Generative Models for Discrete Data

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```
library(tidyverse)
library(BiocManager)
library(Biostrings)
library(BSgenome.Celegans.UCSC.ce2)
```

Questions we will answer in this chapter

- Given a certain model, how can we obtain the probabilities for all possible outcomes?
- How do theoretical frequencies compare with those observed in real data?
- How can we use the Poisson distribution to analyse data on epitope detection
- How can we apply the Multinomial distribution and Monte Carlo simulation to perform power tests?

Our first example

Let X be the number of mutations along a genome of HIV.

We are told that mutations occur at a rate of .00005 per nucleotide per replication cycle. Furthermore we assume that this genome contains 10000 nucleotides per cycle.

Thus, for one cycle, X ~ Poisson(lambda = .00005 * 10000 = 5)

Exercises

1.1

Geometric Distribution:

Given a probability p, how many failures will it take to see the first success?

```
# A random sample of size 5 from a geometric distribution with p=.25
rgeom(5, .25)
```

```
## [1] 6 1 0 6 3
```

```
# What is the probability that we will see 4 failures before the first success?
dgeom(4, .25)
```

```
## [1] 0.07910156
```

```r
# What is the probability that we will see no more than 3 failures before the first success?
pgeom(3, .25)
```

```
## [1] 0.6835938
```

Hypergeometric Distribution:

Given a population of size N where K of the N objects are "success states." How many success state objects will I obtain from drawing a sample of size n without replacement?

```r
# A random sample of size 5 from a hyper geometric distribution with a population of N=25, K=5 success
# given a sample of n=10
rhyper(5, 5, 20, 10)
```

```
## [1] 0 1 0 2 2
```

```r
# What is the probability that we will see 5 success state objects?
dhyper(5, 5, 20, 10)
```

```
## [1] 0.004743083
```

```r
# What is the probability that we will see at least 1 success state object?
phyper(0, 5, 20, 10, lower.tail = F)
```

```
## [1] 0.9434783
```

1.2

$P(X = 2 \mid X \sim Bin(10, .3))$

```r
dbinom(x = 2, size = 10, p = .3)
```

```
## [1] 0.2334744
```

$P(X <= 2 \mid X \sim Bin(10, .3))$

```r
# Using only dbinom()


dbinom(x = 0, size = 10, p = .3) + dbinom(x = 1, size = 10, p = .3) + dbinom(x = 2, size = 10, p = .3)
```

```
## [1] 0.3827828
```

```r
# Using pbinom()
pbinom(q = 2, size = 10, p = .3)
```

```
## [1] 0.3827828
```

1.3

```r
pois_max = function(n, max, lamda) {
  # First calculate P(X >= max) = 1 - P(X <= max - 1)
  prob = ppois(max-1, lamda)
  # Then, as we showed before using order statistics, calculate P(X(n) >= max) = P(X(n) <= max-1)
  prob_max = 1 - prob^n
  return(prob_max)
}
```

1.4

```r
pois_max = function(n = 100, max = 0, lamda = 1) {
  # First calculate P(X >= max) = 1 - P(X <= max - 1)
  prob = ppois(max-1, lamda)
  # Then, as we showed before using order statistics, calculate P(X(n) >= max) = P(X(n) <= max-1)
  prob_max = 1 - prob^n
  return(prob_max)
}
```

1.5

```r
# Real answer
pois_max(100, 9, .5)
```

```
## [1] 3.43549e-07
```

```r
# Simulation

pois_has_max = function(n, max, lamda) {

result_vector = rpois(n, lamda)

