

Discrete distributions for the analysis of Next Generation Sequencing (NGS) data

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First version: 2016-12-10; Last update: 2016-12-12

Introduction

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Introduction

Discrete probabilities and NGS

The advent of Next Generation Sequencing (**NGS**) technologies revived the importance of discrete distributions of probabilities for biologists.

This tutorial aims at providing a rapid overview of some discrete distributions commonly used to analyse NGS data, and highlight the relationship between them.

Overview

Distribution	Applications
Geometric	Local read mapping without mismatch (read extension until first mismatch)
Binomial	Global read mapping with a given number of mismatches
Negative binomial	Local read mapping with m mismatches (waiting time for $(m + 1)^{th}$ mismatch); Detection of differentially expressed genes from RNA-seq data
Poisson	ChIP-seq peak calling
Hypergeometric	Enrichment of a set of differentially expressed genes for functional classes

Perfect match probability

Perfect match probability

We align a library of 50 million short reads of 25 base pairs onto a genome that comprises 23 chromosomes totalling 3 Gigabases. For the sake of simplicity, we assume that nucleotides are equiprobable and independently distributed in the genome. What is the probability to observe the following events by chance?

1. A perfect match for a given read at a given genomic position.
2. A perfect match for a given read anywhere in the genome (searched on two strands).
3. A perfect match for any read of the library at any position of the genome.
4. How many matches do we expect by chance if the whole library is aligned onto the whole genome?

Perfect match - parameters

Let us define the variables of our problem. Since we assume equiprobable and independent nucleotides we can define p as probability to observe a match by chance for a given nucleotide.

$$p = P(A) = P(C) = P(G) = P(T) = 0.25$$

```
k <- 25      # Read length
L <- 50e6    # Library size
C <- 23      # Number of chromosomes
G <- 3e9     # Genome size
p <- 1/4     # Matching probability for a nucleotide
```

Exercise: use these parameters to compute the matching probability for a read (*solution is on next slide*).

Perfect match for a given read at a given genomic position

Since we assume independence, the joint probability (probability to match all the nucleotides) is the product of the individual matching probabilities for each nucleotide.

```
# Matching probability for a given read  
# at a given genomic position  
P.read <- p^k
```

$$P_{\text{read}} = P(n_1 \wedge n_2 \wedge \dots \wedge n_k) = p^k = 0.25^{25} = 8.9e - 16$$

This looks a rather small probability. However we need to take into account that this risk will be challenged many times:

- ▶ the size of the genome (3 000 000 000)
- ▶ the size of the sequencing library (50 000 000)

Number of genomic alignments

The read will be aligned to each genomic position, but we should keep in mind the following facts.

1. For each chromosome, we will skip the last 24 positions, since a 25 bp read cannot be fully aligned there.
2. We double the number of alignments since we try to map the read on two strands.

$$N = 2 \sum_{i=1}^C (L_i - k + 1) = 2 (G - C(k - 1))$$

```
N <- 2 * (G - C * (k - 1))
```

In total, we will thus try to align each read on 5 999 998 896 genomic positions.

Genome-wise matching probability for one read

We reason in 3 steps, by computing the following probabilities.

Formula	Rationale
$1 - P_{\text{read}}$	no match at a given genomic position
$(1 - P_{\text{read}})^N$	not a single match in the genome
$1 - (1 - P_{\text{read}})^N$	at least one match in the genome

```
P.genomic <- 1 - (1 - P.read)^N
```

This gives $P_{\text{genomic}} = 0.00000533$.

Library-wise probability

We can apply the same reasoning for the library-wise probability.

Formula	Rationale
$1 - P_{\text{genomic}} = (1 - P_{\text{read}})^G$	no genomic match for a given read
$(1 - P_{\text{read}})^{GL}$	not a single genomic match in the library
$1 - (1 - P_{\text{read}})^{GL}$	at least one genomic match in the library

```
P.library <- 1 - (1 - P.read)^(G*L)
```

This gives $P_{\text{library}} = 1$, which should however not be literally interpreted as a certainty, but as a probability so close to 1 that it cannot be distinguished from it.

Expected number of matches

The expected number of matches is the read matching probability multiplied by the number of matching trials, i.e. $G \cdot L$ since each read will be matched against each genomic position.

$$E(X) = P_{read} \cdot N \cdot L$$

```
E <- P.read * N * L
```

In total, we expect 266 perfect matches by chance for the whole library against the whole genome.

