummaryStats.PO(partialData); observedSummary;

```

```

      Nplus      Nminus Holdtime
          3          5          28

```

```

> ##Bayesian parameters
> L.mean <- 1; M.mean <- 1.1;
> aL <- .02;
> bL <- aL / L.mean
> aM <- .022;
> bM <- aM / M.mean;
> print(paste("Variances are", aL/bL^2, "and", aM/bM^2))

```

```

[1] "Variances are 50 and 55"

```

```

> N=10
> burn=0

```

Now we run the MCMC. It is set to run only a few iterations, obviously not enough for estimation, but enough to demonstrate the code. You may want to change the sweave code to run more iterations.

```
> ##Rprof(file="mcmc.rprofout")
> timer <- system.time(theMCMC <- BD.MCMC.SC(Lguess=L.mean, Mguess=M.mean,
+                                           alpha.L=aL, beta.L=bL, # mean
+                                           alpha.M=aM, beta.M=bM, #mean of
+                                           beta.immig=beta.immig,
+                                           data= partialData,
+                                           burnIn=burn, N=N));
> ##Rprof(NULL)
> #theMCMC
> mean(theMCMC[,1]); #lambda

[1] 0.722452

> mean(theMCMC[,2]); #mu

[1] 0.9170729

> L;

[1] 0.2

> mu;

[1] 0.4

> timer;

   user  system elapsed
0.489   0.003   0.492

> options(continue=" "); ##undo the setting we changed at top
```

```

> hist(theMCMC[,1], freq=FALSE, breaks=20,
      xlab="Lambda", ylab = "Density",
      main="Posterior of Lambda")
> Lmean <- mean(theMCMC[,1])
> abline(col="red", v=Lmean)
> abline(col="purple", v=L.mean)
> #text(col="red", y=-.3, x=Lmean, labels = "L")
> x <- seq(from=0,to=1, by=.01);
> y <- dgamma(x, shape=aL, rate=bL)
> lines(x,y, col="blue")