return(max(result_vector >= max))
}

a = replicate(1e5, pois_has_max(100, 9, .5))
mean(a)
```

```
## [1] 0
```

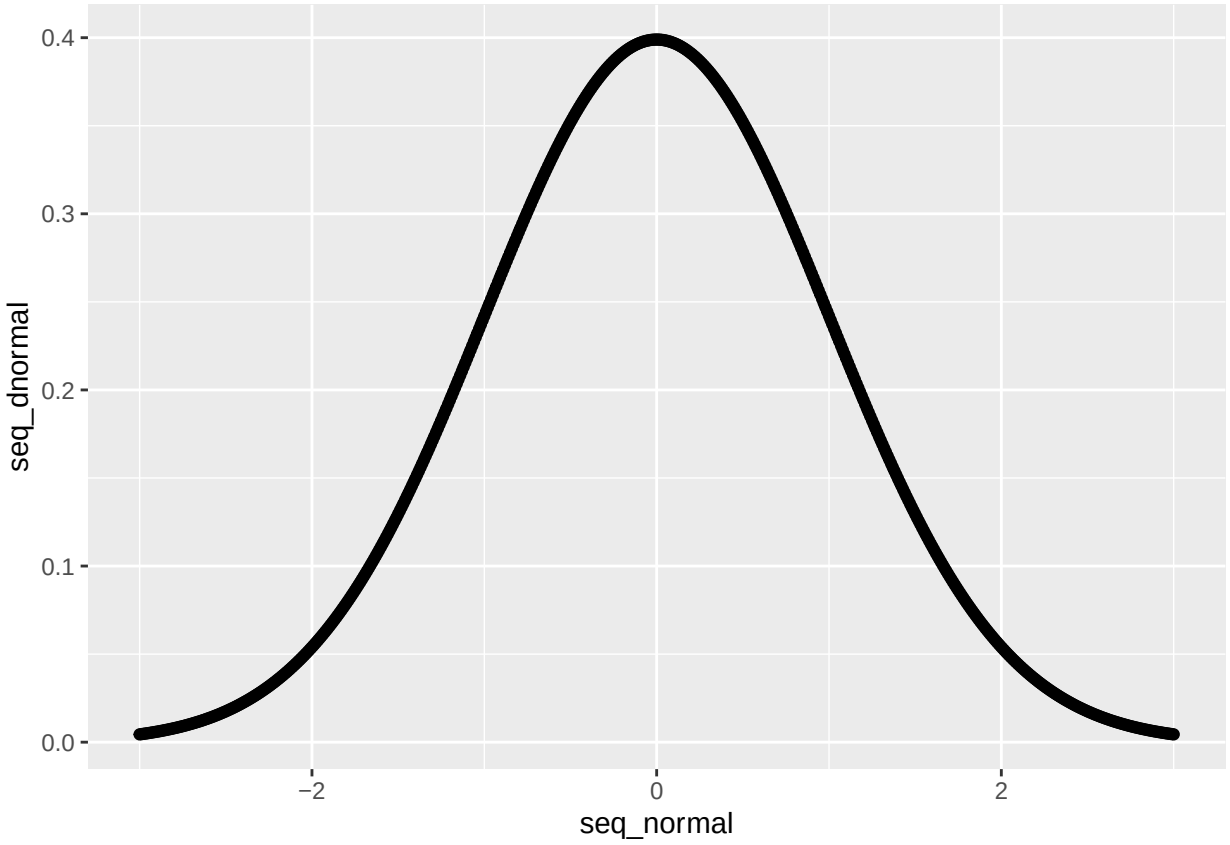
1.6

```r
# Standard normal

seq_normal = seq(-3, 3, .01)

