STA 360/602L: Module 3.8

MCMC and Gibbs sampling II

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Example: bivariate normal

- Consider

$$\begin{pmatrix} \theta_1 \\ \theta_2 \end{pmatrix} \sim \mathcal{N}\left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix}\right]$$

  where ρ is known (and is the correlation between θ_1 and θ_2).

- We will review details of the multivariate normal distribution very soon but for now, let's use this example to explore Gibbs sampling.

- For this density, turns out that we have

$$\theta_1 | \theta_2 \sim \mathcal{N}\left(\rho\theta_2, 1 - \rho^2\right)$$

  and

$$\theta_2 | \theta_1 \sim \mathcal{N}\left(\rho\theta_1, 1 - \rho^2\right)$$

- While we can easily sample directly from this distribution (using the `mvtnorm` or `MASS` packages in R), let's instead use the Gibbs sampler to draw samples from it.

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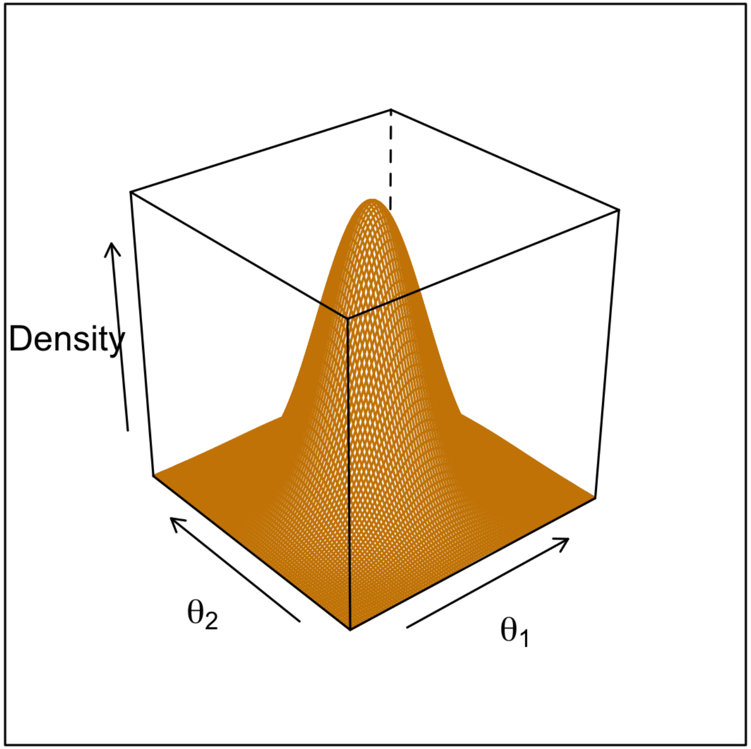
Bivariate normal

First, a few examples of the bivariate normal distribution.

$$\begin{pmatrix} \theta_1 \\ \theta_2 \end{pmatrix} \sim \mathcal{N}\left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}\right]$$



