

# waiting-time-distributions

August 14, 2018

## 1 Waiting time distributions

### 1.1 Nikolas Schnellbächer (2018-08-14)

```
In [246]: import numpy as np
          import matplotlib as mpl
          import matplotlib.pyplot as plt

In [247]: %matplotlib inline
          %config InlineBackend.figure_formats = {'png', 'retina'}

In [248]: # this is how we can use python to sample from an exponential distribution
          # with a given mean value (here meanTime)
          meanTime = 1.5
          sampleTime = np.random.exponential(meanTime)
          print("sample waiting time =", sampleTime)

sample waiting time = 0.2586430977796442

In [249]: # specify the number of samples
          nSamples = 5000
          meanTime = 1.5
          sampleTimes = np.random.exponential(meanTime, nSamples)

          assert sampleTimes.shape == (nSamples,), "Error: Shape assertion failed."
          print(sampleTimes.shape)

(5000,)
```

Next we create the theoretical distribution, which for this case is of course the standard probability density function of the exponential distribution.

```
In [250]: # create the theoretical exponential distribution
          nVisPoints = 300
          meanValue = meanTime
          xVals = np.linspace(0.0, 15.0, nVisPoints)
```

```

yVals = np.array([np.exp(-t / meanValue) / meanValue for t in xVals])
expDist = np.zeros((nVisPoints, 2))
expDist[:, 0] = xVals
expDist[:, 1] = yVals

In [251]: # for an alternative histogram representation I
# create x,y data pairs of the histogram data using
# numpy's histogram function
nBins = 20
hist, bin_edges = np.histogram(sampleTimes, bins = nBins, normed = True)
bin_centers = (bin_edges[1:] + bin_edges[0:-1]) / 2.0
assert hist.shape == bin_centers.shape

scatterData = np.zeros((nBins, 2))
scatterData[:, 0] = bin_centers
scatterData[:, 1] = hist

In [252]: # plotting function to plot the numerically sampled data
# in conjunction with the exponential distribution

def plot_histogram_wDist(X, nBins, dist):

    fig, ax = plt.subplots(1, 1, figsize = (6.5, 4.5))

    ax.hist(X,
            bins = nBins,
            density = True,
            label = r'sampled')

    ax.plot(dist[:, 0], dist[:, 1],
            lw = 1.5,
            color = 'C3',
            label = r'$\mathrm{Exp}(\lambda = \langle t \rangle)$')

    ax.set_xlabel(r'waiting time $t$', fontsize = 16.0)
    ax.set_ylabel(r'frequency', fontsize = 16.0)
    ax.xaxis.labelpad = 10.0
    ax.yaxis.labelpad = 15.0

    major_x_ticks = np.arange(0.0, 15.1, 2.0)
    minor_x_ticks = np.arange(0.0, 15.1, 1.0)
    ax.set_xticks(major_x_ticks)
    ax.set_xticks(minor_x_ticks, minor = True)

    major_y_ticks = np.arange(0.0, 1.1, 0.1)
    minor_y_ticks = np.arange(0.0, 1.1, 0.05)
    ax.set_yticks(major_y_ticks)
    ax.set_yticks(minor_y_ticks, minor = True)

