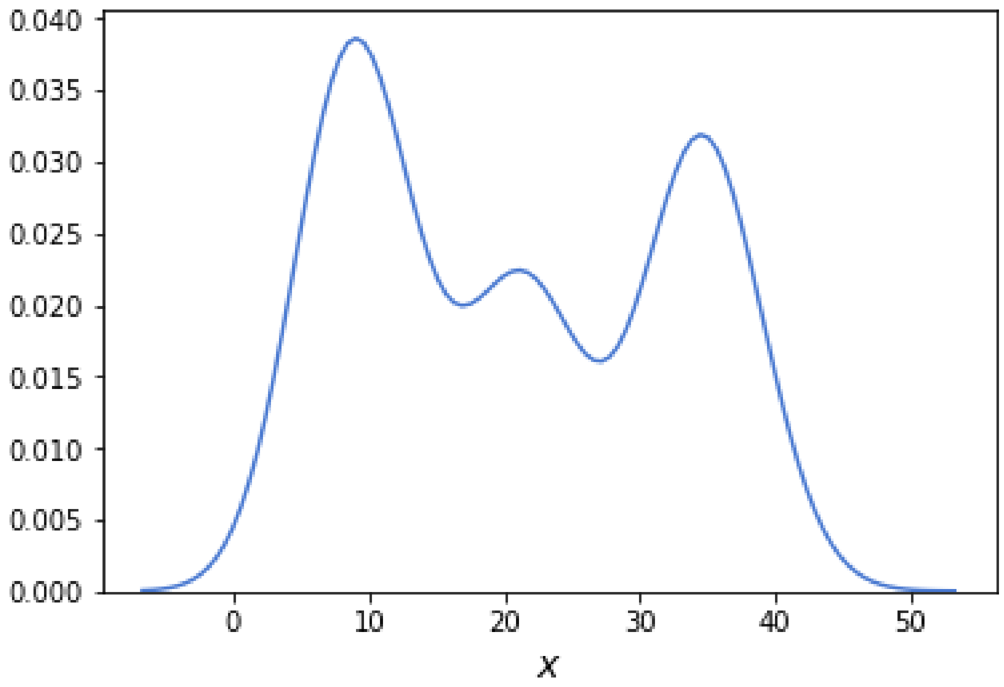
Bayesian Data Analysis Chapter 7

January 20, 2019

```
In [1]: %matplotlib inline
        import pymc3 as pm
        import numpy as np
        import pandas as pd
        import scipy.stats as stats
        import matplotlib.pyplot as plt
        import seaborn as sns
        palette = 'muted'
        sns.set_palette(palette); sns.set_color_codes(palette)
        np.set_printoptions(precision=2)
```

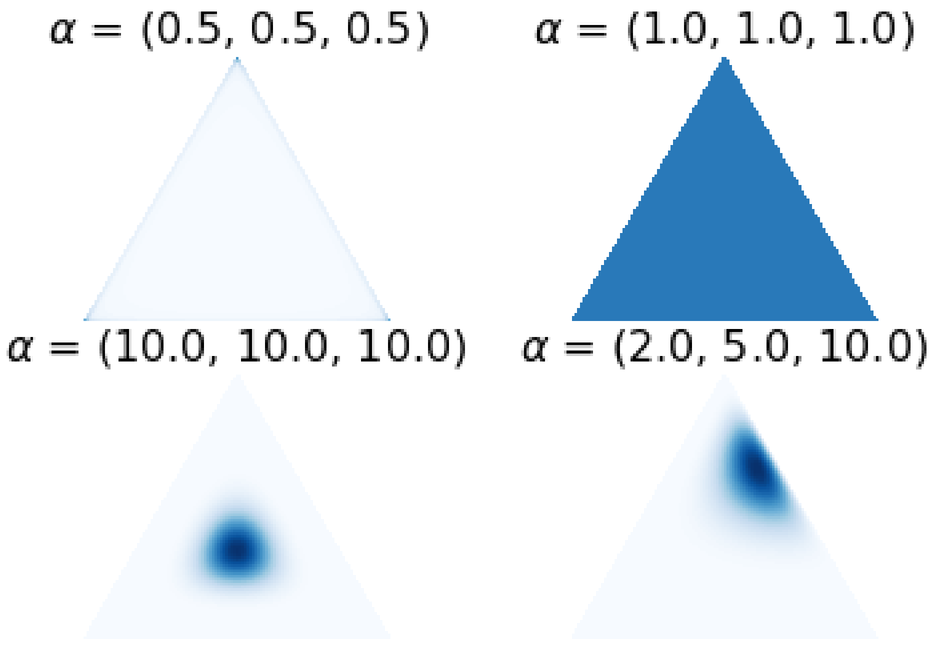
1 Simple example

```
In [2]: clusters = 3

        n_cluster = [90, 50, 75]
        n_total = sum(n_cluster)

        means = [9, 21, 35]
        std_devs = [2, 2, 2]
        # example of mixture data
        mix = np.random.normal(np.repeat(means, n_cluster), np.repeat(std_devs, n_cluster))

In [3]: sns.kdeplot(np.array(mix))
        plt.xlabel('$x$', fontsize=14);
```



```
In [4]: # Author: Thomas Boggs

        import matplotlib.tri as tri
        from functools import reduce
        from matplotlib import ticker, cm

        _corners = np.array([[0, 0], [1, 0], [0.5, 0.75**0.5]])
        _triangle = tri.Triangulation(_corners[:, 0], _corners[:, 1])
        _midpoints = [(_corners[(i + 1) % 3] + _corners[(i + 2) % 3]) / 2.0 for i in range(3)]

        def xy2bc(xy, tol=1.e-3):
            '''Converts 2D Cartesian coordinates to barycentric.
            Arguments:
                xy: A length-2 sequence containing the x and y value.
            '''
