Assignment 3

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Q1a.

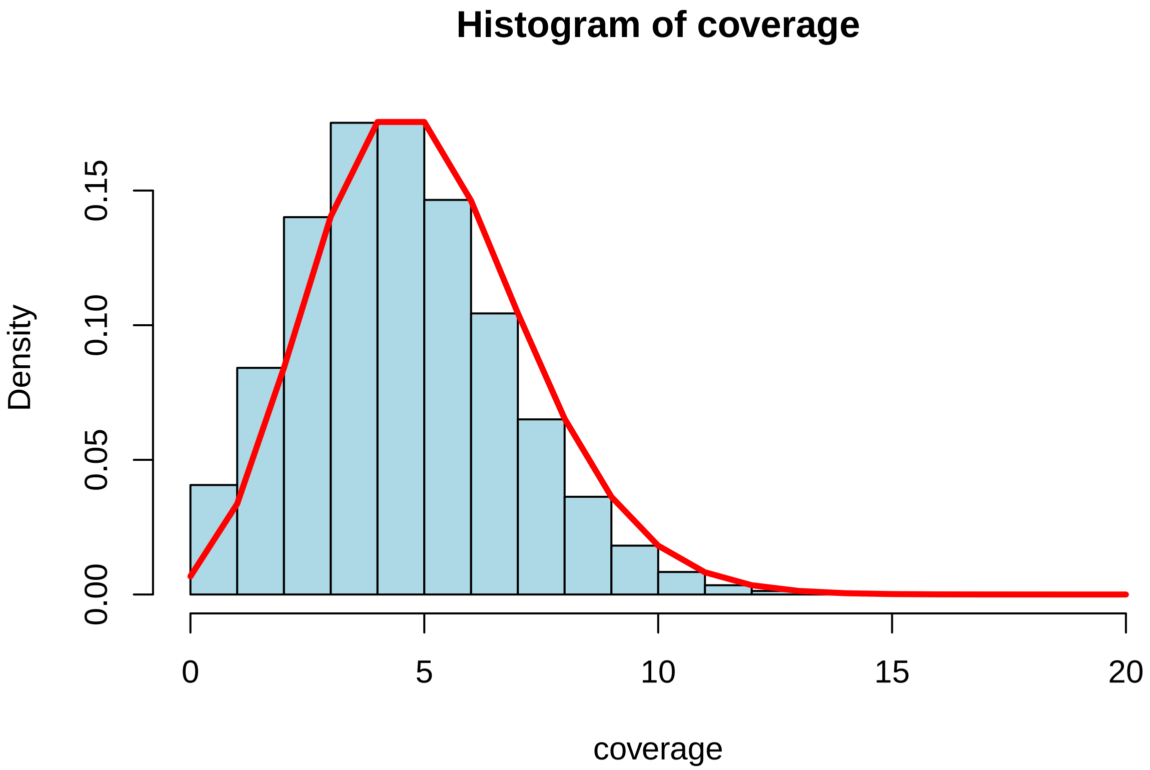
We need $5 * 10^4$ 100bp reads.

$$
\begin{aligned}
n * 100bp &= 1Mbp * 5 \\
n &= \frac{5 * 10^6}{10^2} \\
n &= 5 * 10^4
\end{aligned}
$$

Q1b.

Use following R code to simulate 5x coverage of a 1Mbp genome:

```
set.seed(100)
s = 1000000
n = 5
a = sample(1:s, n*s,replace=TRUE)
coverage = rep(0,s)
for (i in a ){coverage[i] = coverage[i]+1}
hist(coverage,prob=T,col="light blue")
xfit<-seq(min(coverage),max(coverage))
yfit<-dpois(xfit,n)
lines(xfit,yfit,col="red",lwd=3)
```



```
length(which(coverage==0))
```

```
## [1] 6871
```

```
mean(coverage)
```

```
## [1] 5
```