```

```

labelfontsize = 12.0
for tick in ax.xaxis.get_major_ticks():
    tick.label.set_fontsize(labelfontsize)
for tick in ax.yaxis.get_major_ticks():
    tick.label.set_fontsize(labelfontsize)

ax.set_xlim(-0.25, 14.25)
ax.set_ylim(0.0, 0.625)
ax.set_axisbelow(False)

leg = ax.legend(# bbox_to_anchor = [1.0, 1.0],
               # loc = 'upper left',
               fontsize = 16.0,
               handlelength = 1.5,
               scatterpoints = 1,
               markerscale = 1.0,
               ncol = 1)
leg.draw_frame(False)

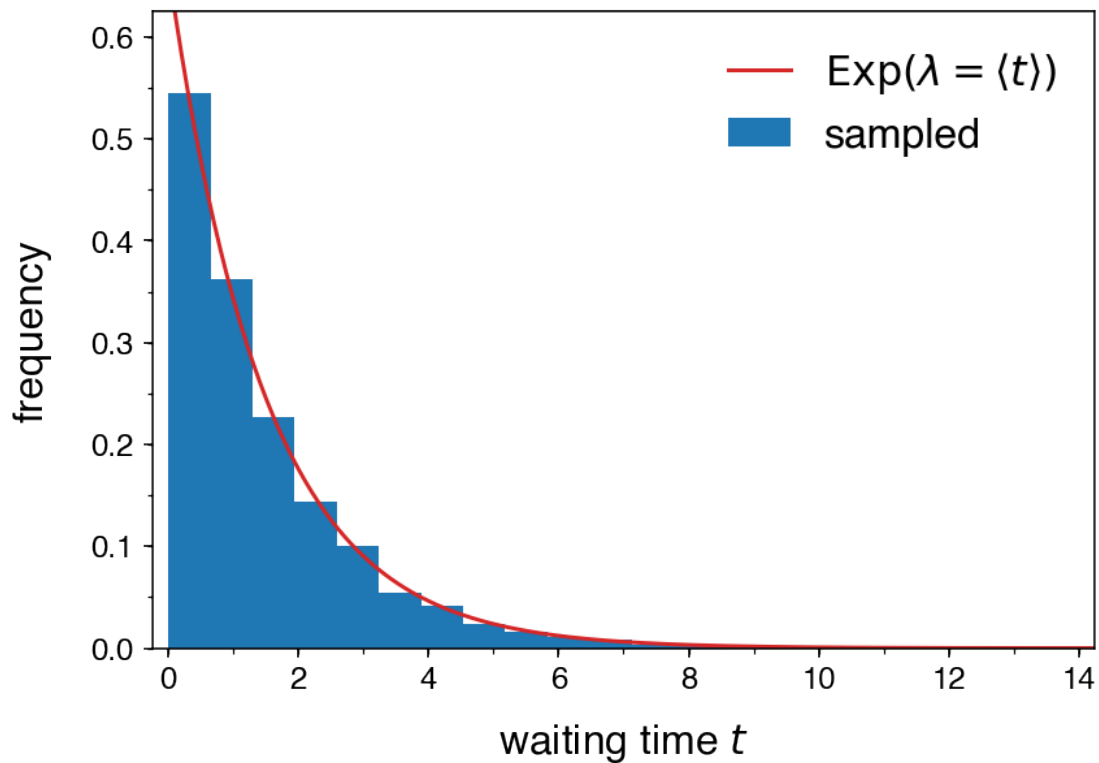
return None

```

```

In [253]: nBins = 20
plot_histogram_wDist(sampleTimes, nBins, expDist)