            s = [(_corners[i] - _midpoints[i]).dot(xy - _midpoints[i]) / 0.75 for i in range(3
            return np.clip(s, tol, 1.0 - tol)

        class Dirichlet(object):
            def __init__(self, alpha):
                '''Creates Dirichlet distribution with parameter `alpha`.'''
                from math import gamma
                from operator import mul
                self._alpha = np.array(alpha)
                self._coef = gamma(np.sum(self._alpha)) /reduce(mul, [gamma(a) for a in self._a
            def pdf(self, x):
                '''Returns pdf value for `x`.'''
                from operator import mul
                return self._coef * reduce(mul, [xx ** (aa - 1)
                                                 for (xx, aa)in zip(x, self._alpha)])
            def sample(self, N):
                '''Generates a random sample of size `N`.'''
                return np.random.dirichlet(self._alpha, N)

        def draw_pdf_contours(dist, nlevels=100, subdiv=8, **kwargs):
            '''Draws pdf contours over an equilateral triangle (2-simplex).
            Arguments:
                dist: A distribution instance with a `pdf` method.
                border (bool): If True, the simplex border is drawn.
                nlevels (int): Number of contours to draw.
                subdiv (int): Number of recursive mesh subdivisions to create.
                kwargs: Keyword args passed on to `plt.triplot`.
