









# problem3

February 13, 2023

Bi/Be/Cs 183 2022-2023: Intro to Computational Biology TAs: Meichen Fang, Tara Chari, Zitong (Jerry) Wang

**Submit your notebooks by sharing a clickable link with Viewer access. Link must be accessible from submitted assignment document.**

Make sure Runtime → Restart and run all works without error

## HW 5 (Midterm) Problem 3c. (8 points)

The sum of  $n$  i.i.d. geometric random variables with parameter  $p$  has a negative binomial distribution with parameters  $r = n$  and  $p$ .

Draw 10,000 samples from a negative binomial distribution with  $r = 10$ ,  $p = 0.5$  and plot your sampled values in the form of a histogram.

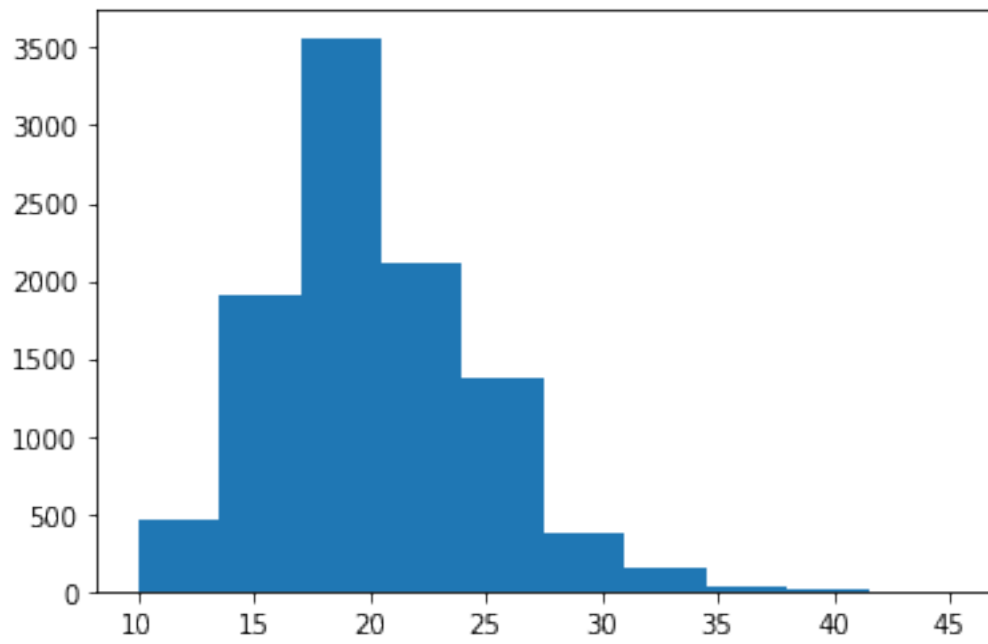
You may **not** use functions that directly generate samples from a negative binomial distribution such as `numpy.random.negative_binomial`. (Hint: a useful function is `numpy.random.geometric`)

```
In [1]: import numpy as np
import matplotlib.pyplot as plt
```

```
In [2]: n = 10000
r = 10
p = 0.5
```

```
In [3]: samples = np.sum(np.random.geometric(p, (r, n)), axis=0)
plt.hist(samples)
```

```
Out[3]: (array([ 468., 1901., 3564., 2116., 1379.,  373.,  157.,  28.,  10.,
                  4.]),
array([10. , 13.5, 17. , 20.5, 24. , 27.5, 31. , 34.5, 38. , 41.5, 45. ]),
<BarContainer object of 10 artists>)
```



# problem5

February 13, 2023

Bi/Be/Cs 183 2022-2023: Intro to Computational Biology TAs: Meichen Fang, Tara Chari, Zitong (Jerry) Wang

**Submit your notebooks by sharing a clickable link with Viewer access. Link must be accessible from submitted assignment document.**

Make sure Runtime → Restart and run all works without error

## HW 5 (Midterm) Problem 5

For this problem you will be exploring various models which can be used to describe count data i.e. the gene-count matrices we use in single-cell.

Single-cell gene counts, which describe stochastically sampled, discrete measurements of UMI counts, are often modeled as being generated from a negative binomial (or Gamma-Poisson) distribution. However, there is a common assumption that droplet-based methods for single-cell RNA seq incur an overabundance of zeros (more zero counts) than would be predicted by random sampling. Thus it is also common to see single-cell data modeled with zero-inflated negative binomials (the ZINB distribution, with an extra parameter for the probability of zero counts).