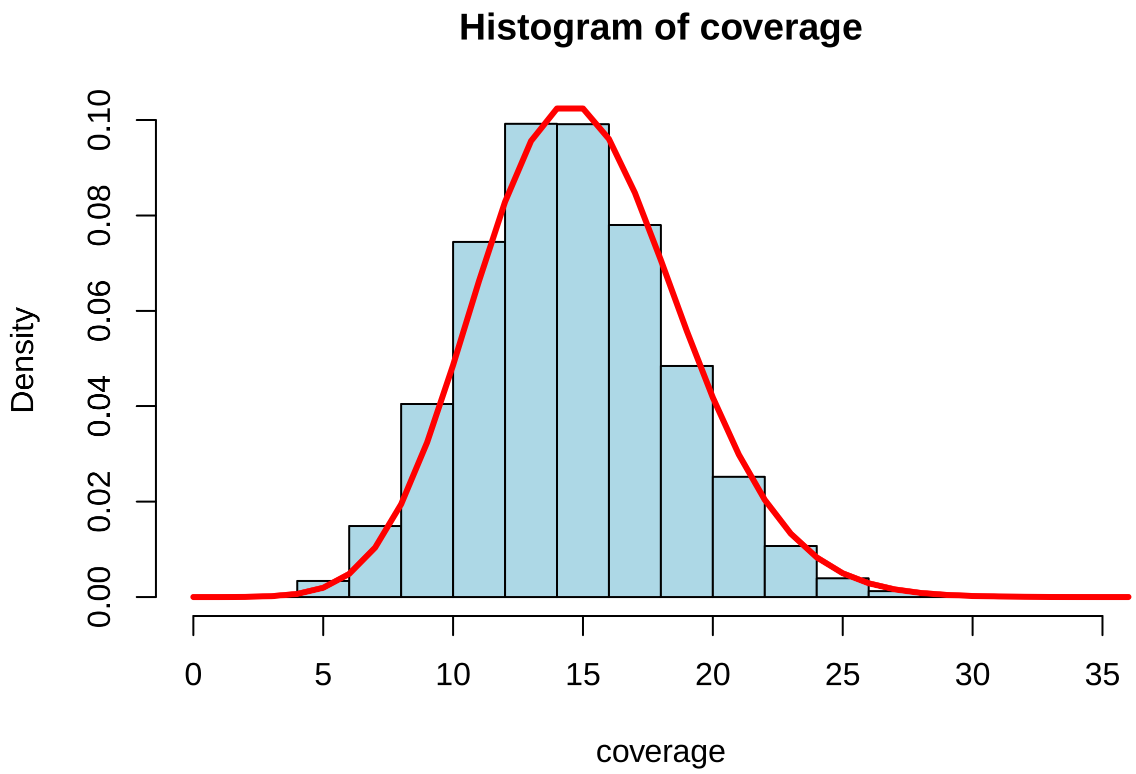
Q1c.

From the results shown in Q1b, 6871 bases have not been sequenced. Theoretically, the Poisson expecation should be the value of coverage:5, which equals to exactly the mean of our simulations.

Q1d.

Use following R code to simulate 15x coverage:

```
set.seed(100)
s = 1000000
n = 15
a = sample(1:s, n*s,replace=TRUE)
coverage = rep(0,s)
for (i in a ){coverage[i] = coverage[i]+1}
hist(coverage,prob=T,col="light blue")
xfit<-seq(min(coverage),max(coverage))
yfit<-dpois(xfit,n)
lines(xfit,yfit,col="red",lwd=3)
```



```
length(which(coverage==0))
```

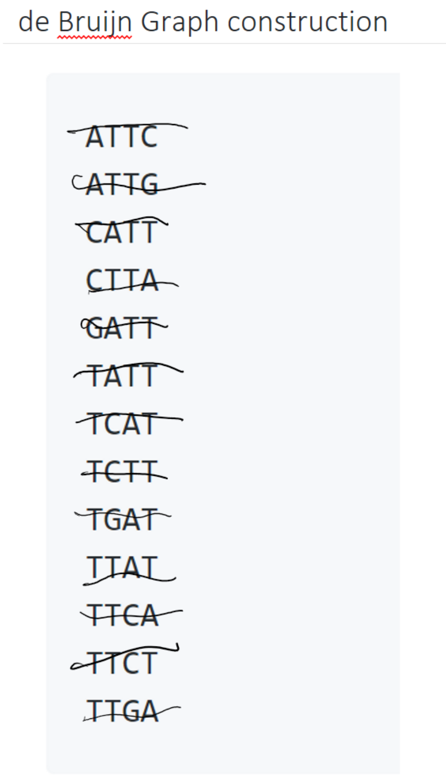
```
## [1] 1
```

```
mean(coverage)
```

```
## [1] 15
```

From the results shown above, 1 base has not been sequenced.Theoretically, the Poisson expecation should be the value of coverage: 15, which equals to exactly the mean of our simulations.

