Stat 102C HW5: Answer Key

Jonathan Arfa, Muzhou Liang

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Problem 1.1

$$
\begin{aligned}
P(X_{t+1} = x, Y_t = y) &= P(Y_t = y)P(X_{t+1} = x | Y_t = y) && (1)\\
&= p_Y(y)p(x|y) && (2)\\
&= p(x, y) && (3)
\end{aligned}
$$

$$
\begin{aligned}
P(X_{t+1} = x, Y_{t+1} = y) &= P(X_{t+1} = x)P(Y_{t+1} = y | X_{t+1} = x) && (4)\\
&= p_X(x)p(y|x) && (5)\\
&= p(x, y) && (6)
\end{aligned}
$$

Thus, $(X_{t+1}, Y_t) \sim p(x, y)$ and $(X_{t+1}, Y_{t+1}) \sim p(x, y)$.

Problem 1.2

```
(probs = matrix(c(0.1, 0.4, 0.3, 0.2), nrow = 2, byrow = TRUE))
```

```
##      [,1] [,2]
## [1,]  0.1  0.4
## [2,]  0.3  0.2
```

```
# marginal probabilities of x: p(x==1), p(x==2)
(px = rowSums(probs))
```

```
## [1] 0.5 0.5
```

```
# marginal probabilities of y
(py = colSums(probs))
```

```
## [1] 0.4 0.6
```

```
# conditional probabilities of x|y==1: p(x==1|y==1), p(x==2|y==1)
(px_y1 = c(probs[1, 1], probs[2, 1])/sum(probs[, 1]))
```

```
## [1] 0.25 0.75

# conditional probabilities of x|y==2
(px_y2 = c(probs[1, 2], probs[2, 2])/sum(probs[, 2]))

## [1] 0.6667 0.3333

# conditional probabilities of y|x==1
(py_x1 = c(probs[1, 1], probs[1, 2])/sum(probs[1, ]))

## [1] 0.2 0.8

# conditional probabilities of y|x==2
(py_x2 = c(probs[2, 1], probs[2, 2])/sum(probs[2, ]))

## [1] 0.6 0.4
```

For the last part of this problem, we need to show that
$p(x, y) = P(X_{t+1} = x|Y_t = y)p_Y(y)$.
So, $p(x = 1, y = 1) = P(X_{t+1} = 1|Y_t = 1)p_Y(1)$.

```
probs[1, 1]

## [1] 0.1

px_y1[1] * py[1]

## [1] 0.1
```

$p(x = 1, y = 2) = P(X_{t+1} = 1|Y_t = 2)p_Y(2)$.

```
probs[1, 2]

## [1] 0.4

px_y2[1] * py[2]

## [1] 0.4
```

$p(x = 2, y = 1) = P(X_{t+1} = 2|Y_t = 1)p_Y(1)$.

```
probs[2, 1]

## [1] 0.3

px_y1[2] * py[1]

## [1] 0.3
```

$p(x = 2, y = 2) = P(X_{t+1} = 2|Y_t = 2)p_Y(2)$.

```
probs[2, 2]
```

```
## [1] 0.2
```

```
px_y2[2] * py[2]
```

```
## [1] 0.2
```

