Homework 6

MacKenzie Ullman

4/9/2021

1. Load data and place into an unmarkedFramePCount object

```
setwd("F:/Quant Eco")
getwd()
## [1] "F:/Quant Eco"
HW6 <- read.csv(file ='count.csv')
head(HW6)
##
     j1 j2 j3
## 1 0 0 0
     1
        1 1
## 3 8 13 12
## 4 2 1 1
## 5 3 8 3
## 6 0 0
summary(HW6)
##
                          j2
                                          j3
          j1
         : 0.00
                          : 0.00
                                    Min.
                                         : 0.00
   Min.
                    Min.
   1st Qu.: 1.00
                    1st Qu.: 1.00
                                    1st Qu.: 1.00
##
   Median: 2.00
                    Median: 2.00
                                    Median: 2.00
##
##
  Mean
          : 3.21
                    Mean
                          : 3.24
                                    Mean
                                          : 3.43
  3rd Qu.: 4.00
                    3rd Qu.: 4.00
                                    3rd Qu.: 5.00
                           :25.00
## Max.
           :24.00
                    Max.
                                    Max.
                                           :17.00
library(unmarked)
## Warning: package 'unmarked' was built under R version 3.6.3
## Loading required package: lattice
count_mat <- as.matrix(HW6)</pre>
nmix_data <- unmarkedFramePCount(y = count_mat)</pre>
```

2. Fit an N-mixture model that assumes conditional detection probability is a function of the detection covariate provided, and expected abundance is an additive function of variables x1 and x2.

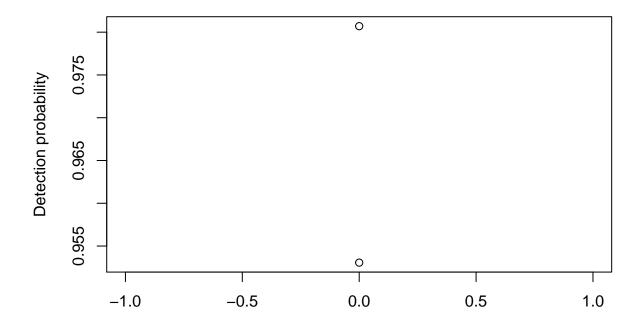
```
## 4 0.7138189 0.857225770 1.5519564
## 5 2.0457416 0.077946090 1.9626749
## 6 0.7596043 -0.356677808 -0.1295560
#Placing detection covariates in an unmarkedFramePCount object
det covs <- list(</pre>
replicate = data.frame(p_covs[, c('j1', 'j2', 'j3')])
)
#Placing the list of detection covariates in to the unmarkedFramePCount object
nmix_data <- unmarkedFramePCount(y = as.matrix(count_mat), obsCovs = det_covs)</pre>
fit <- pcount(formula = ~ replicate ~ 1, data = nmix_data, K = 100)</pre>
#site level covariates
sitecovs <- read.csv('site_covs.csv')</pre>
head(sitecovs)
##
              x1 x2
## 1 -1.06733947 b
## 2 -0.98588873 a
## 3 -0.09409764 d
## 4 1.32241491
## 5 0.45689994 d
## 6 -0.89026419 b
nmix_data <- unmarkedFramePCount(y = as.matrix(count_mat), siteCovs = sitecovs, obsCovs = det_covs)</pre>
fit <- pcount(~ replicate ~ x1 + x2,data = nmix_data, K = 100)</pre>
summary(fit)
##
## Call:
## pcount(formula = ~replicate ~ x1 + x2, data = nmix_data, K = 100)
##
## Abundance (log-scale):
               Estimate
                            SE
                                   z P(>|z|)
## (Intercept)
                  0.915 0.1106 8.27 1.30e-16
## x1
                  0.370 0.0401 9.21 3.14e-20
                 -0.161 0.1382 -1.16 2.45e-01
## x2b
                 -0.189 0.1522 -1.24 2.14e-01
## x2c
## x2d
                 1.335 0.1195 11.17 5.63e-29
##
## Detection (logit-scale):
               Estimate
                            SE
                                   z P(>|z|)
                 1.259 0.0925 13.6 4.01e-42
## (Intercept)
## replicate
                 -0.841 0.0639 -13.2 1.57e-39
##
## AIC: 1736.028
## Number of sites: 200
## optim convergence code: 0
## optim iterations: 46
## Bootstrap iterations: 0
```