You will explore how these assumptions and models fit to real datasets.

In [1]: *#To run a code cell, select the cell and hit Command/Ctrl+Enter or click the run/play button. #Click Insert --> Code Cell or the '+ Code' option to insert a new code cell*

In [2]: *#Click Insert --> Text Cell or the '+ Text' option to insert a cell for text as below*

In [3]: *# This is used to time the running of the notebook*  
`import time`  
`start_time = time.time()`

Text here for descriptions, explanations, etc

## 0.1 Import data and install packages

In [4]: `!pip --quiet install anndata`

In [5]: `import numpy as np`  
`import scipy.io as sio`  
`import pandas as pd`  
`import matplotlib.pyplot as plt` *#Can use other plotting packages like seaborn*  
  
`import anndata`

```

from scipy import optimize
from scipy.special import gammaln
from scipy.special import psi
from scipy.special import factorial
from scipy.optimize import fmin_l_bfgs_b as optim

```

In [6]: # ! allows you to run commands in the command line, as you would in your normal terminal

In [7]: # Download control sample from indrops platform  
# File format is h5ad

```

import requests
from tqdm import trange, tqdm_notebook
def download_file(doi,ext):
    url = 'https://api.datacite.org/doi/'+doi+'/media'
    r = requests.get(url).json()
    netcdf_url = r['data'][0]['attributes']['url']
    r = requests.get(netcdf_url,stream=True)
    #Set file name
    fname = doi.split('/')[0]+ext
    #Download file with progress bar
    if r.status_code == 403:
        print("File Unavailable")
    if 'content-length' not in r.headers:
        print("Did not get file")
    else:
        with open(fname, 'wb') as f:
            total_length = int(r.headers.get('content-length'))
            pbar = trange(int(total_length/1024), unit="B")
            for chunk in r.iter_content(chunk_size=1024):
                if chunk:
                    pbar.update()
                    f.write(chunk)
        return fname

```

```
download_file('10.22002/xsret-sb590','.gz')
```

/tmp/ipykernel\_11951/3748164775.py:21: TqdmDeprecationWarning: Please use `tqdm.notebook.trange`  
pbar = trange(int(total\_length/1024), unit="B")

```
0%|          | 0/19383 [00:00<?, ?B/s]
```

Out[7]: 'xsret-sb590.gz'

In [8]: !gunzip \*.gz  
!mv xsret-sb590 Klein.h5ad

In [9]: indrops = anndata.read('Klein.h5ad')



```
In [10]: indrops
```

```
Out[10]: AnnData object with n_obs = 953 & n_vars = 25435
         obs: 'total_counts'
         var: 'empirical_mean', 'empirical_variance', 'empirical_zero_fraction', 'ml_mean'
         uns: 'global_dispersion', 'name'
```

Use the function below for b).

```
In [82]: # X = numpy array of the data (e.g. 1D array with all the counts for one gene)
         # initial_params is a numpy array representing the initial values of
         # size and prob parameters
         # Returns: Dict with 'r' and 'p' fits
         def fit_nbinom(X, initial_params=None):
             ''' This code is adapted from https://github.com/gokceneraslan/fit_nbinom
             '''
             infinitesimal = np.finfo(float).eps

             def log_likelihood(params, *args):
                 r, p = params
                 X = args[0]
                 N = X.size

                 # MLE estimate based on the formula on Wikipedia:
                 # http://en.wikipedia.org/wiki/Negative_binomial_distribution#Maximum_likelihood_estimation
                 result = np.sum(gammaln(X + r)) \
                     - np.sum(np.log(factorial(X))) \
                     - N * (gammaln(r)) \
                     + N * r * np.log(p) \
                     + np.sum(X * np.log(1 - (p if p < 1 else 1 - infinitesimal)))

                 return -result

             if initial_params is None:
                 # reasonable initial values (from fitdistr function in R)
                 m = np.mean(X)
                 v = np.var(X)
                 size = (m ** 2) / (v - m) if v > m else 10

                 # convert mu/size parameterization to prob/size
                 p0 = size / ((size + m) if size + m != 0 else 1)
                 r0 = size
                 initial_params = np.array([r0, p0])

             bounds = [(infinitesimal, None), (infinitesimal, 1)]
             optimres = optim(log_likelihood,
                             x0=initial_params,
                             args=(X,))
```