Q2a.



de Bruijn Graph construction

~~ATTC~~

~~ATTG~~

~~CATT~~

~~CTTA~~

~~GATT~~

~~TATT~~

~~TCAT~~

~~TCTT~~

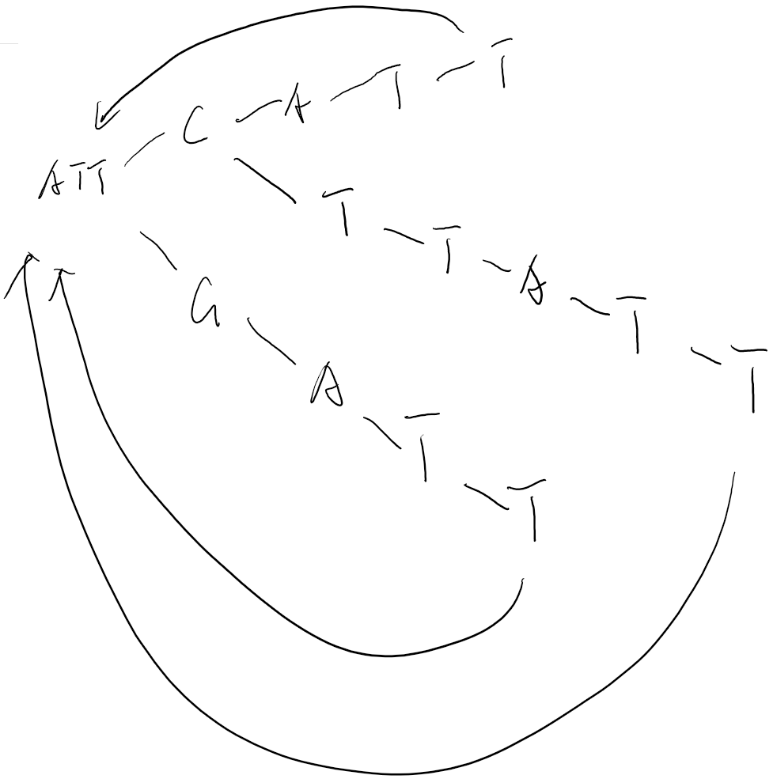
~~TGAT~~

~~TTAT~~

~~TTCA~~

~~TTCT~~

~~TTGA~~

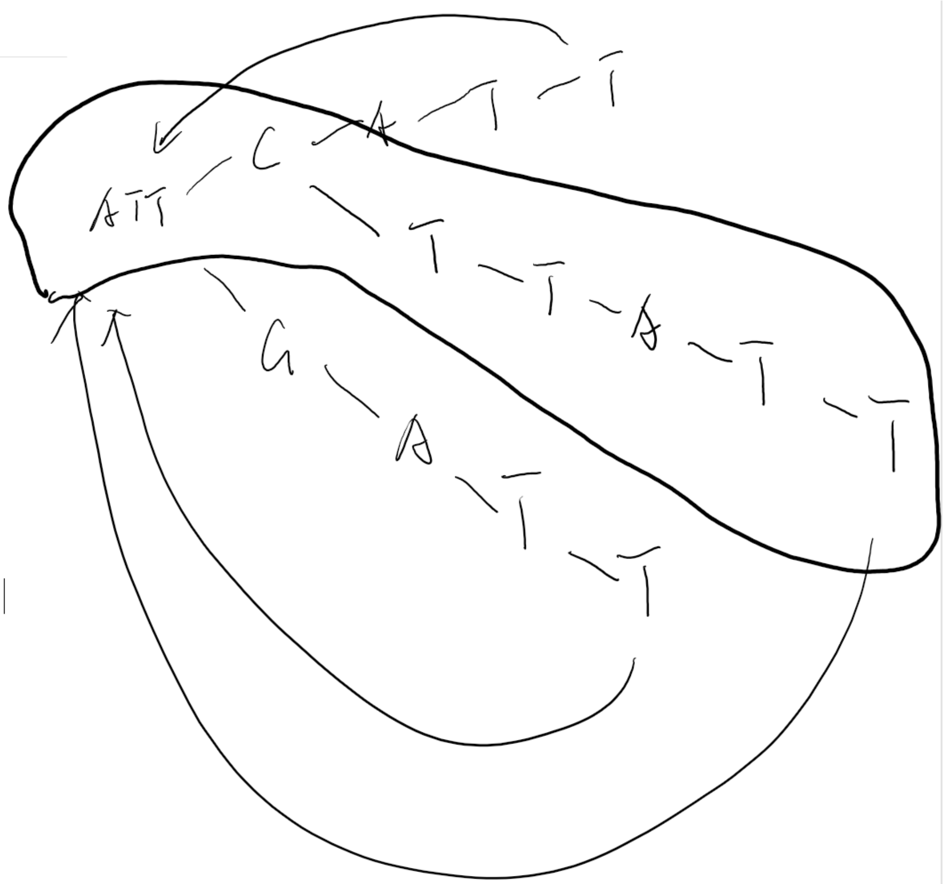


Q2b.

One possible genome sequence could be:
ATTCATTCTTATTG

Q2c.

The longest repeat should be:
ATTCTTATT


ATT
C
A
T
T
T
T
A
T
T
G
A
T
T