```



In [254]: *# plotting function to show that both version of the histogram  
# of course perfectly overlay each other*

```
def plot_histogram_comparison(X, nBins, scatterData, dist):

    fig, ax = plt.subplots(1, 1, figsize = (6.5, 4.5))

    ax.hist(X,
            bins = nBins,
            density = True,
            label = r'sampled',
            zorder = 1)

    ax.plot(dist[:, 0], dist[:, 1],
            lw = 1.5,
            color = 'C3',
            label = r'$\mathrm{Exp}(\lambda = \angle t\angle)$',
            zorder = 3)

    ax.scatter(scatterData[:, 0], scatterData[:, 1],
              s = 50,
              lw = 1.5,
              facecolor = 'None',
              edgecolor = 'C3',
              zorder = 2)

    ax.set_xlabel(r'waiting time $t$', fontsize = 16.0)
    ax.set_ylabel(r'frequency', fontsize = 16.0)
    ax.xaxis.labelpad = 10.0
    ax.yaxis.labelpad = 15.0

    major_x_ticks = np.arange(0.0, 15.1, 2.0)
    minor_x_ticks = np.arange(0.0, 15.1, 1.0)
    ax.set_xticks(major_x_ticks)
    ax.set_xticks(minor_x_ticks, minor = True)

    major_y_ticks = np.arange(0.0, 1.1, 0.1)
    minor_y_ticks = np.arange(0.0, 1.1, 0.05)
    ax.set_yticks(major_y_ticks)
    ax.set_yticks(minor_y_ticks, minor = True)

    labelfontsize = 12.0
    for tick in ax.xaxis.get_major_ticks():
        tick.label.set_fontsize(labelfontsize)
    for tick in ax.yaxis.get_major_ticks():
        tick.label.set_fontsize(labelfontsize)
```

```

ax.set_xlim(-0.25, 14.25)
ax.set_ylim(0.0, 0.625)
ax.set_axisbelow(False)

leg = ax.legend(# bbox_to_anchor = [1.0, 1.0],
               # loc = 'upper left',
               fontsize = 16.0,
               handlelength = 1.5,
               scatterpoints = 1,
               markerscale = 1.0,
               ncol = 1)
leg.draw_frame(False)

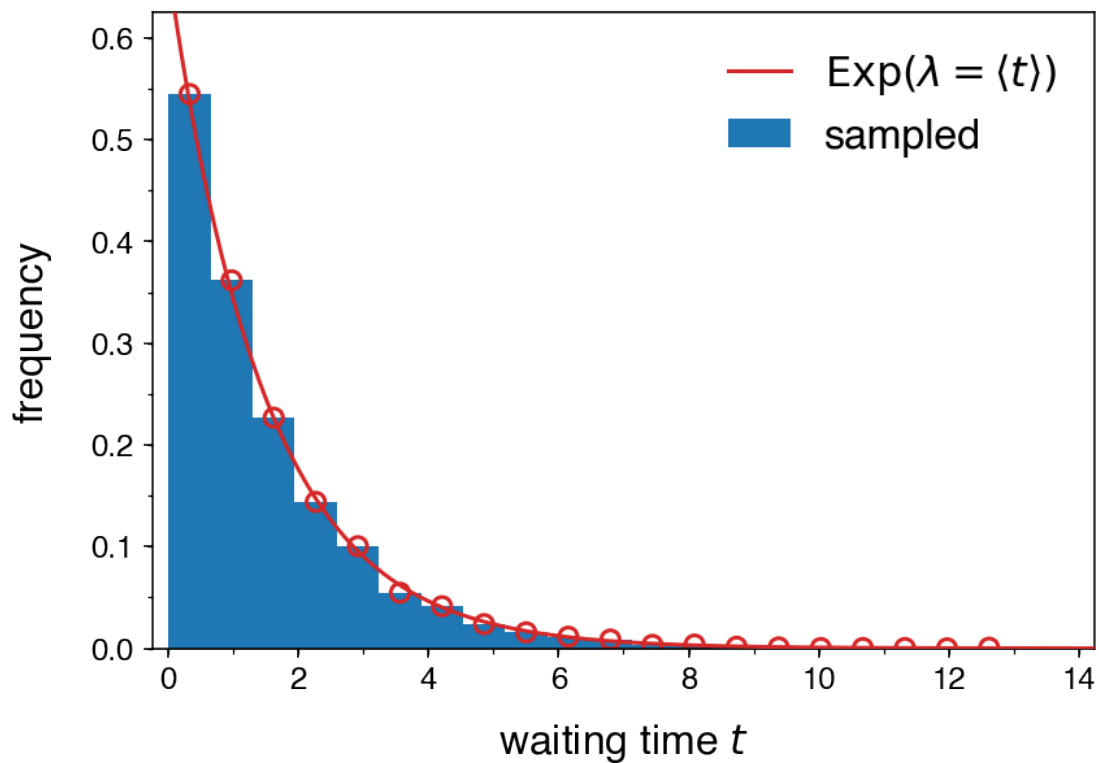
return None

```

```

In [255]: nBins = 20
plot_histogram_comparison(sampleTimes, nBins, scatterData, dist)

```



```

In [256]: def plot_scatter_histogram(X, dist):

fig, ax = plt.subplots(1, 1, figsize = (6.5, 4.5))