seq_dnormal = dnorm(seq_normal, 0, 1)
```

```r
qplot(x = seq_normal, y = seq_dnormal)
```

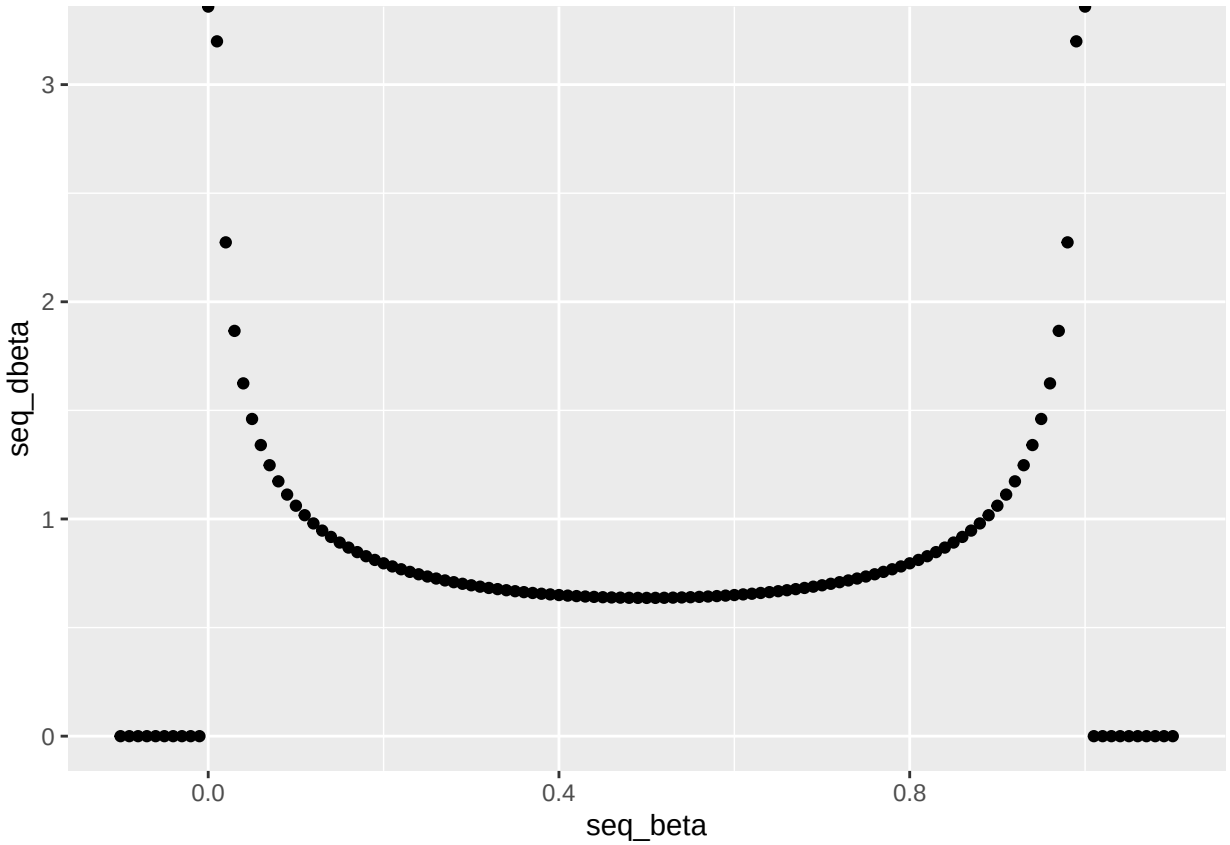



```r
# Beta(.5,.5)

seq_beta = seq(-.1, 1.1, .01)

seq_dbeta = dbeta(seq_beta, .5, .5)