            '''
            refiner = tri.UniformTriRefiner(_triangle)
            trimesh = refiner.refine_triangulation(subdiv=subdiv)
            pvals = [dist.pdf(xy2bc(xy)) for xy in zip(trimesh.x, trimesh.y)]

            plt.tricontourf(trimesh, pvals, nlevels, cmap=cm.Blues, **kwargs)
            plt.axis('equal')
            plt.xlim(0, 1)
            plt.ylim(0, 0.75**0.5)
            plt.axis('off')
```

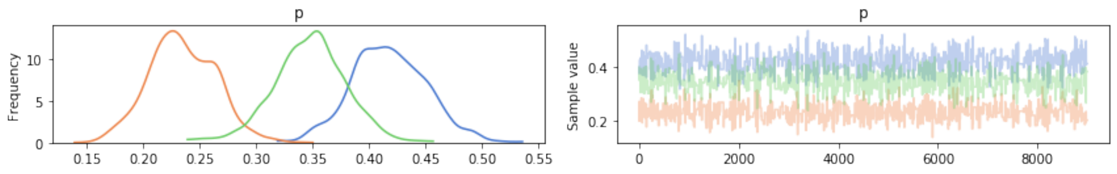
```
In [5]: alphas = [[0.5] * 3, [1] * 3, [10] * 3, [2, 5, 10]]
        for (i, alpha) in enumerate(alphas):
            plt.subplot(2, 2, i + 1)
            dist = Dirichlet(alpha)
            draw_pdf_contours(dist)

            plt.title(r'$\alpha$ = ({:.1f}, {:.1f}, {:.1f})'.format(*alpha), fontsize=16)
```



```
In [6]: with pm.Model() as model_kg:
            # Each observation is assigned to a cluster/component with probability p
            p = pm.Dirichlet('p', a=np.ones(clusters))
            category = pm.Categorical('category', p=p, shape=n_total)

            # Known Gaussians means
            means = pm.math.constant([10, 20, 35])

            y = pm.Normal('y', mu=means[category], sd=2, observed=mix)

            step1 = pm.ElemwiseCategorical(vars=[category], values=range(clusters))
            ## The CategoricalGibbsMetropolis is a recent addition to PyMC3
            ## I have not find the time yet to experiment with it.
            #step1 = pm.CategoricalGibbsMet\ropolis(vars=[category])
            step2 = pm.Metropolis(vars=[p])
            trace_kg = pm.sample(10000, step=[step1, step2],chains=1,njobs=1)

/home/damianos/miniconda3/envs/pymc3/lib/python3.7/site-packages/ipykernel_launcher.py:11: Dep
