

An Intro to Probabilistic Programming using JAGS

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What I'll Assume for This Talk

- ▶ You know what Bayesian inference is:
 - ▶ Inference is the computation of a posterior distribution
 - ▶ All desired results are derived from the posterior
- ▶ You know what typical distributions look like:
 - ▶ Bernoulli / Binomial
 - ▶ Uniform
 - ▶ Beta
 - ▶ Normal
 - ▶ Exponential / Gamma
 - ▶ ...

What is Probabilistic Programming?

**Probabilistic programming uses programming languages
custom-designed for expressing probabilistic models**

A Simple Example of JAGS Code

```
model
{
  alpha <- 1
  beta <- 1

  p ~ dbeta(alpha, beta)

  for (i in 1:N)
  {
    x[i] ~ dbern(p)
  }
}
```

Model Specification vs. Model Use

- ▶ Code in a probabilistic programming languages specifies a model, not a use case
- ▶ A single model specification can be reused in many contexts:
 - ▶ Monte Carlo simulations
 - ▶ Maximum A Posteriori (MAP) estimation
 - ▶ Sampling from a posterior distribution

Imperative versus Declarative Programming

- ▶ Describe a process for generating results:
 - ▶ C
 - ▶ Lisp
- ▶ Describe the structure of the results:
 - ▶ Prolog
 - ▶ SQL
 - ▶ Regular expressions

Existing Probabilistic Programming Systems

- ▶ The BUGS Family
 - ▶ WinBUGS
 - ▶ OpenBUGS
 - ▶ JAGS
 - ▶ Stan
- ▶ Infer.NET
- ▶ Church
- ▶ Factorie

JAGS Syntax: Model Blocks

```
model
{
  ...
}
```


JAGS Syntax: Deterministic Assignment

```
alpha <- 1
```

JAGS Syntax: Stochastic Assignment

```
p ~ dbeta(1, 1)
```

JAGS Semantics: Probability Distributions

- ▶ `dbern / dbinom`
- ▶ `dunif`
- ▶ `dbeta`
- ▶ `dnorm`
- ▶ `dexp / dgamma`
- ▶ ...

JAGS Syntax: For Loops

```
for (i in 1:N)
{
  x[i] ~ dbern(p)
}
```

Putting It All Together

```
model
{
  alpha <- 1
  beta <- 1

  p ~ dbeta(alpha, beta)

  for (i in 1:N)
  {
    x[i] ~ dbern(p)
  }
}
```

An Equivalent Translation If $N == 3$

```
model
{
  p ~ dbeta(1, 1)

  x[1] ~ dbern(p)
  x[2] ~ dbern(p)
  x[3] ~ dbern(p)
}
```

For Loops are not Sequential

```
model
{
  p ~ dbeta(1, 1)

  x[2] ~ dbern(p)
  x[3] ~ dbern(p)
  x[1] ~ dbern(p)
}
```

For Loops do not Introduce a New Scope

```
model
{
  for (i in 1:N)
  {
    x[i] ~ dnorm(mu, 1)
    epsilon ~ dnorm(0, 1)
    x.pair[i] <- x[i] + epsilon
  }

  mu ~ dunif(-1000, 1000)
}
```


A Translation of a Broken For Loop

```
model
{
  x[1] ~ dnorm(mu, 1)
  epsilon ~ dnorm(0, 1)
  x.pair[1] <- x[1] + epsilon

  x[2] ~ dnorm(mu, 1)
  epsilon ~ dnorm(0, 1)
  x.pair[2] <- x[2] + epsilon

  mu ~ dunif(-1000, 1000)
}
```

Stochastic vs. Deterministic Nodes

- ▶ Observed data *must* correspond to stochastic nodes
- ▶ All constants like N must be known at compile-time
- ▶ Deterministic nodes are nothing more than shorthand
 - ▶ A deterministic node can always be optimized out!
- ▶ Stochastic nodes are the essence of the program

Observed Data Must Use Stochastic Nodes

Two valid mathematical formulations:

$$y_i \sim \mathcal{N}(ax_i + b, 1)$$

$$y_i = ax_i + b + \epsilon_i$$

$$\text{where } \epsilon_i \sim \mathcal{N}(0, 1)$$

Observed Data Must Use Stochastic Nodes

Valid jags code:

```
y[i] ~ dnorm(a * x[i] + b, 1)
```

Invalid jags code:

```
epsilon[i] ~ dnorm(0, 1)  
y[i] <- a * x[i] + b + epsilon[i]
```

What's Badly Missing from JAGS Syntax?

- ▶ if / else
- ▶ Can sometimes get away with a `dsum()` function
- ▶ Some cases would require a non-existent `dprod()` function

This is *NOT* Valid JAGS Code

```
model
{
  p ~ dbeta(1, 1)

  for (i in 1:N)
  {
    exp[i] ~ dexp(1)
    norm[i] ~ dnorm(5, 1)
    alpha[i] ~ dbern(p)
    x[i] ~ dsum(alpha[i] * exp[i],
                (1 - alpha[i]) * norm[i])
  }
}
```

But Valid Code Does Exist for Many Important Models!