Geometric distribution: local alignment without mismatch

Local alignment until the first mismatch

A local read-mapping algorithm starts by aligning the 5' base of a read, and extends the alignment until either the first mismatch or the end of the read. In the example below, the alignment stops after 11 nucleotides.

```
      ATGCG ACTAG CATAC GAGTG ACTAA
      11111 11111 10
... ATGCG ACTAG CGTTC GACTG ACTAA ...
```

What is the probability to obtain by chance:

1. an alignment of exactly 25 nucleotides?
2. an alignment of at least 25 nucleotides?

Local alignment – parameters

```
p <- 0.25  # Matching probability for each nucleotide  
x <- 25    # Number of matches before the first mismatch  
P.x <- p^x * (1-p)  
Pval.x <- p^x
```

$$P(X = 25) = p^x(1 - p) = 0.25^{25}0.75 = 6.66e - 16$$

$$P(X \geq 25) = p^x = 0.25^{25} = 8.88e - 16$$

Geometric distribution

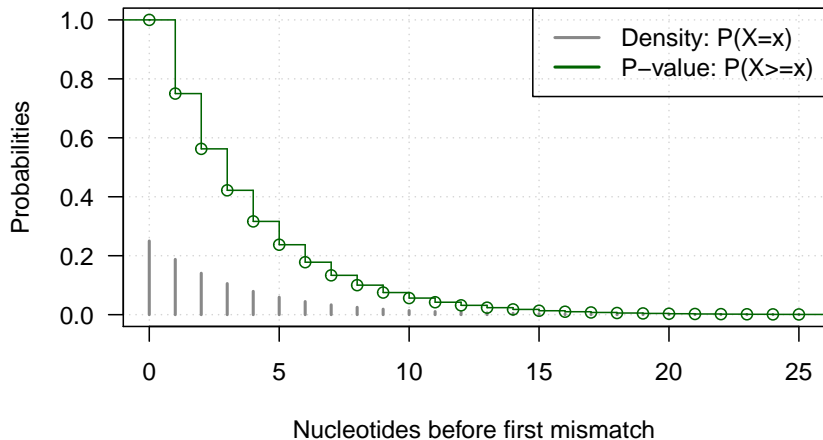


Figure 1: Geometric distribution.

- └ Geometric distribution: local alignment without mismatch

Binomial: global alignment with m mismatches

Global alignment with mismatches

What is the probability to observe a global alignment with at most $m = 3$ mismatches for a given read of 25bp aligned on a particular genomic position?

This question can be formulated as a Bernoulli schema, where each nucleotide is a trial, which can result in either a success (nucleotide match between the read and the genome) or a failure (mismatch). We can label each position of the alignment with a Boolean value indicating whether it matches (1) or not (0), as exemplified below.

ATGCG	ACTAG	CATAC	GAGTG	ACTAA			
11111	11111	10101	11011	11111			
...	ATGCG	ACTAG	CGTTC	GA	CTG	ACTAA	...

At each position, we have a probability of success $p = 0.25$, and a probability of failure $q = 1 - p = 0.75$.

Probability to observe exactly k matches

```

n <- 25      # Number of trials, i.e. the length of the ali
m <- 3       # Maximal number of accepted mismatches
k <- n - m   # Number of matches
p <- 1/4     # Matching probability for one nucleotide

```

Let us denote by k the number of matching residues. The probability to observe k successes in a Bernoulli schema with n trials and

$$P(X = k) = \mathcal{B}(k; n, p) = \binom{n}{k} p^k (1-p)^{n-k} = \frac{n!}{k!(n-k)!} p^k (1-p)^{n-k}$$

Properties of the binomial distribution

- ▶ Mean = $n \cdot p$
- ▶ Variance = $n \cdot p \cdot (1 - p)$
- ▶ Shape:
 - ▶ i-shaped when p is close to 0,
 - ▶ j-shaped when p is close to 1,
 - ▶ bell-shaped for intermediate values of p .