qplot(x = seq_beta, y = seq_dbeta)
```

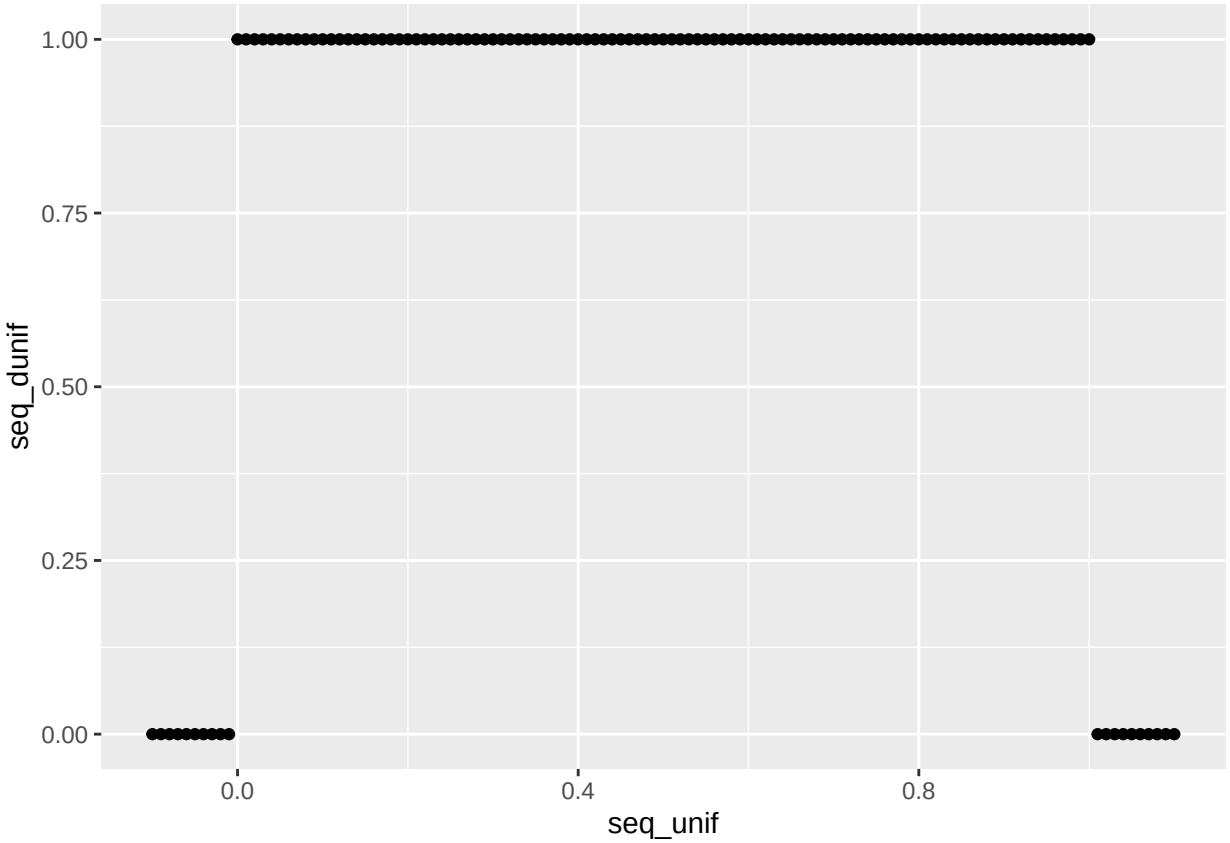



```
# Uniform (0,1)

seq_unif = seq(-.1, 1.1, .01)

seq_dunif = dunif(seq_unif, 0, 1)

qplot(x = seq_unif, y = seq_dunif)
```

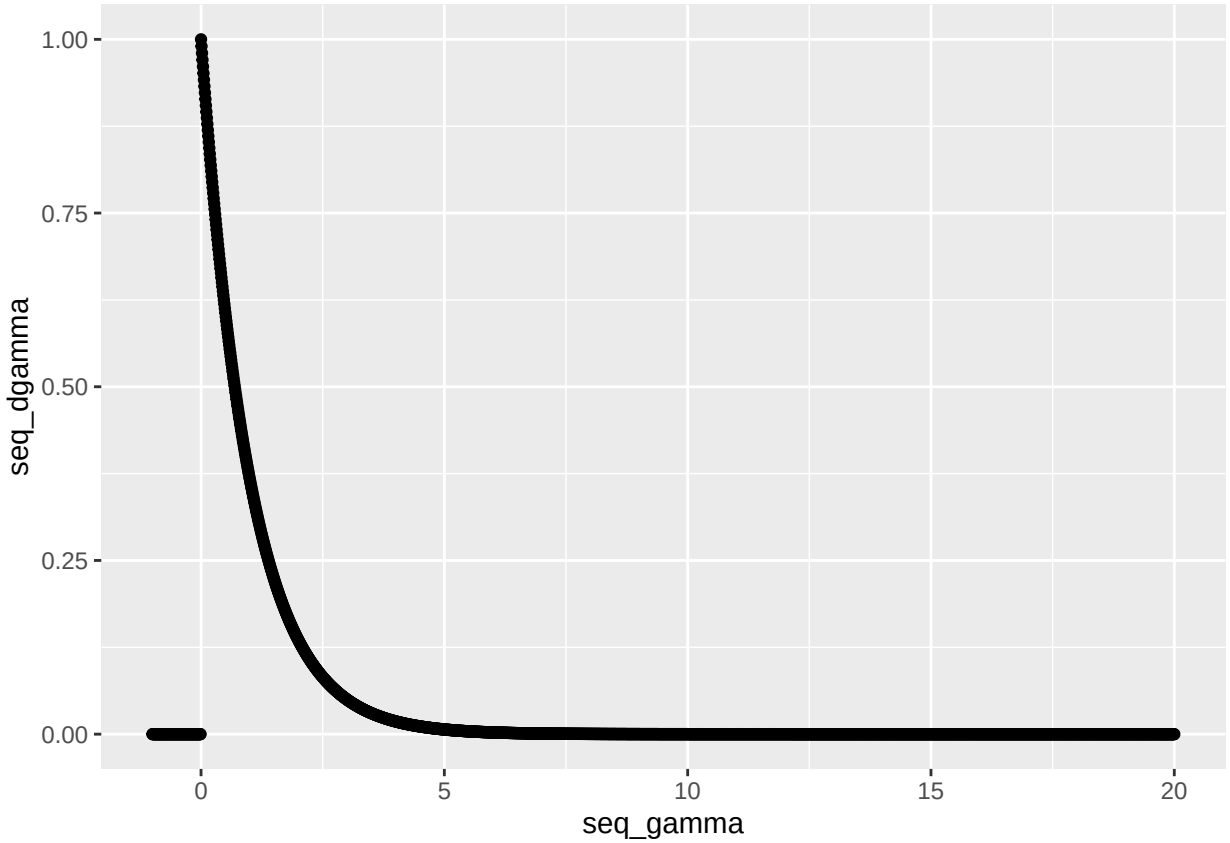



```
# Gamma(1,1)