Problem 1.3

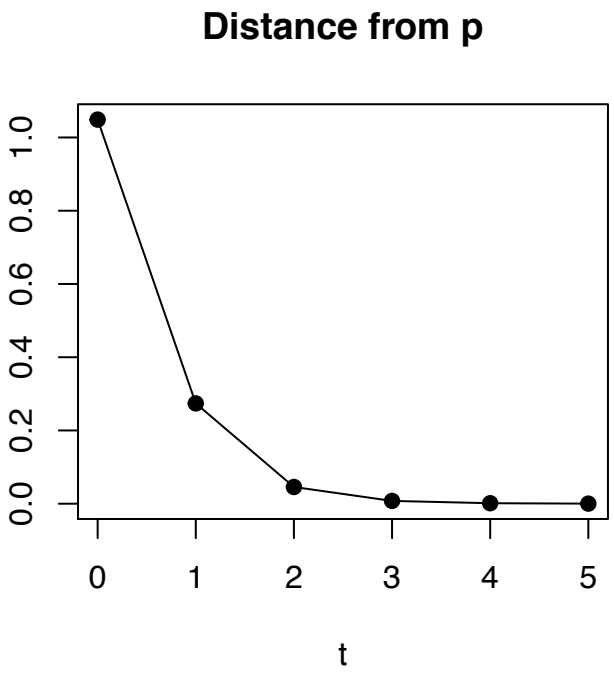
```
n = 5
# initialize a 3-dimensional array
jointdist = array(dim = c(2, 2, n + 1))
# set the first matrix of that array to p0
jointdist[, , 1] <- matrix(c(1, 0, 0, 0), nrow = 2)
for (t in 2:(n + 1)) {
    # get x_t|y_(t-1)
    x1y1 = px_y1[1] * sum(jointdist[, 1, t - 1])
    x2y1 = px_y1[2] * sum(jointdist[, 1, t - 1])
    x1y2 = px_y2[1] * sum(jointdist[, 2, t - 1])
    x2y2 = px_y2[2] * sum(jointdist[, 2, t - 1])
    jointdist[, , t] = matrix(c(x1y1, x1y2, x2y1, x2y2), 2, byrow = TRUE)

    # get y_t|x_t
    x1y1 = py_x1[1] * sum(jointdist[1, , t])
    x1y2 = py_x1[2] * sum(jointdist[1, , t])
    x2y1 = py_x2[1] * sum(jointdist[2, , t])
    x2y2 = py_x2[2] * sum(jointdist[2, , t])
    jointdist[, , t] = matrix(c(x1y1, x1y2, x2y1, x2y2), 2, byrow = TRUE)
}
for (t in 0:n) {
    print(paste("Joint distribution at t =", t))
    print(jointdist[, , t + 1])
}
```

```
## [1] "Joint distribution at t = 0"
##      [,1] [,2]
## [1,]    1    0
## [2,]    0    0
## [1] "Joint distribution at t = 1"
##      [,1] [,2]
## [1,] 0.05  0.2
```

```
## [2,] 0.45  0.3
## [1] "Joint distribution at t = 2"
##         [,1]   [,2]
## [1,] 0.09167 0.3667
## [2,] 0.32500 0.2167
## [1] "Joint distribution at t = 3"
##         [,1]   [,2]
## [1,] 0.09861 0.3944
## [2,] 0.30417 0.2028
## [1] "Joint distribution at t = 4"
##         [,1]   [,2]
## [1,] 0.09977 0.3991
## [2,] 0.30069 0.2005
## [1] "Joint distribution at t = 5"
##         [,1]   [,2]
## [1,] 0.09996 0.3998
## [2,] 0.30012 0.2001
```

This isn't required by the homework, but we can create a metric of how close our approximate joint distribution is to p at each value of t.

```
distance = apply(jointdist, 3, function(mat) {
    # the distance between two matrices is the sqrt of the sum of the squared
    # differences
    sqrt(sum((mat - probs)^2))
})
plot(0:n, distance, xlab = "t", ylab = "", type = "o", pch = 19, main = "Distance from p")
```



Problem 1.4

```
Nsim = 20
M = 1e+05
# create a data frame of each person's x&y value
distribution = data.frame(x = rep(1, M), y = rep(1, M))
jointdist = array(0, dim = c(2, 2, Nsim))
for (t in 1:Nsim) {
    # get (x_t|y_t-1)
    r = runif(M)  #generate a random number for each person
    indy1 = which(distribution$y == 1)  #indices of which people have y_(t-1)==1
    indy2 = which(distribution$y == 2)
    distribution$x[indy1] = ifelse(r[indy1] < px_y1[1], 1, 2)
    distribution$x[indy2] = ifelse(r[indy2] < px_y2[1], 1, 2)

    # get (y_t|x_t)
    r = runif(M)
    indx1 = which(distribution$x == 1)
    indx2 = which(distribution$x == 2)
```