  # This is added back by InteractiveShellApp.init_path()
Sequential sampling (1 chains in 1 job)
CompoundStep
>ElemwiseCategorical: [category]
>Metropolis: [p]
100%|| 10500/10500 [00:30<00:00, 349.40it/s]
```

```
Only one chain was sampled, this makes it impossible to run some convergence checks
```

```
In [7]: chain_kg = trace_kg[1000:]
        varnames_kg = ['p']
        pm.traceplot(chain_kg, varnames_kg);
```



```
In [8]: print(pm.summary(chain_kg, varnames_kg))
        n_cluster_array = np.array(n_cluster)
        print('\n')
        print('Actual values of cluster fractions: {}'.format(n_cluster_array/n_cluster_array.
```

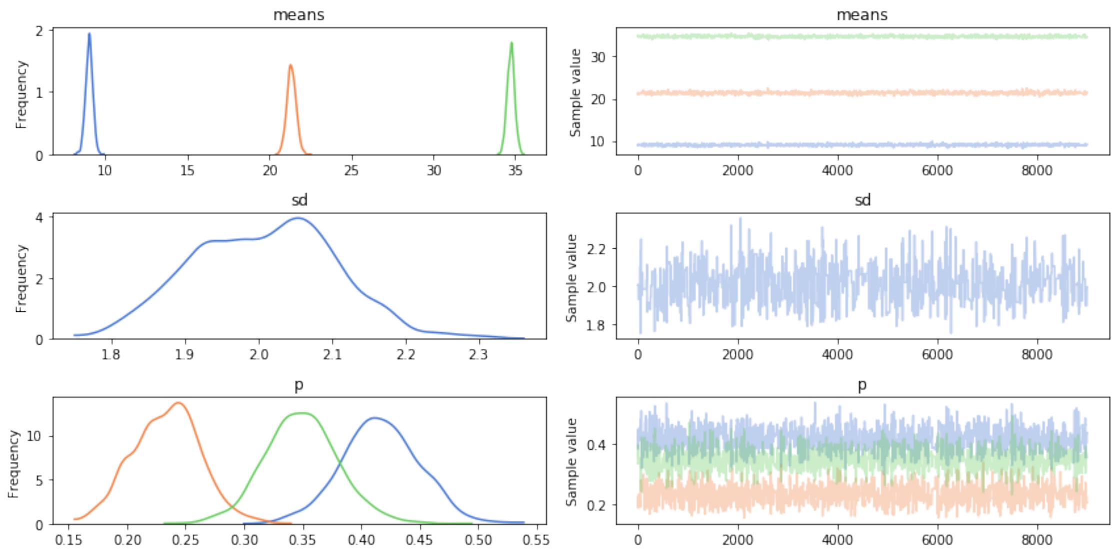
```
          mean        sd  mc_error   hpd_2.5  hpd_97.5
p__0  0.418133  0.032734  0.001302  0.347043  0.475764
p__1  0.234513  0.029194  0.001281  0.173813  0.285907
p__2  0.347354  0.032026  0.001378  0.281533  0.406833


Actual values of cluster fractions: [0.42 0.23 0.35]
```

```
In [9]: with pm.Model() as model_ug:
            # Each observation is assigned to a cluster/component with probability p
            p = pm.Dirichlet('p', a=np.ones(clusters))
            category = pm.Categorical('category', p=p, shape=n_total)

            # We estimate the unknown gaussians means and standard deviation
            means = pm.Normal('means', mu=[10, 20, 35], sd=2, shape=clusters)
            sd = pm.HalfCauchy('sd', 5)

            y = pm.Normal('y', mu=means[category], sd=sd, observed=mix)

            step1 = pm.ElemwiseCategorical(vars=[category], values=range(clusters))
            step2 = pm.Metropolis(vars=[means, sd, p])
            trace_ug = pm.sample(10000, step=[step1, step2],chains=1,njobs=1)