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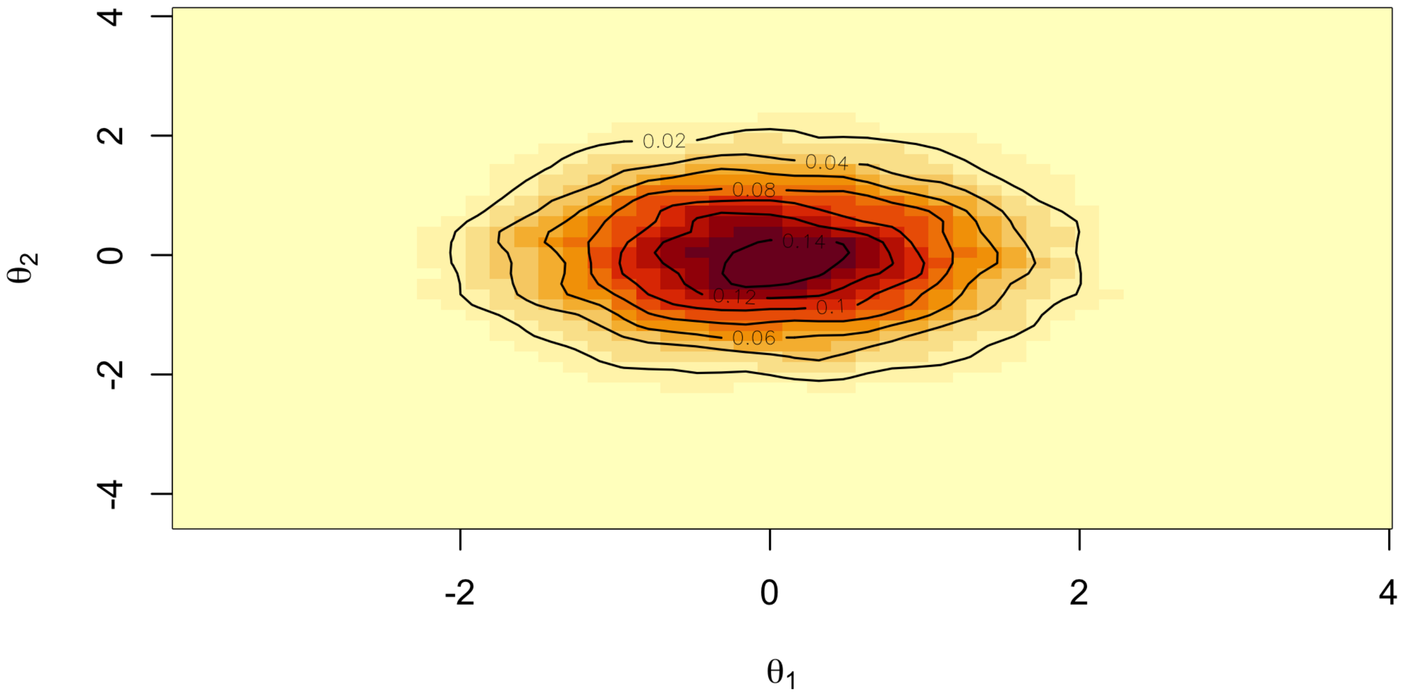
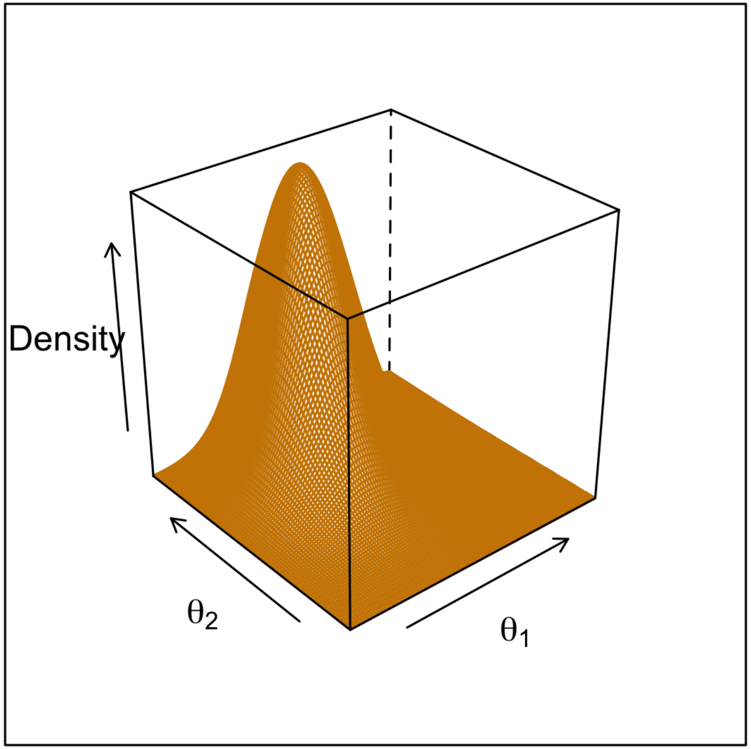
Bivariate normal

$$\begin{pmatrix} \theta_1 \\ \theta_2 \end{pmatrix} \sim \mathcal{N}\left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}\right]$$