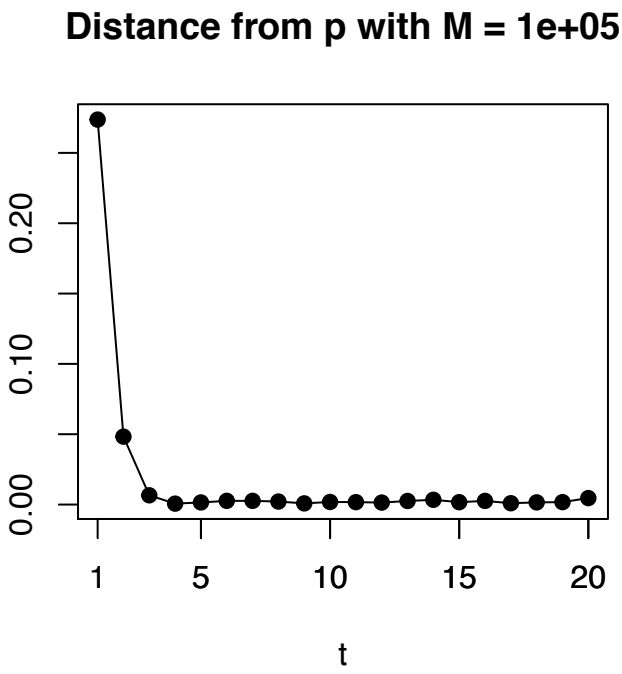
```
    distribution$y[indx1] = ifelse(r[indx1] < py_x1[1], 1, 2)
    distribution$y[indx2] = ifelse(r[indx2] < py_x2[1], 1, 2)
    for (x in 1:2) for (y in 1:2) {
        # fill in each cell of the joint dist.
        jointdist[x, y, t] = sum(distribution$x == x & distribution$y == y)
    }
    # convert from number of people to proportion
    jointdist[, , t] = jointdist[, , t]/M
}
jointdist[, , Nsim]
```

```
##         [,1]   [,2]
## [1,] 0.09889 0.3968
## [2,] 0.30230 0.2021
```

```
probs
```

```
##      [,1] [,2]
## [1,]  0.1  0.4
## [2,]  0.3  0.2
```

```
distance = apply(jointdist, 3, function(mat) {
    sqrt(sum((mat - probs)^2))
})
plot(1:Nsim, distance, xlab = "t", ylab = "", type = "o", pch = 19, main = paste0("Distance
    M))
axis(1, at = c(1, seq(5, Nsim, by = 5)))
```