```

```
/home/damianos/miniconda3/envs/pymc3/lib/python3.7/site-packages/ipykernel_launcher.py:12: Dep
  if sys.path[0] == '':
Sequential sampling (1 chains in 1 job)
CompoundStep
```

```
>ElemwiseCategorical: [category]
>CompoundStep
>>Metropolis: [p]
>>Metropolis: [sd]
>>Metropolis: [means]
100%|| 10500/10500 [00:35<00:00, 297.53it/s]
Only one chain was sampled, this makes it impossible to run some convergence checks
```

```
In [10]: chain_ug = trace_ug[1000:]
         varnames_ug = ['means', 'sd', 'p']
         pm.traceplot(chain_ug, varnames_ug);
```



```
In [11]: print(pm.summary(chain_ug, varnames_ug))
         means_array = np.array([9, 21, 35])
         std_devs = [2, 2, 2]
         print('\n')
         print('Actual values of cluster fractions: {}'.format(n_cluster_array/n_cluster_array
         print('Actual values of cluster means: {}'.format(means_array))
         print('Actual values of cluster sd: {}'.format(std_devs))
```

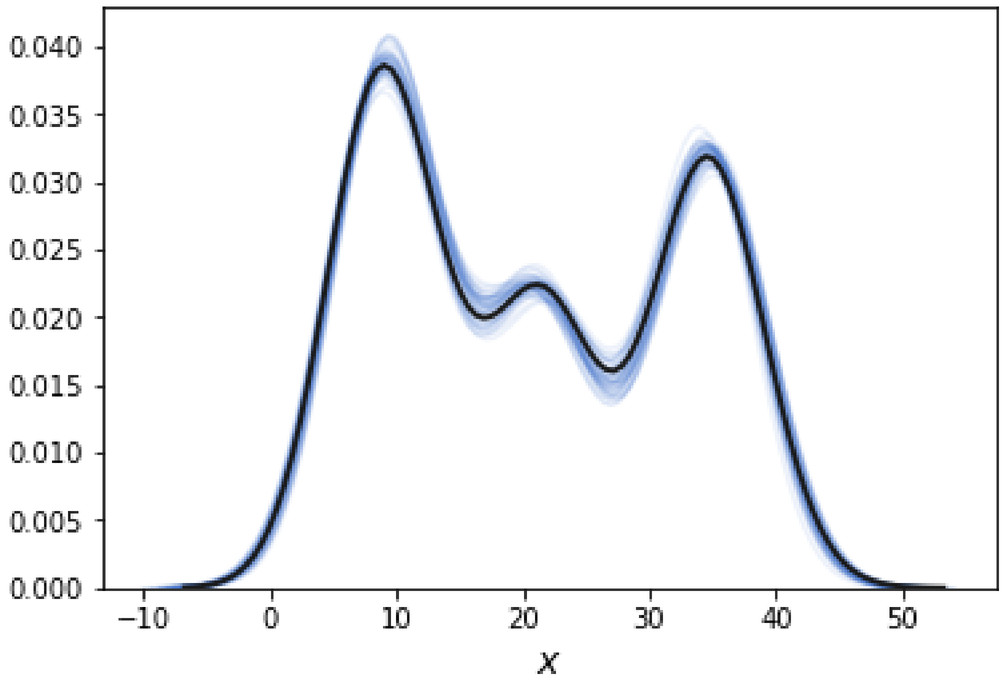
```
                mean        sd  mc_error    hpd_2.5   hpd_97.5
means__0    9.008717  0.217561  0.007712   8.613627   9.463408
means__1   21.356761  0.275587  0.010145  20.812555  21.887742
means__2   34.742823  0.225639  0.008249  34.304095  35.202331
sd          2.008365  0.097757  0.004210   1.821559   2.183144
p__0        0.417117  0.033083  0.001022   0.351142   0.480680
p__1        0.233721  0.028664  0.000926   0.172529   0.283838
p__2        0.349161  0.030978  0.001001   0.288788   0.411532
```

```
Actual values of cluster fractions: [0.42 0.23 0.35]
Actual values of cluster means: [ 9 21 35]
Actual values of cluster sd: [2, 2, 2]
```