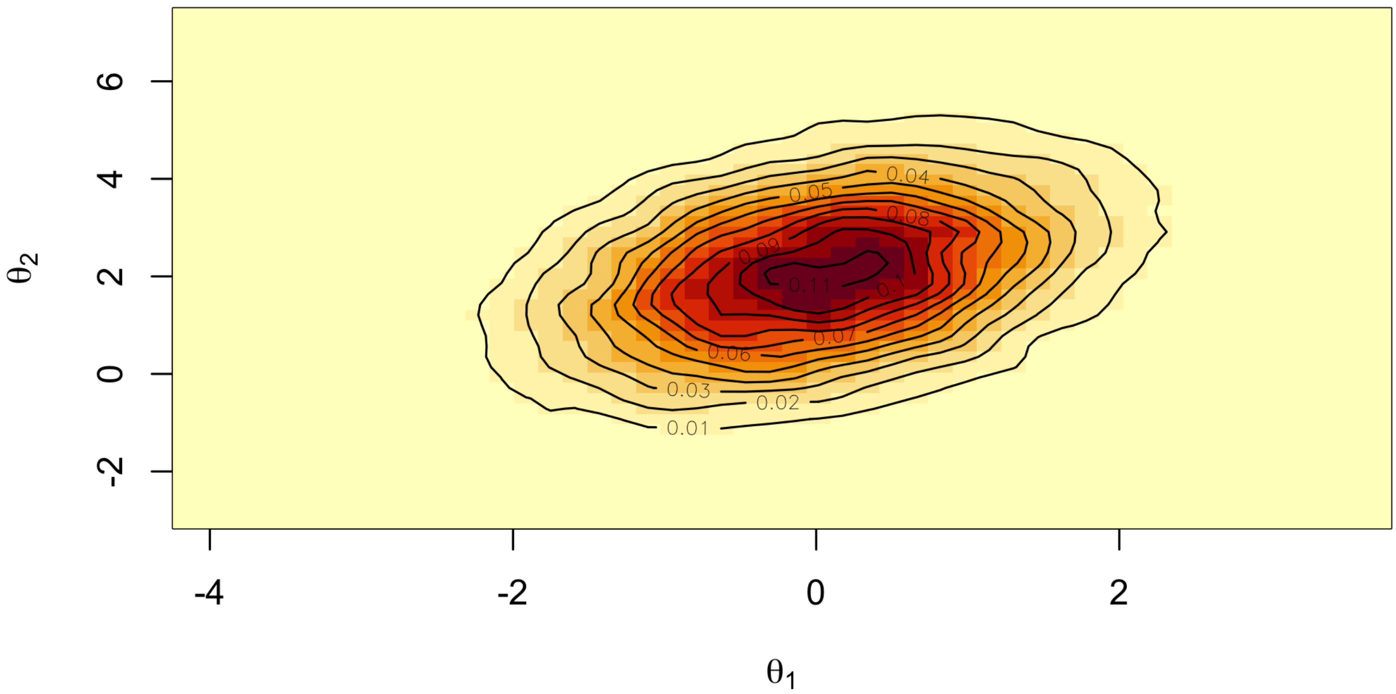
Bivariate normal

$$\begin{pmatrix}\theta_1\\ \theta_2\end{pmatrix} \sim \mathcal{N}\left[\begin{pmatrix}0\\ 2\end{pmatrix}, \begin{pmatrix}1 & 0.5\\ 0.5 & 2\end{pmatrix}\right]$$



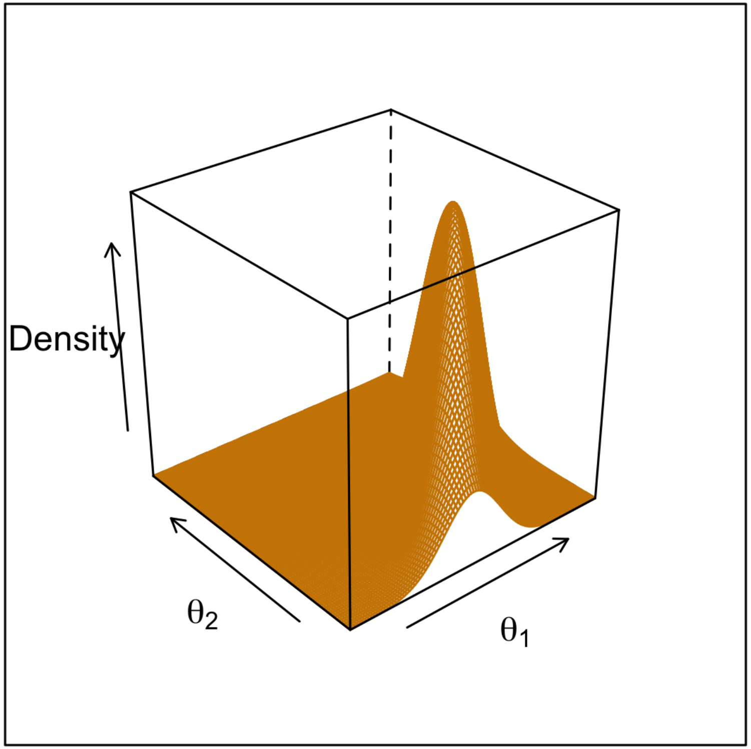
Bivariate normal

$$\begin{pmatrix}\theta_1\\ \theta_2\end{pmatrix} \sim \mathcal{N}\left[\begin{pmatrix}0\\ 2\end{pmatrix}, \begin{pmatrix}1 & 0.5\\ 0.5 & 2\end{pmatrix}\right]$$