Binomial and perfect match

Remark: the perfect match probability seen above is a particular case of the binomial.

$$P(X = n) = \frac{n!}{n!0!} p^n (1 - p)^{n-n} = p^n$$

Probability of hit with at most m mismatches

We can sum the probabilities for all possible values of matches from $k = n - m$ (m mismatches) to $k = n$ (no mismatch).

$$P(M \leq m) = \sum_{k=n-m}^n \binom{n}{k} p^k (1-p)^{n-k}$$

Binomial density

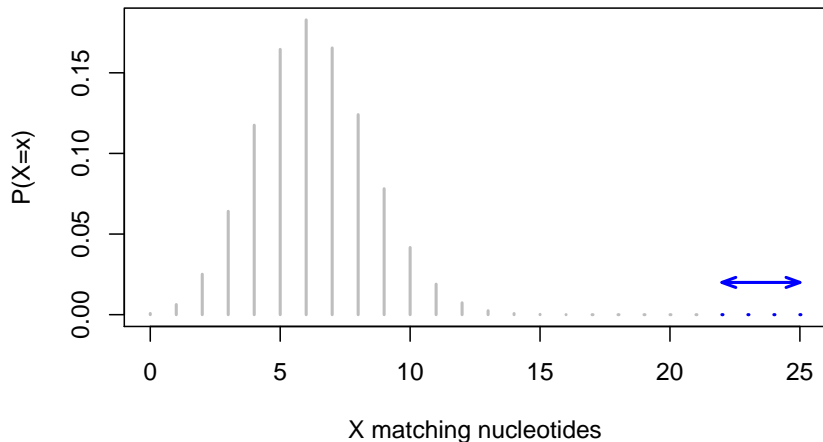


Figure 2: Binomial density function. Alignments with at most m mismatches are highlighted in blue.

Binomial P-value

Binomial P-value

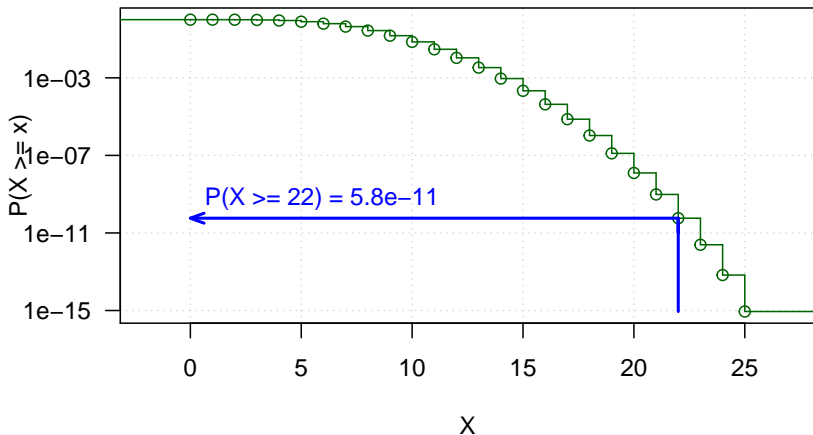


Figure 3: Binomial p-value. The ordinate indicates the probability to

Simulated sequences

We can generate random sequences with equiprobable and independent residues from the nucleotide alphabet.

$$\mathcal{A} = \{A, C, G, T\}$$

```
CAGTGCTATATAAATAGACACACAA
TGACCAGTTAGACATCAATCTTAGT
GAATTGCTTTTAAAAATTCAAACCTT
ACGTAGACAGTCTTTTTTGATGAAAA
GCAAGGATGTCCGGAGCATTCCACG
...
```