- ▶ Linear regression
- ▶ Logistic regression
- ▶ Hierarchical linear regression
- ▶ Mixtures of Gaussians

Linear Regression

```
model
{
  a ~ dnorm(0, 0.0001)
  b ~ dnorm(0, 0.0001)

  tau <- pow(sigma, -2)
  sigma ~ dunif(0, 100)

  for (i in 1:N)
  {
    mu[i] <- a * x[i] + b
    y[i] ~ dnorm(mu[i], tau)
  }
}
```


Logistic Regression

```
model
{
  a ~ dnorm(0, 0.0001)
  b ~ dnorm(0, 0.0001)

  for (i in 1:N)
  {
    y[i] ~ dbern(p[i])
    logit(p[i]) <- a * x[i] + b
  }
}
```

Hierarchical Linear Regression

```
model
{
  mu.a ~ dnorm(0, 0.0001)
  mu.b ~ dnorm(0, 0.0001)
  ...

  for (j in 1:K)
  {
    a[j] ~ dnorm(mu.a, tau.a)
    b[j] ~ dnorm(mu.b, tau.b)
  }
  for (i in 1:N)
  {
    mu[i] <- a[g[i]] * x[i] + b[g[i]]
    y[i] ~ dnorm(mu[i], tau)
  }
}
```

Clustering via Mixtures of Normals

```
model
{
  p ~ dbeta(1, 1)

  mu1 ~ dnorm(0, 0.0001)
  mu2 ~ dnorm(1, 0.0001)

  tau <- pow(sigma, -2)
  sigma ~ dunif(0, 100)

  for (i in 1:N)
  {
    z[i] ~ dbern(p)
    mu[i] <- z[i] * mu1 + (1 - z[i]) * mu2
    x[i] ~ dnorm(mu[i], tau)
  }
}
```

MCMC in 30 Seconds

- ▶ If we can write down a distribution, we can sample from it
- ▶ Every piece of JAGS code defines a probability distribution
- ▶ But we have to use Markov chains to draw samples
- ▶ May require hundreds of steps to produce one sample
- ▶ MCMC == Markov Chain Monte Carlo

Using JAGS from R

```
library("rjags")

jags <- jags.model("logit.bugs",
                  data = list("x" = x,
                              "N" = N,
                              "y" = y),
                  n.chains = 4,
                  n.adapt = 1000)

mcmc.samples <- coda.samples(jags, c("a", "b"), 50)

summary(mcmc.samples)

plot(mcmc.samples)
```

Summarizing the Results

```
> summary(mcmc.samples)
```

```
Iterations = 1:50
```

```
Thinning interval = 1
```

```
Number of chains = 4
```

```
Sample size per chain = 50
```

1. Empirical mean and standard deviation for each variable,
plus standard error of the mean:

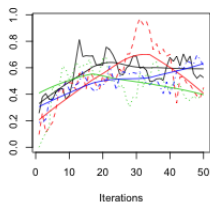
	Mean	SD	Naive SE	Time-series SE
a	0.5504	0.1404	0.009929	0.01868
b	-2.7125	0.8504	0.060134	0.10579

2. Quantiles for each variable:

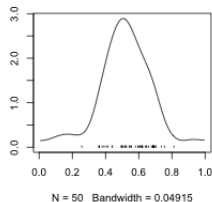
	2.5%	25%	50%	75%	97.5%
a	0.2669	0.4669	0.5414	0.6144	0.8234
b	-4.3907	-3.1135	-2.6842	-2.3118	-0.3475

Plotting the Samples

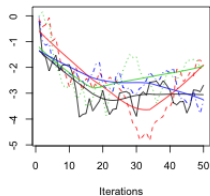
Trace of a



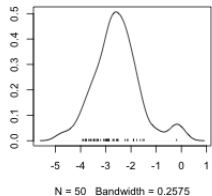
density.default(density, width = width)



Trace of b



density.default(density, width = width)



Burn-In

- ▶ Markov chains do not start in the right position
- ▶ Need time to reach and then settle down near MAP values
- ▶ The initial sampling period is called burn-in
- ▶ We discard all of these samples

Adaptive Phase

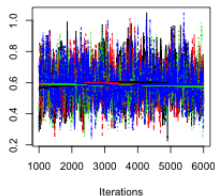
- ▶ JAGS has tunable parameters that need to adapt to the data
- ▶ Controlled by `n.adapt` parameter
- ▶ JAGS allows you to treat adaptive phase as part of burn-in
- ▶ For simple models, adaptation may not be necessary

Mixing

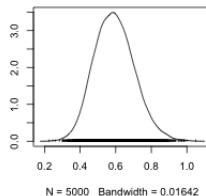
- ▶ How do we know that burn-in is complete?
- ▶ Run multiple chains
- ▶ Test that they all produce similar results
- ▶ All test for mixing are heuristic methods

Plotting the Samples after Burn-In

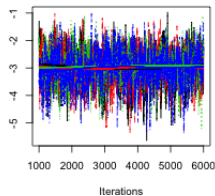
Trace of a



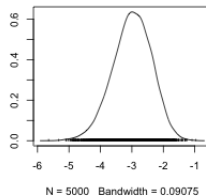
density.default(density(a), width = width)



Trace of b



density.default(density(b), width = width)



Other Practical Issues

- ▶ Autocorrelation between samples
- ▶ Thinning
- ▶ Initializing parameters
- ▶ Numeric stability

Additional References

- ▶ The BUGS Book
- ▶ The JAGS Manual
- ▶ My GitHub Repo of JAGS Examples
- ▶ 2012 NIPS Workshop on Probabilistic Programming

Appendix 1: Basic Sampler Design

- ▶ Slice sampler
- ▶ Metropolis-Hastings sampler
- ▶ Adaptive rejection sampling
- ▶ CDF inversion

Appendix 2: Gibbs Sampling

- ▶ Conjugacy
- ▶ Any closed form posterior