```

```

ax.plot([-1.0, 20.0], [0.0, 0.0],
        dashes = [6.0, 3.0],
        color = '#CCCCCC',
        lw = 1.0,
        zorder = 1)

ax.plot(dist[:, 0], dist[:, 1],
        lw = 1.5,
        color = 'C3',
        label = r'$\mathrm{Exp}(\lambda = \langle t \rangle)$',
        zorder = 3)

ax.scatter(X[:, 0], X[:, 1],
           s = 50,
           lw = 1.5,
           facecolor = 'None',
           edgecolor = 'C3',
           zorder = 2,
           label = r'sampled')

ax.set_xlabel(r'waiting time $t$', fontsize = 16.0)
ax.set_ylabel(r'frequency', fontsize = 16.0)
ax.xaxis.labelpad = 10.0
ax.yaxis.labelpad = 15.0

major_x_ticks = np.arange(0.0, 15.1, 2.0)
minor_x_ticks = np.arange(0.0, 15.1, 1.0)
ax.set_xticks(major_x_ticks)
ax.set_xticks(minor_x_ticks, minor = True)

major_y_ticks = np.arange(0.0, 1.1, 0.1)
minor_y_ticks = np.arange(0.0, 1.1, 0.05)
ax.set_yticks(major_y_ticks)
ax.set_yticks(minor_y_ticks, minor = True)

labelfontsize = 12.0
for tick in ax.xaxis.get_major_ticks():
    tick.label.set_fontsize(labelfontsize)
for tick in ax.yaxis.get_major_ticks():
    tick.label.set_fontsize(labelfontsize)

ax.set_xlim(-0.25, 14.25)
ax.set_ylim(-0.025, 0.625)
ax.set_axisbelow(False)

leg = ax.legend(# bbox_to_anchor = [1.0, 1.0],
               # loc = 'upper left',

```

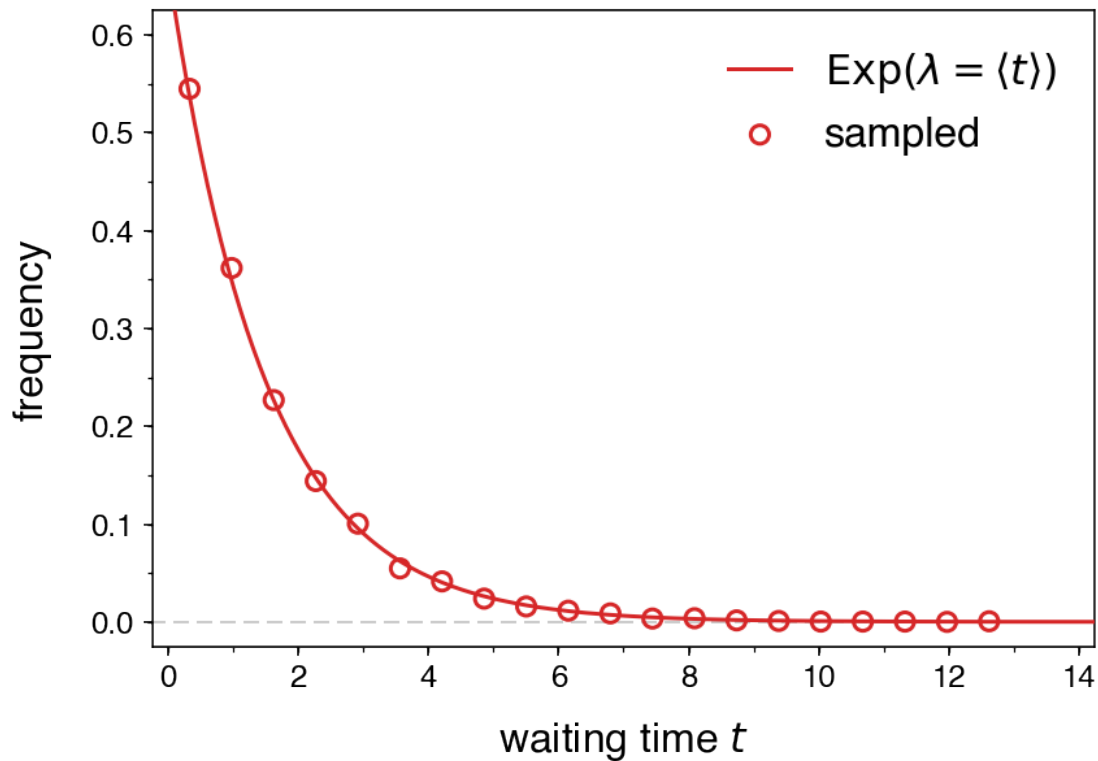
```

        fontsize = 16.0,
        handlelength = 1.5,
        scatterpoints = 1,
        markerscale = 1.0,
        ncol = 1)
    leg.draw_frame(False)

    return None