Mismatch count simulation

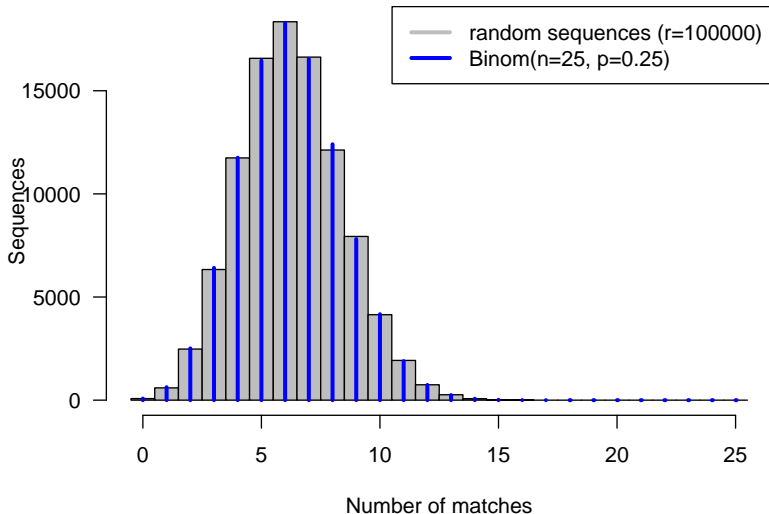


Figure 4: Global alignment simulation. A random read is aligned on

Exercise – binomial Parameters

Each student will take a custom prior probability (p) among the following values: $\{0.001, 0.01, 0.1, 0.25, 0.5, 0.75, 0.9, 0.99, 0.999\}$.

1. Draw 10000 random numbers from a binomial distribution (`rbinom()`) with the custom p and 25 trials.
2. Compute the expected mean and variance.
3. Compute the classical descriptive statistics: mean, variance, standard deviation.
4. Fill up the form on the collective result table
5. Plot an histogram of the numbers drawn.
6. Overlay the theoretical distribution and check the consistency.

Solution – binomial

```

rand.rep <- 10000 # Random sample size
p <- 0.1          # Prior probability
n <- 25           # Number of trials for the binomial
exp.mean <- n*p   # Expected number of successes
exp.var <- n*p*(1-p)

# Generate random numbers
x <- rbinom(n = rand.rep, size = n, prob = p)

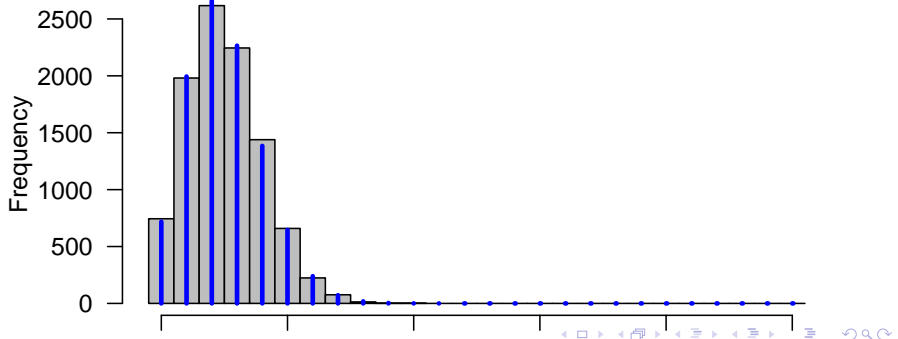
# Compute statistics
stats <- data.frame(p = p, n = n, exp.mean=exp.mean, mean=mean(x),
  exp.var = exp.var, variance=var(x), sd=sd(x))
kable(stats, digits=4)

```


Solution – binomial plot

```
hist(x, breaks=(0:26)-0.5, col="grey", main=paste("Binomial",  
          xlab="Successes", ylab="Frequency", las=1)  
lines(0:25, rand.rep*dbinom(x = 0:25, size = n, prob = p),
```

Binomial simulation, $p = 0.1$



- └ Binomial: global alignment with m mismatches

Negative binomial: local alignment with at most m mismatches

Local alignment with mismatches: problem statement

A local alignment algorithm starts from the 5' end of a read, and stops either at the x^{th} mismatch or when the end of the read is reached. What is the probability to obtain by chance an alignment of exactly 25 nucleotides with exactly $m = 3$ mismatches?

This amounts to obtain exactly $k = 22$ matches and $m = 3$ mismatches (in any order), followed by a mismatch at the $(k + m + 1)^{th}$ position.

We show here some examples of local alignments with at most 5 mismatches. Note that the last residue can be either a match (uppercase) or a mismatch (lowercase).

GGCAAGCTTGATATATGATCGCGGG

cagtg

tGacca

GaattGCTTt

Number of successes before the r^{th} failure

The **negative binomial** distribution (also called **Pascal distribution**) indicates the probability of the number of successes (k) before the r^{th} failure, in a Bernoulli schema with success probability p .

$$\mathcal{NB}(k|r, p) = \binom{k+r-1}{k} p^k (1-p)^r$$

This formula is a simple adaptation of the binomial, with the difference that we know that the last trial must be a failure. The binomial coefficient is thus reduced to choose the k successes among the $n-1 = k+r-1$ trials preceding the r^{th} failure.

Alternative formulation

It can also be adapted to indicate related probabilities.