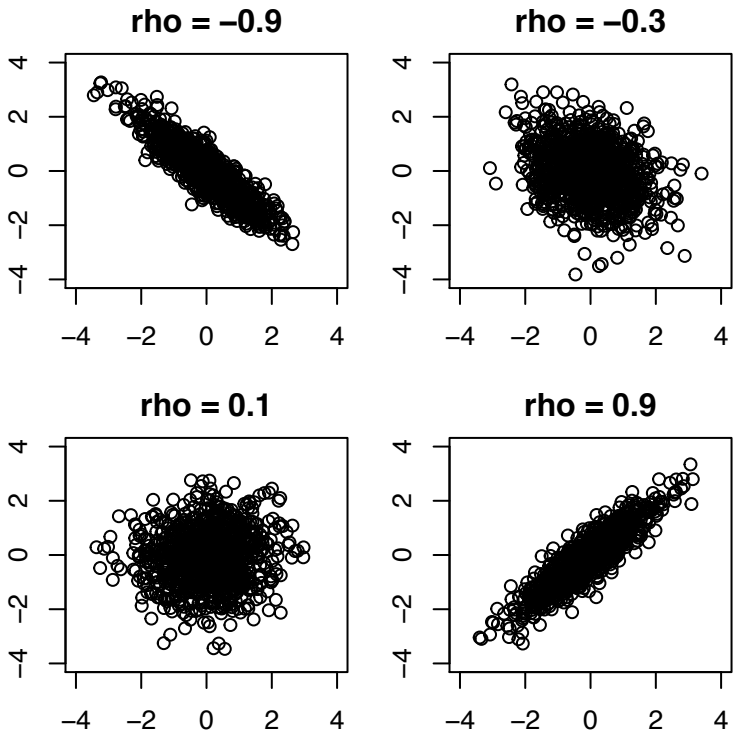


Problem 2

Since we want to test out various values of ρ, let's create a function that we can run with different parameters.

```
gibbsBivarNorm = function(rho, Nsim = 2000, burnin = 1000, x0 = 0, y0 = 0, returnvals = TRUE
    plotit = TRUE) {
    x = y = numeric(Nsim)
    # first iteration happens outside the for loop
    x[1] = rnorm(1, rho * y0, sqrt(1 - rho^2))
    y[1] = rnorm(1, rho * x[1], sqrt(1 - rho^2))
    for (t in 2:Nsim) {
        x[t] = rnorm(1, rho * y[t - 1], sqrt(1 - rho^2))  #conditional dist. of x|y
        y[t] = rnorm(1, rho * x[t], sqrt(1 - rho^2))  #conditional dist. of y|x
    }
    # remove the samples from the burn-in period.
    x = x[(burnin + 1):Nsim]
    y = y[(burnin + 1):Nsim]
    if (plotit)
        plot(x, y, main = paste("rho =", rho), xlim = c(-4, 4), ylim = c(-4,
```

```
            4))
    # note that I'm keeping the limits of the graph constant regardless of rho
    if (returnvals)
        return(list(x = x, y = y, expec_val = mean(sqrt(x^2 + y^2))))
}
par(mfrow = c(2, 2), mar = c(2.5, 2, 2, 1) + 0.1)
# FYI, default margins are mar=c(5, 4, 4, 2) + 0.1
gibbsBivarNorm(-0.9)$expec_val

## [1] 1.177

gibbsBivarNorm(-0.3)$expec_val

## [1] 1.254

gibbsBivarNorm(0.1)$expec_val

## [1] 1.276

gibbsBivarNorm(0.9)$expec_val

## [1] 1.16
```