```

In [257]: `plot_scatter_histogram(scatterData, dist)`



Next we consider a two-step process. The first process has a mean waiting time  $\tau_A$  and the second process a mean waiting time  $\tau_B$ .

```

In [258]: # set the mean waiting times for the two-step process
          tau_A = 1.0
          tau_B = 1.5

          # specify the number of samples
          nSamples = 500000

          tauAs = np.random.exponential(tau_A, nSamples)
          tauBs = np.random.exponential(tau_B, nSamples)

```

```

assert tauAs.shape == tauBs.shape

observedTimes = tauAs + tauBs # a sequential two step process
assert observedTimes.shape == (nSamples,), "Error: Shape assertion failed."
print(observedTimes.shape)

(500000,)

In [259]: # create the theoretical distribution
# Here this distribution is the convolution of two exponential distributions.
nVisPoints = 300
tau_A = 1.0
tau_B = 1.5
xVals = np.linspace(0.0, 20.0, nVisPoints)
yVals = np.array([(np.exp(-t / tau_B) - np.exp(-t / tau_A)) / (tau_B - tau_A) for t in xVals])
dist2 = np.zeros((nVisPoints, 2))
dist2[:, 0] = xVals
dist2[:, 1] = yVals

In [260]: # for an alternative histogram representation I
# create x,y data pairs of the histogram data using
# numpy's histogram function
nBins = 40
hist, bin_edges = np.histogram(observedTimes, bins = nBins, normed = True)
bin_centers = (bin_edges[1:] + bin_edges[0:-1]) / 2.0
assert hist.shape == bin_centers.shape

scatterData2 = np.zeros((nBins, 2))
scatterData2[:, 0] = bin_centers
scatterData2[:, 1] = hist

In [261]: # plotting function to plot the numerically sampled data
# in conjunction with the exponential distribution

def plot_histogram_wDist_2step(X, nBins, dist):

    fig, ax = plt.subplots(1, 1, figsize = (6.5, 4.5))

    ax.hist(X,
            bins = nBins,
            density = True,
            label = r'sampled')

    ax.plot(dist[:, 0], dist[:, 1],
            lw = 1.5,
            color = 'C3',
            label = r'$p(t)$')