> hist(theMCMC[,2], freq=FALSE, breaks=20,
      xlab="Mu", ylab = "Density",
      main="Posterior of Mu")
> Mmean <- mean(theMCMC[,2])
> abline(col="red", v=Mmean)
> abline(col="purple", v=M.mean)
> x <- seq(from=0,to=1, by=.01);
> y <- dgamma(x, shape=aM, rate=bM)
> lines(x,y, col="blue")

```

References

Doss, C., Suchard, M., Holmes, I., Kato-Maeda, M., and Minin, V. (2010). Great Expectations: EM Algorithms for Discretely Observed Linear Birth-Death-Immigration Processes. *Arxiv preprint arXiv:1009.0893*.

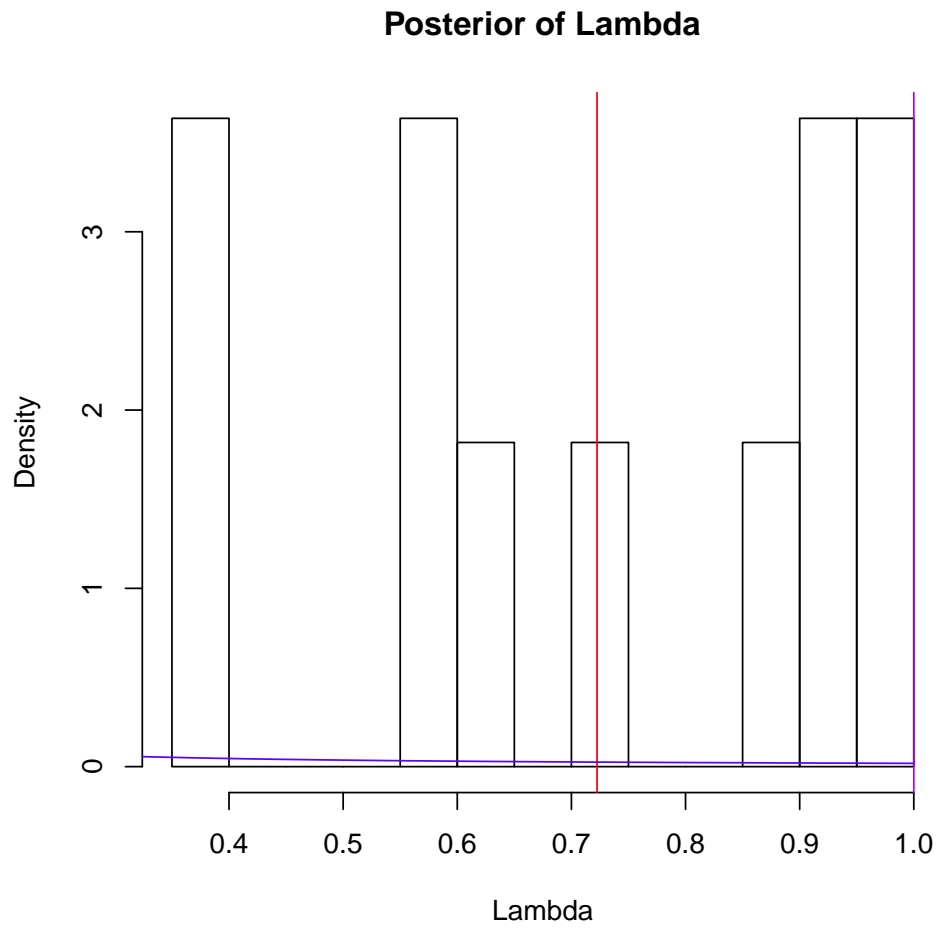


Figure 1: Posterior Density Estimation of Lambda

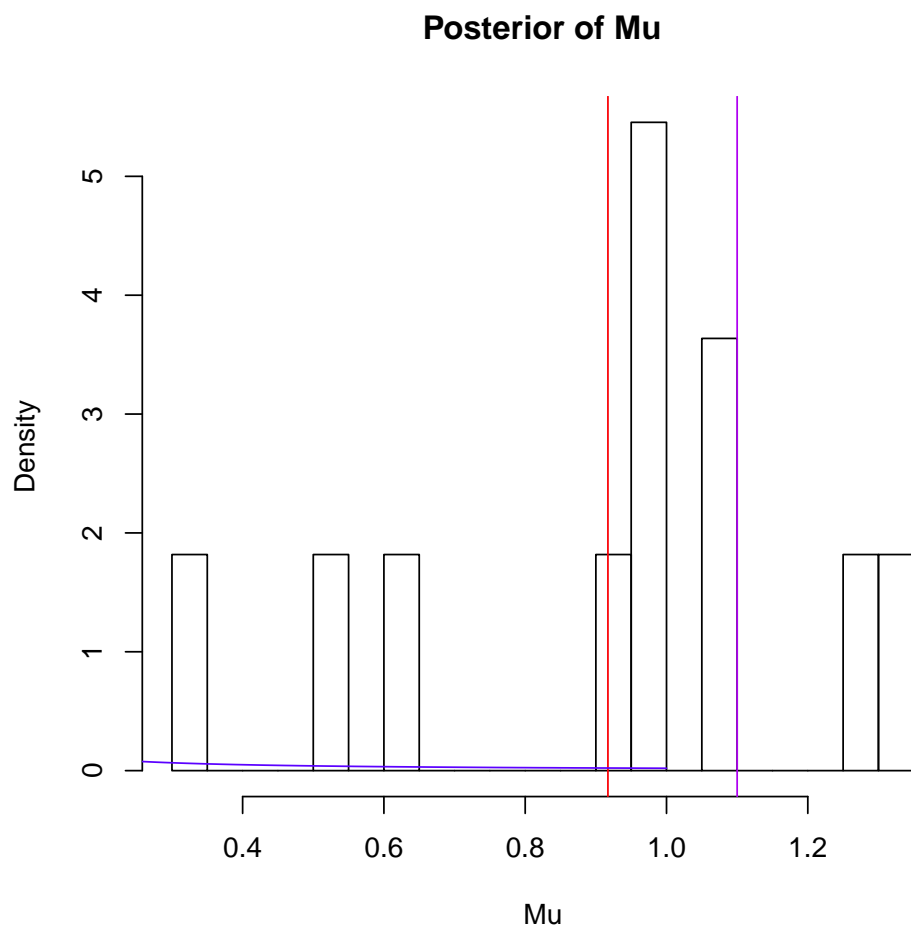


Figure 2: Posterior Density Estimation of μ