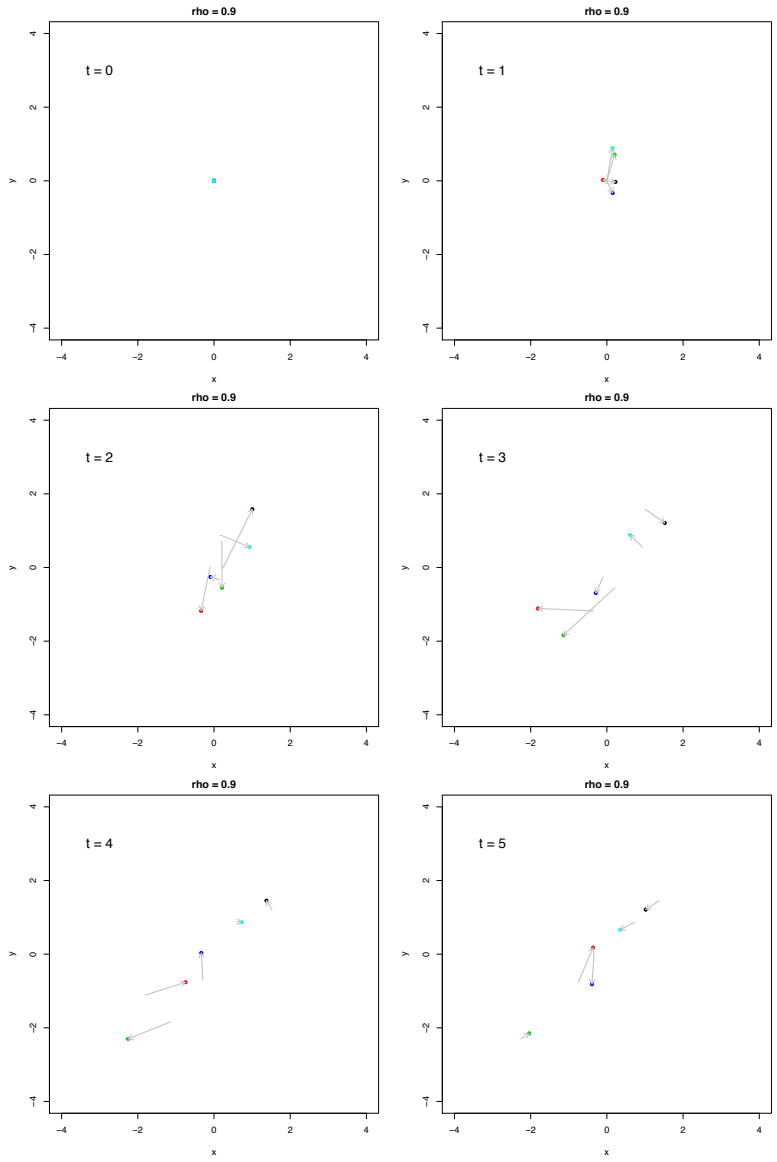
Problem 2-Bonus

We'll create a function that outputs a series of plots, interrupted by pauses. If we wrap this function in the saveGIF() function it should create an animated gif.

```
library(animation)
gibbsBivarNorm_walk = function(rho, M, x0 = 0, y0 = 0, Nsim = 50, burnin = 0,
    arrow = TRUE) {
    xvals = yvals = matrix(nrow = Nsim + 1, ncol = M)
    for (i in 1:M) {
        # get the samples from each walk separately
        samples = gibbsBivarNorm(rho, Nsim, burnin, x0, y0, plotit = FALSE)
        xvals[, i] = c(x0, samples$x)
        yvals[, i] = c(y0, samples$y)
    }
    for (t in (burnin + 1):(Nsim + 1)) {
        # plot all samples from a given t together
        plot(xvals[t, ], yvals[t, ], type = "p", col = 1:M, xlim = c(-4, 4),
            ylim = c(-4, 4), xlab = "x", ylab = "y", pch = 16, main = paste("rho =",
                rho))
        # draw arrows from previous points
        if (arrow & t > 1)
            arrows(xvals[t - 1, ], yvals[t - 1, ], xvals[t, ], yvals[t, ], length = 0.1,
                col = "grey")
        # write t (notice that I'm placing the text where it's less likely to
        # overlap text)
        if (rho >= 0) {
            text(-3, 3, paste("t =", t - 1), cex = 1.5)
        } else text(3, 3, paste("t =", t - 1), cex = 1.5)
        ani.pause()
    }
}
```