- ▶ Number of **failures** (r) before the k^{th} **success**.

$$\mathcal{NB}(r|k, p) = \binom{k+r-1}{r} p^k (1-p)^r$$

- ▶ Number of **trials** ($n = k + r - 1$) before the r^{th} **failure**.

$$\mathcal{NB}(n|r, p) = \binom{n-1}{r-1} p^{n-r} (1-p)^r$$

Properties of the negative binomial

Negative binomial density

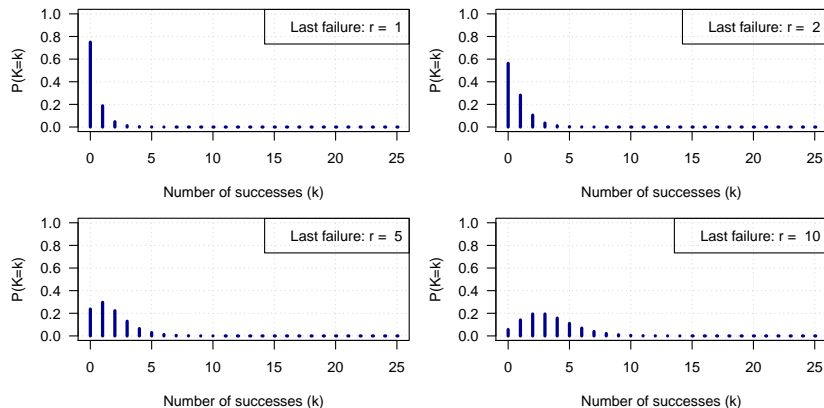
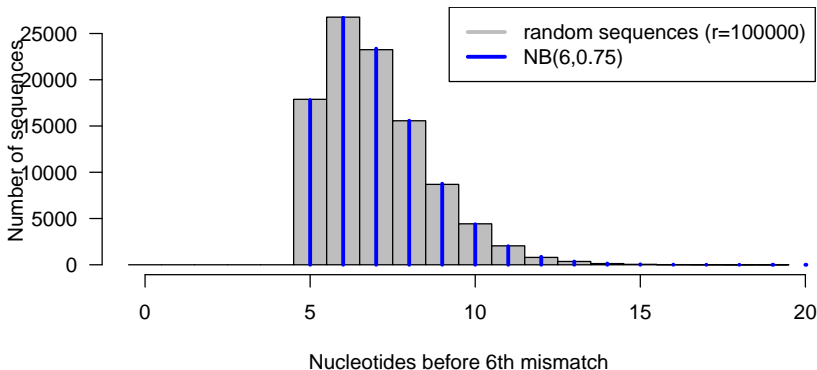


Figure 5: Negative binomial.

Local alignment with simulated sequences

Local alignment, at most 5 mismatches



Exercise – Negative binomial

Each student chooses a value for the maximal number of failures (r).

1. Read carefully the help of the negative binomial functions:
`help(NegBinomial)`
2. **Random sampling:** draw of $rep = 100000$ random numbers from a negative binomial distribution (`rndbinom()`) to compute the distribution of the number of successes (k) before the r^{th} failure.
3. Compute the expected mean and variance of the negative binomial.
4. Compute the mean and variance from your sampling distribution.
5. Draw an histogram with the number of successes before the r^{th} failure.
6. Fill up the form on the collective result table

Solution to the exercise – negative binomial

```

r <- 6          # Number of failures
p <- 0.75       # Failure probability
rep <- 100000
k <- rnbinom(n = rep, size = r, prob = p)
max.k <- max(k)
exp.mean <- r*(1-p)/p
rand.mean <- mean(k)
exp.var <- r*(1-p)/p^2
rand.var <- var(k)
hist(k, breaks = -0.5:(max.k+0.5), col="grey", xlab="Number
      las=1, ylab="", main="Random sampling from negative b
abline(v=rand.mean, col="darkgreen", lwd=2)
abline(v=exp.mean, col="green", lty="dashed")
arrows(rand.mean, rep/20, rand.mean+sqrt(rand.var), rep/20,
      angle=20, length = 0.1, col="purple", lwd=2)
text(x = rand.mean, y = rep/15, col="purple")

```

- └ Negative binomial: local alignment with at most m mismatches

Negative binomial for over-dispersed counts

To be treated in the afternoon !