Exercise 1:

```r
> n = 100
> x = runif(n, min = 0, max = 10)
> a = 1
> b = 0.5
> s = 3
> y_det = a * x * exp(-b * x)
> y = rgamma(n, shape = s, scale = y_det/s)
> plot(x, y)
> curve(a * x * exp(-b * x), add = TRUE)
```
Exercise 2:
Redo spatial distribution simulation:

```r
> set.seed(1001)
> nparents = 50
> noffspr = 10
> L = 30
> parent_x = runif(nparents, min = 0, max = L)
> parent_y = runif(nparents, min = 0, max = L)
> angle = runif(nparents * noffspr, min = 0, max = 2 * pi)
> dist = rexp(nparents * noffspr, 0.5)
> offspr_x = rep(parent_x, each = noffspr) + cos(angle) * dist
> offspr_y = rep(parent_y, each = noffspr) + sin(angle) * dist
> dist = sqrt((outer(offspr_x, offspr_x, "-"))^2 + (outer(offspr_y, 
+    offspr_y, 
+    "-"))\(^2\))
> nbrcrowd = apply(dist < 2, 1, sum) - 1
```

Calculate mean and standard deviation of neighborhood crowding:

```r
> m = mean(nbrcrowd)
> s2 = var(nbrcrowd)
```

Method of moments: \( \mu = m; \) variance \( \sigma^2 = \mu(1 + \mu/k) \) or \( k = \mu/(\sigma^2/\mu - 1). \)

```r
> k.est = m/(s2/m - 1)
```

Plot distribution of neighborhood crowding:

```r
> b1 = barplot(table(factor(nbrcrowd, levels = 0:max(nbrcrowd)))/length(nbrcrowd), 
+    xlab = "Number of neighbors", ylab = "Proportion")
> points(b1, dnbinom(0:max(nbrcrowd), mu = m, size = k.est), pch = 16)
```
Exercise 3:
Continue with pigweed simulation:

```r
> ci = nbrcrowd * 3
> M = 2.3
> alpha = 0.49
> mass_det = M/(1 + ci)
> mass = rgamma(length(mass_det), scale = mass_det, shape = alpha)
> b = 271.6
> k = 0.569
> seed_det = b * mass
> seed = rnbinom(length(seed_det), mu = seed_det, size = k)
```

Calculate the median: the median is identical to the 50% quantile of the distribution, or `qbinom(0.5)`.

```r
> logxvec = seq(-7, 1, length = 100)
> xvec = 10^logxvec
> med = qbinom(0.5, mu = b * xvec, size = k)
> plot(mass, 1 + seed, log = "xy", xlab = "Mass", ylab = "1+Seed set")
> curve(b * x + 1, add = TRUE)
> lower = qbinom(0.025, mu = b * xvec, size = k)
> upper = qbinom(0.975, mu = b * xvec, size = k)
```
The median is lower than the mean because the distribution is right-skewed; like the upper and lower quantiles, the median of the (discrete) negative binomial distribution changes by discrete steps rather than smoothly like the mean.

**Exercise 4:**
Set up simulation:

```r
> rzinbinom = function(n, mu, size, zprob) {
+   ifelse(runif(n) < zprob, 0, rbinom(n, mu = mu, size = size))
+ }
> a = 0.696
> b = 9.79
> recrprob = function(x, a = 0.696, b = 9.79) {
+   a/(1 + (a/b) * x)
+ }
> scoefs = c(mu = 25.32, k = 0.932, zprob = 0.123)
> settlers = rzinbinom(603, mu = scoefs["mu"], size = scoefs["k"],
+   zprob = scoefs["zprob")
> recr = rbinom(603, prob = recrprob(settlers), size = settlers)
```

Draw the figure:
Exercise 5:
Using the relationships \( \text{shape1} = a = P\theta \) and \( \text{shape2} = b = (1 - P)\theta \) relating the Morris \((P, \theta)\) to the standard statistical parameterization:

\[
\begin{align*}
&\text{rmrbinom} = \text{function}(n, \text{size}, p, \theta) \{ \\
&\quad \text{rbinom}(n, \text{size} = \text{size}, \text{prob} = \text{rbeta}(n, \text{shape1} = p * \theta, \\
&\quad \quad \text{shape2} = (1 - p) * \theta)) \\
&\} \\
&\text{a} = 0.696 \\
&\text{b} = 9.79 \\
&\text{recrprob} = \text{function}(x, a = 0.696, b = 9.79) \ a / (1 + (a/b) * x) \\
&\text{scoefs} = c(\text{mu} = 25.32, k = 0.932, \text{zprob} = 0.123) \\
&\text{settlers} = \text{rzinbinom}(603, \text{mu} = \text{scoefs}[^\text{mu}], \text{size} = \text{scoefs}[^\text{k}], \\
&\quad \text{zprob} = \text{scoefs}[^\text{zprob}]) \\
&\text{recr} = \text{rmrbinom}(603, p = \text{recrprob}(\text{settlers}), \theta = 10, \text{size} = \text{settlers})
\end{align*}
\]
Recruits
0 10 20 30 40 50
Settlers
0 10 20 30 40 50