Bivariate normal

$$\begin{pmatrix} \theta_1 \\ \theta_2 \end{pmatrix} \sim \mathcal{N}\left[\begin{pmatrix} 1 \\ -1 \end{pmatrix}, \begin{pmatrix} 1 & 0.9 \\ 0.9 & 1.5 \end{pmatrix}\right]$$



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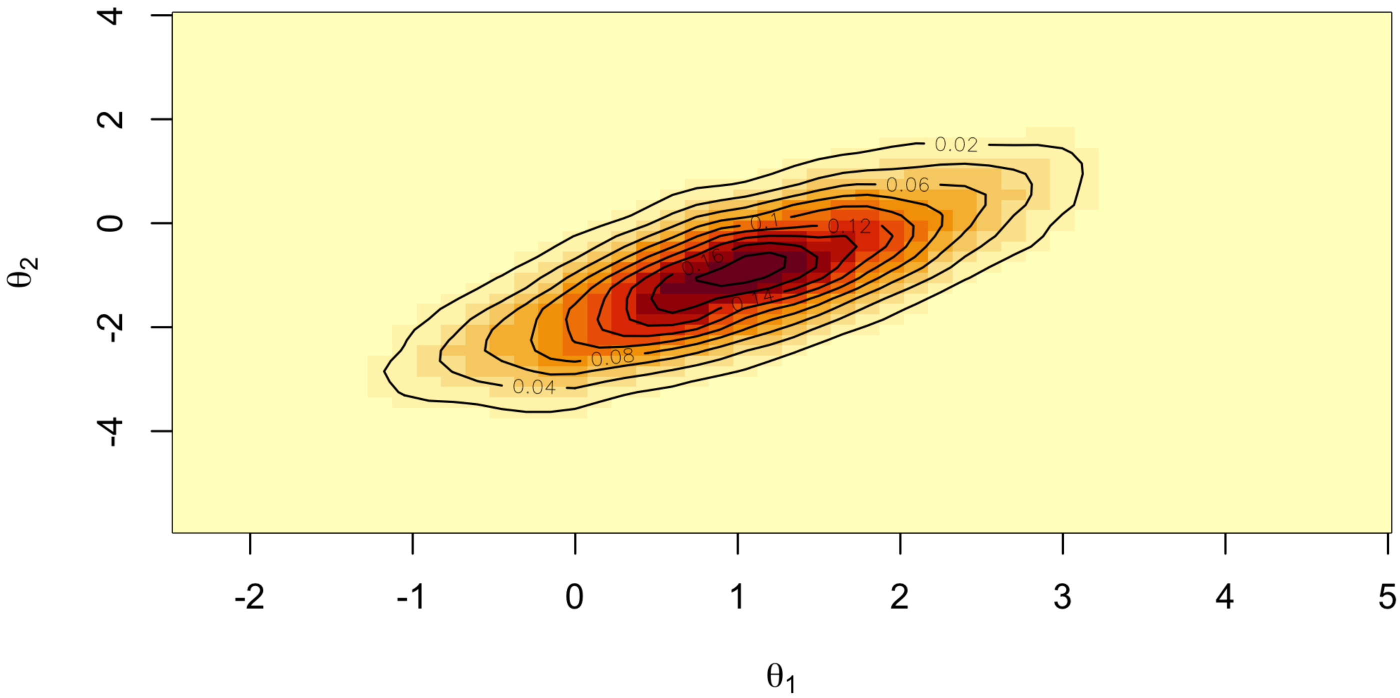
Bivariate normal

$$\begin{pmatrix}\theta_1\\ \theta_2\end{pmatrix} \sim \mathcal{N}\left[\begin{pmatrix}1\\ -1\end{pmatrix}, \begin{pmatrix}1 & 0.9\\ 0.9 & 1.5\end{pmatrix}\right]$$



Back to the example

- Again, we have

$$\theta_1|\theta_2 \sim \mathcal{N}\left(\rho\theta_2, 1-\rho^2\right); \quad \theta_2|\theta_1 \sim \mathcal{N}\left(\rho\theta_1, 1-\rho^2\right)$$