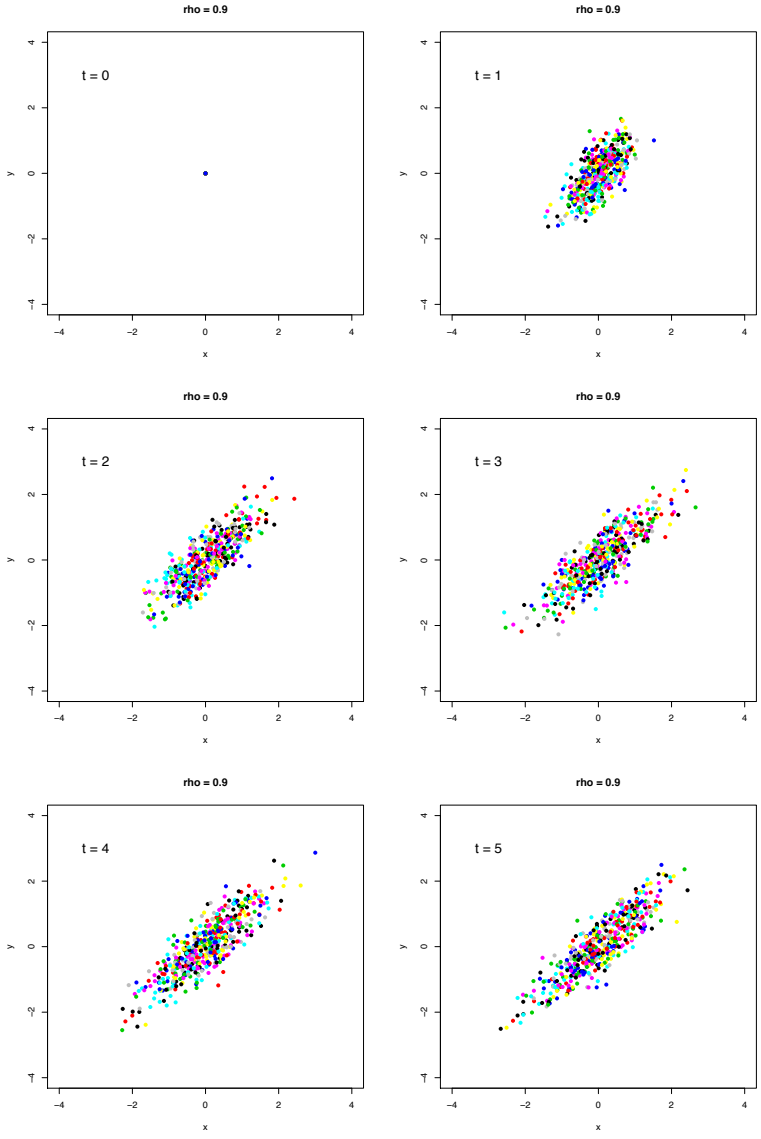
Let's check out a few of these visualizations. Here we're using a low M, starting all of our chains at $(0, 0)$, and using arrows to see how each point is moving.

```
par(mfrow = c(1, 1), mar = c(4, 4, 2, 1))
ani.options(interval = 0.1)
# the next 2 lines will generate the 'video' in your plotting window
gibbsBivarNorm_walk(rho = 0.9, M = 5, Nsim = 5)
```



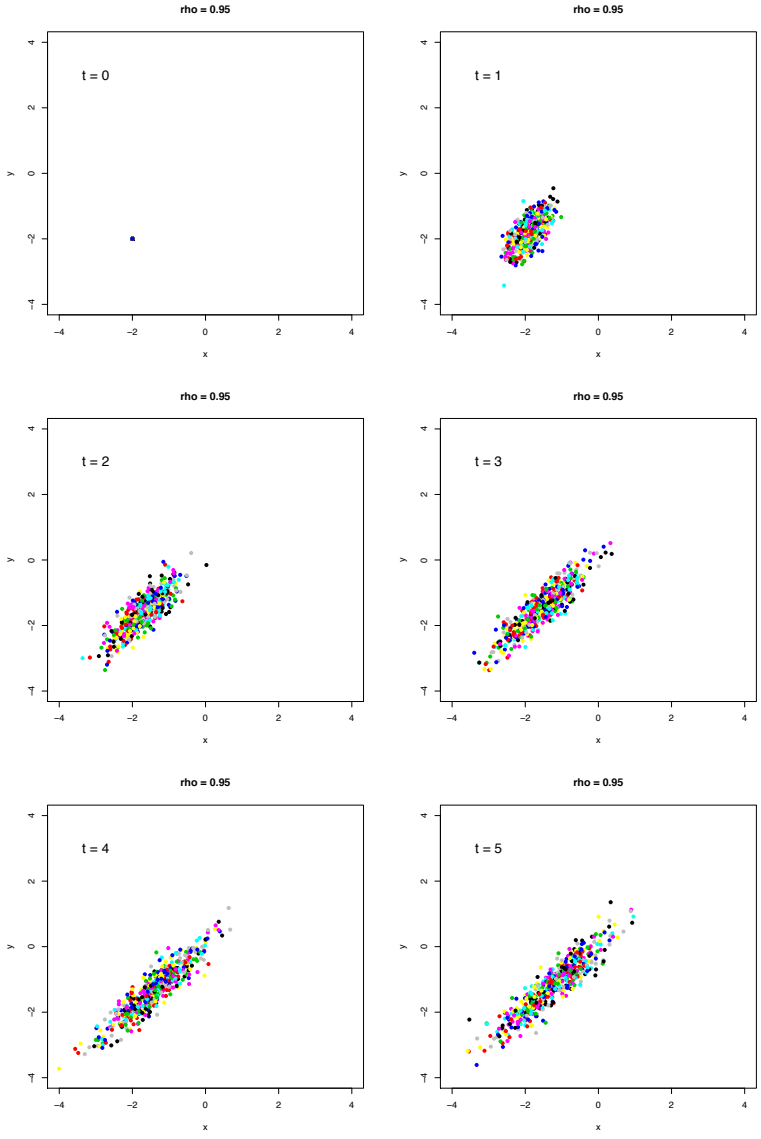
Here's a much larger M. See how the distribution is coverging to the joint distribution $p(x, y)$?