3. Interpret the effect of x1 on the expected count at each site. Verity your interpretation in R. The expected count per each site increases by 0.3696188 when x1 increases by 1 unit.

```
#verify
beta <- coef(fit)
##
       lam(Int)
                     lam(x1)
                                  lam(x2b)
                                               lam(x2c)
                                                             lam(x2d)
                                                                            p(Int)
##
      0.9151447
                   0.3696188
                               -0.1606306
                                             -0.1891303
                                                            1.3351914
                                                                         1.2585992
## p(replicate)
     -0.8410807
a <- beta[2]*1
     lam(x1)
## 0.3696188
b <- beta[2] *2
     lam(x1)
## 0.7392376
c <- b-a
##
     lam(x1)
## 0.3696188
  4. Predict and plot the effect of the supplied detection covariate. Do this over the range of this covariate.
new <- data.frame(replicate = seq(from = min(det_covs$replicate), to = max(det_covs$replicate), length.</pre>
prd <- predict(object = fit, newdata = new, type = 'det')</pre>
prd
##
       Predicted
                          SE
                                  lower
      0.9698079 0.006852513 0.9530609 0.9807009
       0.9682779 0.007075790 0.9510610 0.9795680
## 2
       0.9666731 0.007303550 0.9489797 0.9783704
      0.9649900 0.007535662 0.9468141 0.9771046
## 4
      0.9632251 0.007771974 0.9445612 0.9757669
## 6
       0.9613748 0.008012310 0.9422177 0.9743534
       0.9594353 0.008256468 0.9397807 0.9728603
## 7
## 8
       0.9574028 0.008504222 0.9372466 0.9712832
       0.9552732 0.008755319 0.9346122 0.9696180
## 10 0.9530423 0.009009476 0.9318739 0.9678600
## 11 0.9507059 0.009266382 0.9290284 0.9660045
## 12 0.9482595 0.009525696 0.9260719 0.9640466
## 13 0.9456987 0.009787044 0.9230009 0.9619813
       0.9430188 0.010050021 0.9198115 0.9598031
## 15 0.9402149 0.010314193 0.9165001 0.9575068
## 16 0.9372823 0.010579089 0.9130626 0.9550866
## 17 0.9342159 0.010844209 0.9094952 0.9525366
## 18 0.9310105 0.011109020 0.9057939 0.9498510
## 19 0.9276611 0.011372959 0.9019547 0.9470235
## 20 0.9241624 0.011635433 0.8979735 0.9440478
## 21 0.9205089 0.011895821 0.8938462 0.9409174
```

```
0.9166952 0.012153478 0.8895686 0.9376257
       0.9127160 0.012407735 0.8851365 0.9341660
       0.9085656 0.012657908 0.8805457 0.9305315
       0.9042386 0.012903296 0.8757921 0.9267154
  25
       0.8997295 0.013143191 0.8708713 0.9227107
##
  27
       0.8950326 0.013376884 0.8657791 0.9185104
       0.8901426 0.013603670 0.8605112 0.9141077
## 29
       0.8850540 0.013822859 0.8550635 0.9094957
   30
       0.8797616 0.014033785 0.8494316 0.9046677
##
  31
       0.8742601 0.014235818 0.8436114 0.8996171
   32
       0.8685446 0.014428373 0.8375987 0.8943375
##
   33
       0.8626100 0.014610928 0.8313894 0.8888228
##
   34
       0.8564518 0.014783035 0.8249792 0.8830671
##
   35
       0.8500656 0.014944339 0.8183643 0.8770651
       0.8434471 0.015094592 0.8115404 0.8708119
##
  36
##
  37
       0.8365927 0.015233675 0.8045037 0.8643030
       0.8294989 0.015361615 0.7972503 0.8575347
##
  38
##
       0.8221625 0.015478606 0.7897762 0.8505039
       0.8145811 0.015585027 0.7820778 0.8432084
##
  40
##
       0.8067524 0.015681463 0.7741513 0.8356466
##
  42
       0.7986748 0.015768722 0.7659930 0.8278182
       0.7903474 0.015847852 0.7575996 0.8197237
##
  44
       0.7817696 0.015920156 0.7489676 0.8113649
       0.7729417 0.015987197 0.7400939 0.8027446
##
  46
       0.7638646 0.016050804 0.7309753 0.7938668
       0.7545398 0.016113068 0.7216092 0.7847370
       0.7449697 0.016176327 0.7119931 0.7753618
##
  48
##
   49
       0.7351575 0.016243147 0.7021249 0.7657491
       0.7251071 0.016316280 0.6920032 0.7559080
##
  50
  51
       0.7148232 0.016398621 0.6816268 0.7458488
## 52
       0.7043114 0.016493146 0.6709958 0.7355829
##
  53
       0.6935783 0.016602837 0.6601108 0.7251227
##
       0.6826312 0.016730598 0.6489737 0.7144814
       0.6714782 0.016879164 0.6375876 0.7036725
##
  55
       0.6601284 0.017051003 0.6259572 0.6927104
##
       0.6485917 0.017248225 0.6140886 0.6816094
##
  57
  58
       0.6368788 0.017472490 0.6019899 0.6703840
##
  59
       0.6250012 0.017724941 0.5896711 0.6590483
       0.6129713 0.018006141 0.5771438 0.6476165
##
       0.6008018 0.018316041 0.5644221 0.6361021
##
  61
       0.5885067 0.018653966 0.5515216 0.6245182
       0.5761000 0.019018627 0.5384600 0.6128772
##
  63
##
   64
       0.5635966 0.019408154 0.5252566 0.6011912
       0.5510119 0.019820144 0.5119323 0.5894716
##
   65
  66
       0.5383615 0.020251728 0.4985093 0.5777293
  67
       0.5256615 0.020699645 0.4850108 0.5659748
##
##
  68
       0.5129282 0.021160318 0.4714609 0.5542183
##
  69
       0.5001781 0.021629942 0.4578842 0.5424694
  70
       0.4874278 0.022104559 0.4443057 0.5307379
##
  71
       0.4746938 0.022580134 0.4307502 0.5190329
       0.4619927 0.023052628 0.4172427 0.5073636
##
  72
## 73
       0.4493407 0.023518058 0.4038075 0.4957390
## 74
       0.4367539 0.023972554 0.3904683 0.4841679
## 75 0.4242480 0.024412411 0.3772482 0.4726591
```

```
## 76 0.4118384 0.024834124 0.3641692 0.4612212
## 77
      0.3995399 0.025234429 0.3512523 0.4498626
## 78 0.3873668 0.025610326 0.3385173 0.4385917
## 79 0.3753328 0.025959101 0.3259825 0.4274165
## 80 0.3634508 0.026278344 0.3136650 0.4163450
## 81
     0.3517331 0.026565958 0.3015806 0.4053850
## 82 0.3401913 0.026820162 0.2897432 0.3945439
## 83 0.3288362 0.027039495 0.2781656 0.3838289
## 84
       0.3176776 0.027222811 0.2668589 0.3732469
## 85
      0.3067246 0.027369275 0.2558327 0.3628045
     0.2959854 0.027478348 0.2450952 0.3525080
      0.2854674 0.027549779 0.2346530 0.3423633
## 87
      0.2751770 0.027583590 0.2245115 0.3323757
## 88
## 89
      0.2651200 0.027580055 0.2146747 0.3225506
## 90
      0.2553011 0.027539685 0.2051451 0.3128925
## 91
      0.2457242 0.027463210 0.1959243 0.3034058
      0.2363925 0.027351553 0.1870126 0.2940944
## 93 0.2273084 0.027205817 0.1784092 0.2849616
## 94 0.2184736 0.027027255 0.1701124 0.2760107
## 95 0.2098888 0.026817258 0.1621195 0.2672441
## 96 0.2015544 0.026577327 0.1544271 0.2586642
## 97 0.1934699 0.026309060 0.1470310 0.2502726
## 98 0.1856342 0.026014125 0.1399262 0.2420708
## 99 0.1780459 0.025694249 0.1331074 0.2340598
## 100 0.1707027 0.025351199 0.1265685 0.2262402
plot(x = c(0,0), y = prd[1, c('lower', 'upper')],
ylab = 'Detection probability', xlab = '',)
```



