

A `title: "Distribution of generations in a long-term evolution experiment"`
`output: html_document`
`---`

```
```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE, messages = FALSE, warnings = F)
```
```

```
```{r}
library(ggplot2)
```
```

This plot shows the number of samples sequenced at each generation in a long-term evolution experiment.

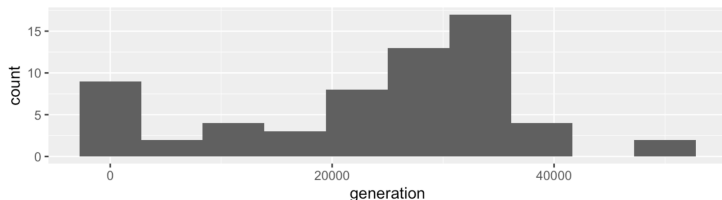
```
```{r, fig.height = 2}
metadata <- read.csv("Ecoli_metadata_composite.tsv", sep = "\t")
ggplot(metadata, aes(x = generation)) +
 geom_histogram(bins = 10)
```
```

B Distribution of generations in a long-term evolution experiment

```
library(ggplot2)
```

This plot shows the number of samples sequenced at each generation in a long-term evolution experiment.

```
metadata <- read.csv("Ecoli_metadata_composite.tsv", sep = "\t")
ggplot(metadata, aes(x = generation)) +
  geom_histogram(bins = 10)
```



C Distribution of generations in a long-term evolution experiment

```
In [1]: import pandas as pd
import matplotlib
```

This plot shows the number of samples sequenced at each generation in a long-term evolution experiment.

```
In [2]: metadata = pd.read_csv("Ecoli_metadata_composite.tsv",
                                sep = "\t")
plt = metadata['generation'].plot(kind = "hist")
plt.set_xlabel("Generation")
```

```
Out[2]: Text(0.5, 0, 'Generation')
```