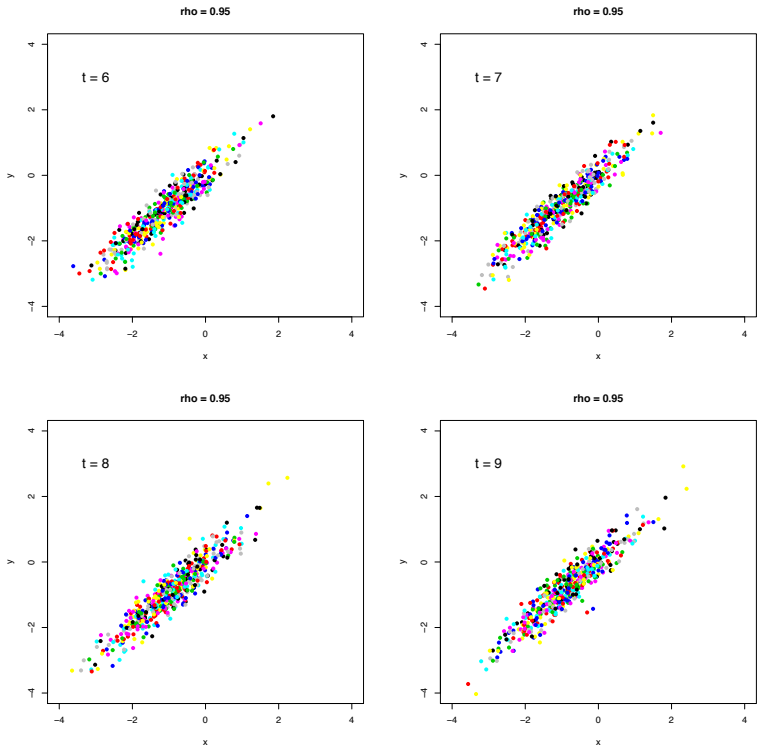
```
gibbsBivarNorm_walk(rho = 0.9, M = 500, arrow = FALSE, Nsim = 5)
```



And finally, here are 500 Markove chains that are starting far from the center and with $\rho = 0.95$.

```
gibbsBivarNorm_walk(rho = 0.95, M = 500, arrow = FALSE, x0 = -2, y0 = -2, Nsim = 9)
```


rho = 0.95
t = 0
rho = 0.95
t = 1
rho = 0.95
t = 2
rho = 0.95
t = 3
rho = 0.95
t = 4
rho = 0.95
t = 5
x
y



The following code chunk isn't being run, but will save GIFs of the sequences.

```
# The file should pop up separately, make sure you save it somewhere useful.
saveGIF(gibbsBivarNorm_walk(rho = 0.9, M = 5, Nsim = 50), movie.name = "smallM.gif")
saveGIF(gibbsBivarNorm_walk(rho = 0.9, M = 500, arrow = FALSE, Nsim = 50), movie.name = "big
saveGIF(gibbsBivarNorm_walk(rho = 0.95, M = 500, arrow = FALSE, x0 = -3, y0 = -3,
    Nsim = 50), movie.name = "bigM2.gif")
```