seq_gamma = seq(-1, 20, .01)

seq_dgamma = dgamma(seq_gamma, 1, 1)

qplot(x = seq_gamma, y = seq_dgamma)
```

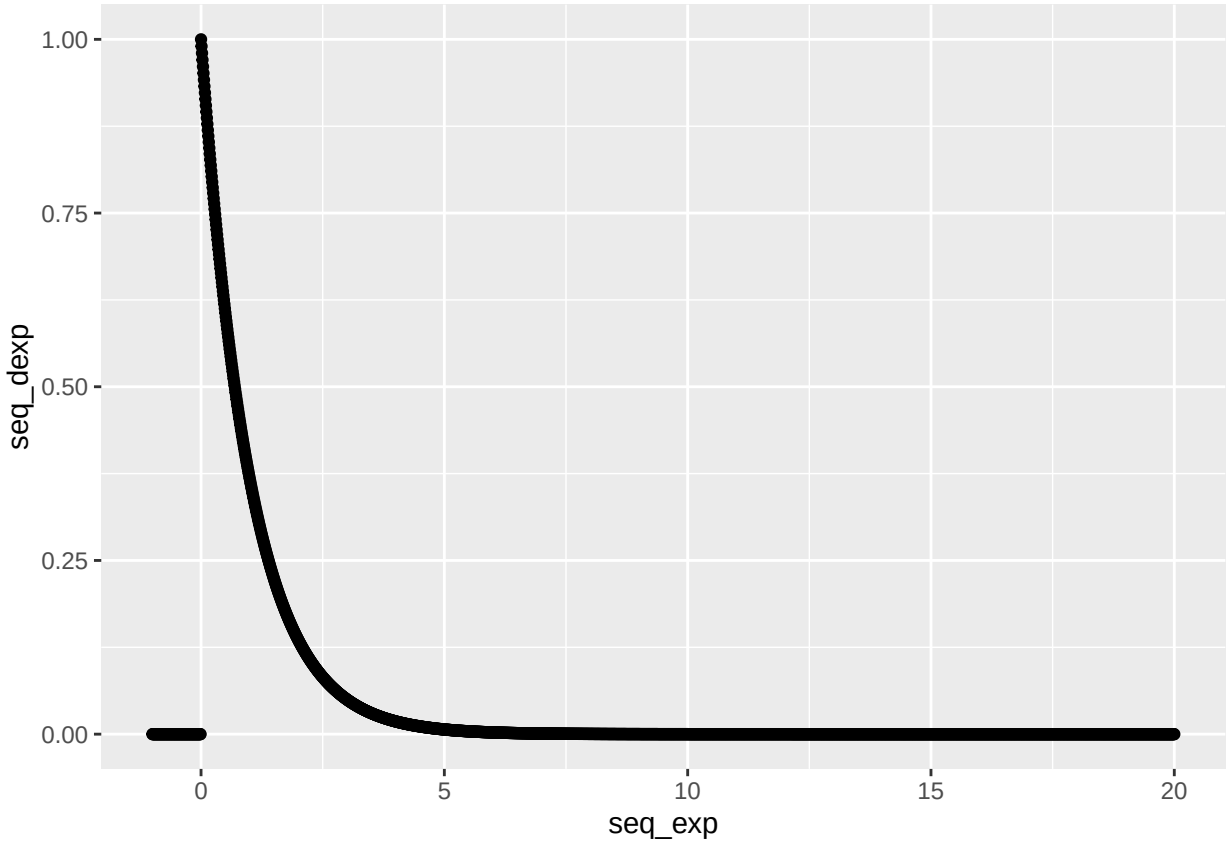



```
# Exponential(1)

seq_exp = seq(-1, 20, .01)

seq_dexp = dexp(seq_exp, 1)

qplot(x = seq_exp, y = seq_dexp)
```



1.7

Note that the mean of a pois(3) is 3, and the variance is also 3.

```
poisson_rv = rpois(100,3)

mean(poisson_rv)
```

```
## [1] 2.85
```

```
var(poisson_rv)
```

```
## [1] 3.138889
```

1.8

```
cel = BSgenome.Celegans.UCSC.ce2

dna_seq = cel$chrM
```