## Lab 5: stochastic simulation — solutions

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©2005 Ben Bolker Exercise 1: > 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:

```
> 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</pre>
```

Calculate mean and standard deviation of neighborhood crowding:

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

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

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

Plot distribution of neighborhood crowding:

```
> 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:

```
> 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 qnbinom(0.5).

```
> logxvec = seq(-7, 1, length = 100)
> xvec = 10^logxvec
> med = qnbinom(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 = qnbinom(0.025, mu = b * xvec, size = k)
> upper = qnbinom(0.975, mu = b * xvec, size = k)
```

```
> lines(xvec, lower + 1, lty = 2, type = "s")
> lines(xvec, upper + 1, lty = 2, type = "s")
> lines(xvec, med + 1, lwd = 2, type = "s")
```



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:

```
> rzinbinom = function(n, mu, size, zprob) {
+     ifelse(runif(n) < zprob, 0, rnbinom(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  $\mathtt{shape1}=a=P\theta$  and  $\mathtt{shape2}=b=(1-P)\theta$  relating the Morris  $(P, \theta)$  to the standard statistical parameterization:

> 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)
+
+ }
```

Draw the figure:

```
> 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:

```
> 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:

> nsim = 1000 > nt = 30

```
> p = 0.95
> NO = 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, NO = NO, 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[,</pre>
      "slope.lo"] > null.value)
+
> slope.pow = tapply(reject.null, faclist, sum)/nsim
   Some plots:
```

```
> par(mfrow = c(2, 2))
> matplot(nvec, slope.mean, type = "b")
> matplot(nvec, slope.sd, type = "b")
> matplot(nvec, slope.cov, type = "b")
> matplot(nvec, slope.pow, type = "b")
```



## Exercise 8:

Redo code with quadratic function, testing against a null value of zero:

```
> nvec = c(3, 5, 7, 10, 15, 20)
> nsim = 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, NO = NO, 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):

```
> quad.mean = tapply(powsimresults[, "quad"], nfac, mean)
> quad.sd = tapply(powsimresults[, "quad"], nfac, sd)
> nsim = 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:

> 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)