- Here's a code to do Gibbs sampling using those full conditionals:

```r
rho <- #set correlation
S <- #set number of MCMC samples
thetamat <- matrix(0,nrow=S,ncol=2)
theta <- c(10,10) #initialize values of theta
for (s in 1:S) {
theta[1] <- rnorm(1,rho*theta[2],sqrt(1-rho^2)) #sample theta1
theta[2] <- rnorm(1,rho*theta[1],sqrt(1-rho^2)) #sample theta2
thetamat[s,] <- theta
}
```

- Here's a code to do sample directly instead:

```r
library(mvtnorm)
rho <- #set correlation; no need to set again once you've used previous code
S <- #set number of MCMC samples; no need to set again once you've used previous code
Mu <- c(0,0)
Sigma <- matrix(c(1,rho,rho,1),ncol=2)
thetamat_direct <- rmvnorm(S, mean = Mu,sigma = Sigma)
```

-->

More code

See how the chain actually evolves with an overlay on the true density:

```r
rho <- #set correlation
Sigma <- matrix(c(1,rho,rho,1),ncol=2); Mu <- c(0,0)
x.points <- seq(-3,3,length.out=100)
y.points <- x.points
z <- matrix(0,nrow=100,ncol=100)
for (i in 1:100) {
  for (j in 1:100) {
    z[i,j] <- dmvnorm(c(x.points[i],y.points[j]),mean=Mu,sigma=Sigma)
  }
}
contour(x.points,y.points,z,xlim=c(-3,10),ylim=c(-3,10),col="orange2",
        xlab=expression(theta[1]),ylab=expression(theta[2]))

S <- #set number of MCMC samples;
thetamat <- matrix(0,nrow=S,ncol=2)
theta <- c(10,10)
points(x=theta[1],y=theta[2],col="black",pch=2)
for (s in 1:S) {
  theta[1] <- rnorm(1,rho*theta[2],sqrt(1-rho^2))
  theta[2] <- rnorm(1,rho*theta[1],sqrt(1-rho^2))
  thetamat[s,] <- theta
  if(s < 20){
    points(x=theta[1],y=theta[2],col="red4",pch=16); Sys.sleep(1)
  } else {
    points(x=theta[1],y=theta[2],col="green4",pch=16); Sys.sleep(0.1)
  }
}
```

MCMC

- Gibbs sampling is one of several flavors of Markov chain Monte Carlo (MCMC).
  - Markov chain: a stochastic process in which future states are independent of past states conditional on the present state.
  - Monte Carlo: simulation.
- MCMC provides an approach for generating samples from posterior distributions.
- From these samples, we can obtain summaries (including summaries of functions) of the posterior distribution for θ, our parameter of interest.

How does MCMC work?

- Let $\theta^{(s)} = (\theta_1^{(s)}, \ldots, \theta_p^{(s)})$ denote the value of the $p \times 1$ vector of parameters at iteration s.
- Let $\theta^{(0)}$ be an initial value used to start the chain (*should not be sensitive*).
- MCMC generates $\theta^{(s)}$ from a distribution that depends on the data and potentially on $\theta^{(s-1)}$, but not on $\theta^{(1)}, \ldots, \theta^{(s-2)}$.
- This results in a Markov chain with **stationary distribution** $\pi(\theta|Y)$ under some conditions on the sampling distribution.
- The theory of Markov Chains (structure, convergence, reversibility, detailed balance, stationarity, etc) is well beyond the scope of this course so we will not dive into it.
- If you are interested, consider taking courses on stochastic process.

Properties

- **Note**: Our Markov chain is a collection of draws of θ that are (slightly we hope!) dependent on the previous draw.

- The chain will wander around our parameter space, only remembering where it had been in the last draw.

- We want to have our MCMC sample size, S, big enough so that we can
  - Move out of areas of low probability into regions of high probability (convergence)
  - Move between high probability regions (good mixing)
  - Know our Markov chain is stationary in time (the distribution of samples is the same for all samples, regardless of location in the chain)

- At the start of the sampling, the samples are **not** from the posterior distribution. It is necessary to discard the initial samples as a burn-in to allow convergence. We'll talk more about that in the next class.

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Different flavors of MCMC

- The most commonly used MCMC algorithms are:
  - Metropolis sampling (Metropolis et al., 1953).
  - Metropolis-Hastings (MH) (Hastings, 1970).
  - Gibbs sampling (Geman & Geman, 1984; Gelfand & Smith, 1990).
- Overview of Gibbs - Casella & George (1992, The American Statistician, 46, 167-174). the first two
- Overview of MH - Chib & Greenberg (1995, The American Statistician).
- We will get to Metropolis and Metropolis-Hastings later in the course.

What's next?

Move on to the readings for the next module!