5. Use contrasts to compare expected abundance between all pairwise levels of variable x2. Obtain p-values associated with each contrast and tell me whether you reject or fail to reject each null hypothesis tested.

```
x <- matrix(
c(0, 0, 1, -1, 0,
0, 0, 1, 0, -1,
0, 0, 0, 1, -1),
nrow = 3, byrow = T
)
Х
        [,1] [,2] [,3] [,4] [,5]
   [1,]
           0
                 0
##
                      1
                          -1
## [2,]
           0
                 0
                      1
                            0
                                -1
           0
                 0
                      0
                            1
                                -1
## [3,]
lin_com <- linearComb(obj = fit, coefficients = x, type = 'state')</pre>
lin_com
## Linear combination(s) of Abundance estimate(s)
##
##
     Estimate
                   SE (Intercept) x1 x2b x2c x2d
## 1
       0.0285 0.1332
                                 0
                                    0
                                            -1
                                                 0
## 2
     -1.4958 0.0935
                                 0
                                    0
                                        1
                                             0
                                               -1
     -1.5243 0.1140
w <- coef(lin_com) / SE(lin_com)
```

```
## [1] 0.2140043 -15.9929898 -13.3713082
```

```
#Calculating p-values
2 * pnorm(-1 * abs(w))
```

[1] 8.305437e-01 1.430000e-57 8.896231e-41

We reject all the null hypotheses. There is a difference between b and c, a difference between b and d, and a difference between c and d, in terms of abundance probability