```



```

ax.set_xlabel(r'waiting time $t$', fontsize = 16.0)
ax.set_ylabel(r'frequency', fontsize = 16.0)
ax.xaxis.labelpad = 10.0
ax.yaxis.labelpad = 15.0

major_x_ticks = np.arange(0.0, 15.1, 2.0)
minor_x_ticks = np.arange(0.0, 15.1, 1.0)
ax.set_xticks(major_x_ticks)
ax.set_xticks(minor_x_ticks, minor = True)

major_y_ticks = np.arange(0.0, 1.1, 0.1)
minor_y_ticks = np.arange(0.0, 1.1, 0.05)
ax.set_yticks(major_y_ticks)
ax.set_yticks(minor_y_ticks, minor = True)

labelfontsize = 12.0
for tick in ax.xaxis.get_major_ticks():
    tick.label.set_fontsize(labelfontsize)
for tick in ax.yaxis.get_major_ticks():
    tick.label.set_fontsize(labelfontsize)

ax.set_xlim(-0.25, 15.75)
ax.set_ylim(0.0, 0.315)
ax.set_axisbelow(False)

leg = ax.legend(# bbox_to_anchor = [1.0, 1.0],
                # loc = 'upper left',
                fontsize = 16.0,
                handlelength = 1.5,
                scatterpoints = 1,
                markerscale = 1.0,
                ncol = 1)
leg.draw_frame(False)

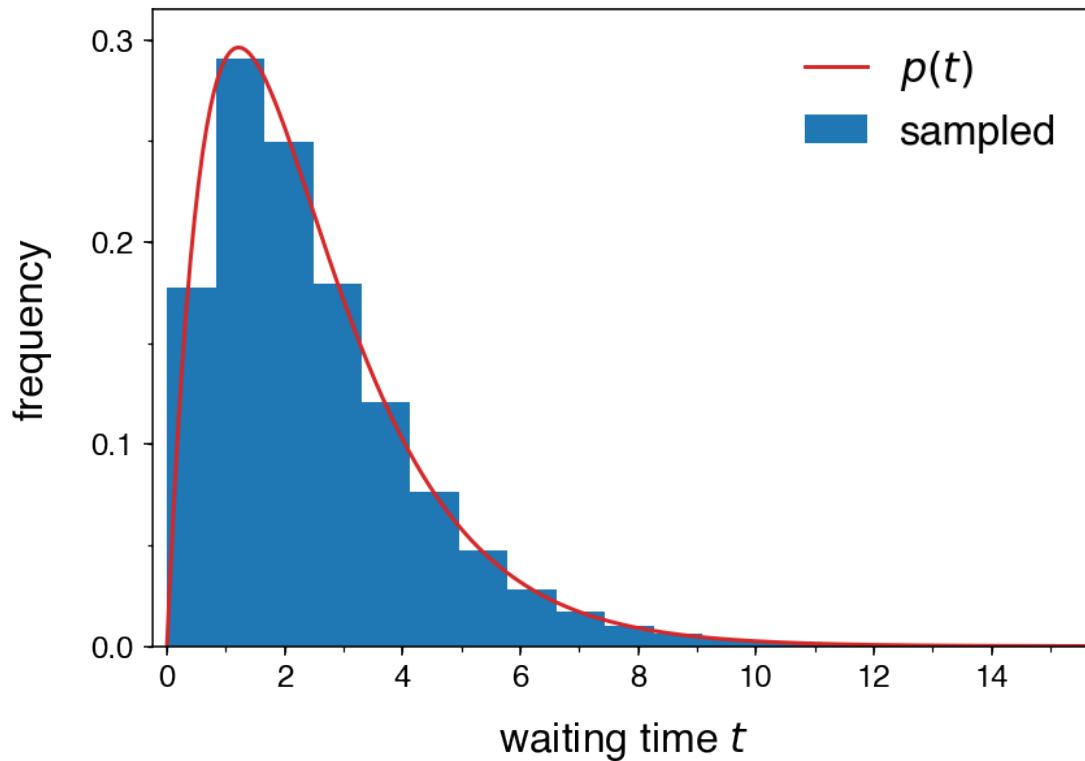
return None

```

```

In [262]: nBins = 30
          plot_histogram_wDist_2step(observedTimes, nBins, dist2)