> plot(settlers, recr, xlab = "Settlers", ylab = "Recruits")
> curve(a * x/(1 + (a/b) * x), add = TRUE)

Exercise 6: Redefine linear simulation function:

> linsim = function(nt = 20, NO = 2, dN = 1, sd_process = sqrt(2),
+   sd_obs = sqrt(2)) {
+   cur_N = NO
+   Nobs = numeric(nt)
+   Nobs[1] = cur_N + rnorm(1, sd = sd_obs)
+   for (i in 2:nt) {
+     cur_N = cur_N + rnorm(1, mean = dN, sd = sd_process)
+     Nobs[i] = cur_N + rnorm(1, sd = sd_obs)
+   }
+   return(Nobs)
+ }

Run it 1000 times:

> nsim = 1000
> Nmat = matrix(nrow = 20, ncol = nsim)
> for (i in 1:nsim) {
+   Nmat[, i] = linsim(sd_process = 2, sd_obs = 2)
+ }

6
Draw the figure:

```r
> matplot(1:20, Nmat, col = "gray", type = "l", lty = 1)
> lines(1:20, rowMeans(Nmat), lwd = 2)
> matlines(1:20, t(apply(Nmat, 1, quantile, c(0.025, 0.975))),
+   lty = 2, col = 1)
```

Exercise 7:
Redefine `immigsim` with negative binomial instead of Poisson growth:

```r
> immignbsim = function(nt = 20, N0 = 2, immig, surv, k) {
+   N = numeric(nt)
+   N[1] = N0
+   for (i in 2:nt) {
+     Nsurv = rbinom(1, size = N[i - 1], prob = surv)
+     N[i] = Nsurv + rnbinom(1, mu = immig, size = k)
+   }
+   return(N)
+ }
```

Define parameters:

```r
> nsim = 1000
> nt = 30
```
> p = 0.95
> N0 = 2
> immig = 10
> k = 0.5

> nvec = c(3, 5, 7, 10, 15, 20)
> kvec = c(5, 1, 0.5)
> nsim = 500
> powsimresults = matrix(nrow = length(nvec) * length(kvec) * nsim,
+   ncol = 6)
> colnames(powsimresults) = c("n", "k", "sim", "slope", "slope.lo",
+   "slope.hi")
> ctr = 1
> for (j in 1:length(kvec)) {
+   k = kvec[j]
+   for (i in 1:length(nvec)) {
+     nt = nvec[i]
+     tvec = 1:nt
+     for (sim in 1:nsim) {
+       current.sim = immignbsim(nt = nt, N0 = N0, surv = p,
+         immig = immig, k = k)
+       lm1 = lm(current.sim ~ tvec)
+       slope = coef(lm1)["tvec"]
+       ci.slope = confint(lm1)["tvec",]
+       powsimresults[ctr, ] = c(nt, k, sim, slope, ci.slope)
+       ctr = ctr + 1
+     }
+   }
+ }

Construct a list of factors for cross-tabulating:

> faclist = list(factor(powsimresults[, "n"],), factor(powsimresults[, 
+ "k"],))

Calculate all the cross-tabulated summary statistics:

> slope.mean = tapply(powsimresults[, "slope"], faclist, mean)
> slope.sd = tapply(powsimresults[, "slope"], faclist, sd)
> ci.good = (powsimresults[, "slope.hi"] > immig) & (powsimresults[, 
+ "slope.lo"] < immig)
> nsim = 500
> slope.cov = tapply(ci.good, faclist, sum)/nsim
> null.value = 0
> reject.null = (powsimresults[, "slope.hi"] < null.value) | (powsimresults[, 
+ "slope.lo"] > null.value)
> slope.pow = tapply(reject.null, faclist, sum)/nsim

Some plots:
Exercise 8:
Redo code with quadratic function, testing against a null value of zero:

```r
nvec = c(3, 5, 7, 10, 15, 20)
sim = 500
powsimresults = matrix(nrow = length(nvec) * nsim, ncol = 5)
colnames(powsimresults) = c("n", "sim", "quad", "quad.lo", "quad.hi")
ctr = 1
for (i in 1:length(nvec)) {
  nt = nvec[i]
  tvec = 1:nt
  for (sim in 1:nsim) {
    current.sim = immigsim(nt = nt, N0 = N0, surv = p, immig = immig)
    lm1 = lm(current.sim ~ tvec + I(tvec^2))
    quad = coef(lm1)[3]
    ci.quad = confint(lm1)[3, ]
    powsimresults[ctr, ] = c(nt, sim, quad, ci.quad)
  }
  ctr = ctr + 1
}
```
Calculate all the tabulated summary statistics (skipping coverage):

```r
quad.mean = tapply(powsimresults[, "quad"], nfac, mean)
quad.sd = tapply(powsimresults[, "quad"], nfac, sd)
n = 500
null.value = 0
reject.null = (powsimresults[, "quad.hi"] < null.value) | (powsimresults[, + "quad.lo"] > null.value)
quad.pow = tapply(reject.null, nfac, sum)/nsim
```

Some plots:

```r
op = par(mfrow = c(2, 2))
plot(nvec, quad.mean, type = "b")
plot(nvec, quad.sd, type = "b")
plot(nvec, quad.pow, type = "b")
par(op)
```