```



```
In [263]: def plot_scatter_histogram(X, dist):

    fig, ax = plt.subplots(1, 1, figsize = (6.5, 4.5))

    ax.plot([-1.0, 20.0], [0.0, 0.0],
            dashes = [6.0, 3.0],
            color = '#CCCCCC',
            lw = 1.0,
            zorder = 1)

    ax.plot(dist[:, 0], dist[:, 1],
            lw = 1.5,
            color = 'C3',
            label = r'$p(t)$',
            zorder = 3)

    ax.scatter(X[:, 0], X[:, 1],
               s = 50,
               lw = 1.5,
               facecolor = 'None',
               edgecolor = 'C3',
               zorder = 2,
```

```

        label = r'sampled')

ax.set_xlabel(r'waiting time $t$', fontsize = 16.0)
ax.set_ylabel(r'frequency', fontsize = 16.0)
ax.xaxis.labelpad = 10.0
ax.yaxis.labelpad = 15.0

major_x_ticks = np.arange(0.0, 15.1, 2.0)
minor_x_ticks = np.arange(0.0, 15.1, 1.0)
ax.set_xticks(major_x_ticks)
ax.set_xticks(minor_x_ticks, minor = True)

major_y_ticks = np.arange(0.0, 1.1, 0.1)
minor_y_ticks = np.arange(0.0, 1.1, 0.05)
ax.set_yticks(major_y_ticks)
ax.set_yticks(minor_y_ticks, minor = True)

labelfontsize = 12.0
for tick in ax.xaxis.get_major_ticks():
    tick.label.set_fontsize(labelfontsize)
for tick in ax.yaxis.get_major_ticks():
    tick.label.set_fontsize(labelfontsize)

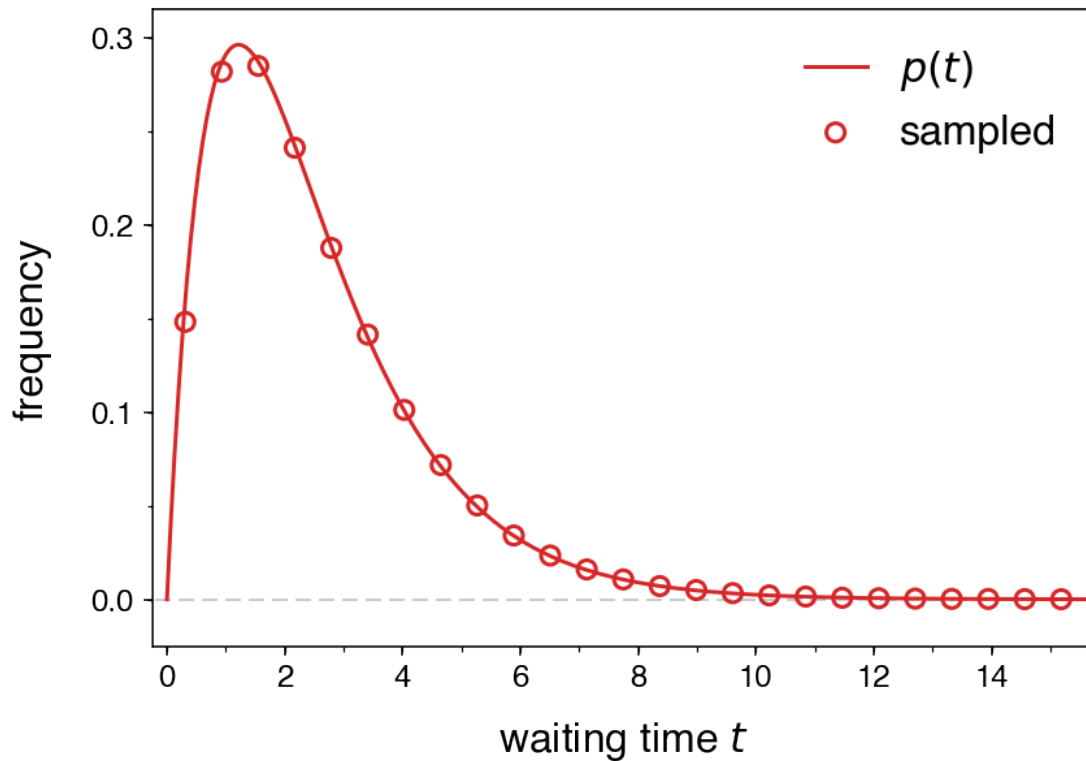
ax.set_xlim(-0.25, 15.75)
ax.set_ylim(-0.025, 0.315)
ax.set_axisbelow(False)

leg = ax.legend(# bbox_to_anchor = [1.0, 1.0],
               # loc = 'upper left',
               fontsize = 16.0,
               handlelength = 1.5,
               scatterpoints = 1,
               markerscale = 1.0,
               ncol = 1)
leg.draw_frame(False)

return None

```

In [264]: `plot_scatter_histogram(scatterData2, dist2)`



For further information on this topic, have a look at the following two sources:

- Rob Phillips et al. - **Physical Biology of the Cell** (2nd edition, 2013). They discuss this issue in the context of molecular motors, where multiple internal states of a molecular motor are often hidden, i.e. not accessible to direct experimental observation. However sometimes one can reveal the existence of such states by analyzing the corresponding waiting-time distributions.
- D. L. Floyd et al. - Analysis of Kinetic Intermediates in Single-Particle Dwell-Time Distributions, *Biophysical Journal*, **99**, 360-366, 2010.