```
In [12]: ppc = pm.sample_ppc(chain_ug, 50, model_ug)
```

```
/home/damianos/miniconda3/envs/pymc3/lib/python3.7/site-packages/ipykernel_launcher.py:1: Depre
  """Entry point for launching an IPython kernel.
100%|| 50/50 [00:00<00:00, 998.86it/s]
```

```
In [13]: for i in ppc['y']:
             sns.kdeplot(i, alpha=0.1, color='b')
         sns.kdeplot(np.array(mix), lw=2, color='k');
         plt.xlabel('$x$', fontsize=14);
```



Note the higher uncertainty where the data overlap and the reduced uncertainty at the high/low limits

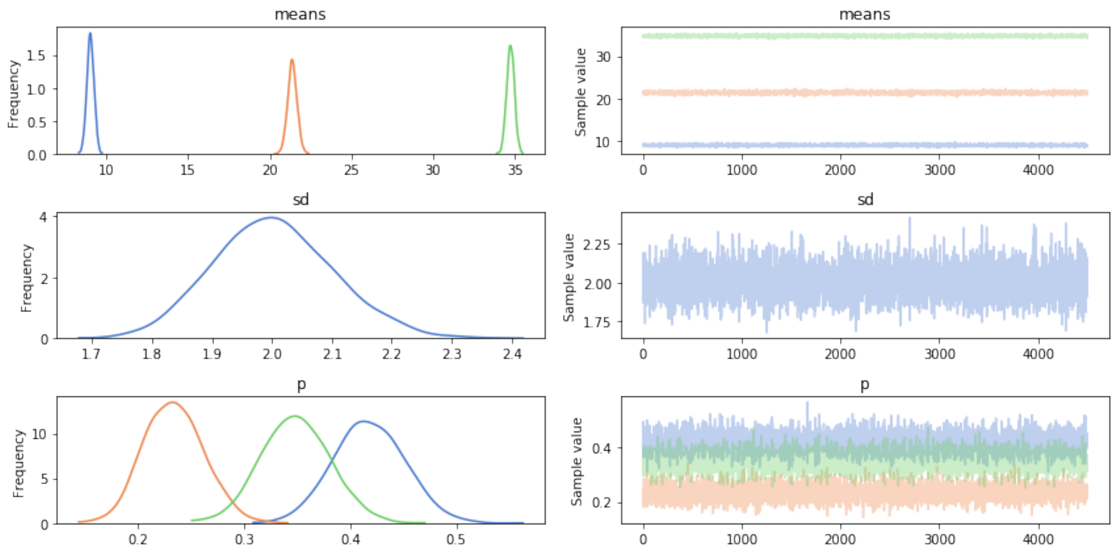
1.1 Marginalized Gaussian Mixture model

1.1.1 In the previous models we have explicitly defined the latent variable z in the model. This is ineffective in terms of sampling. PyMC3 offers the ability to model the outcome conditionaly on z as $p(y|z,\theta)$ and marginalise it to get $p(y|\theta)$

```
In [14]: with pm.Model() as model_mg:
             p = pm.Dirichlet('p', a=np.ones(clusters))

             means = pm.Normal('means', mu=[10, 20, 35], sd=2, shape=clusters)
             sd = pm.HalfCauchy('sd', 5)

             y = pm.NormalMixture('y', w=p, mu=means, sd=sd, observed=mix)

             trace_mg = pm.sample(5000, chains=1,njobs=1)
```

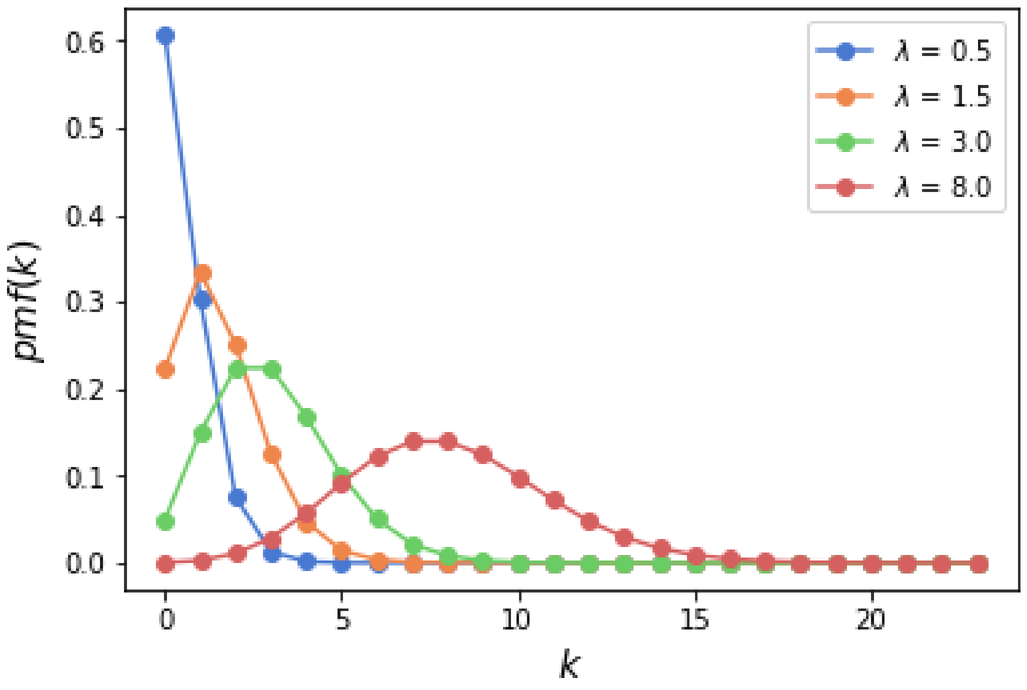
```
Auto-assigning NUTS sampler...
Initializing NUTS using jitter+adapt_diag...
Sequential sampling (1 chains in 1 job)
NUTS: [sd, means, p]
100%|| 5500/5500 [00:08<00:00, 637.72it/s]
Only one chain was sampled, this makes it impossible to run some convergence checks
```

```
In [15]: chain_mg = trace_mg[500:]
         varnames_mg = ['means', 'sd', 'p']
         pm.traceplot(chain_mg, varnames_mg);
```

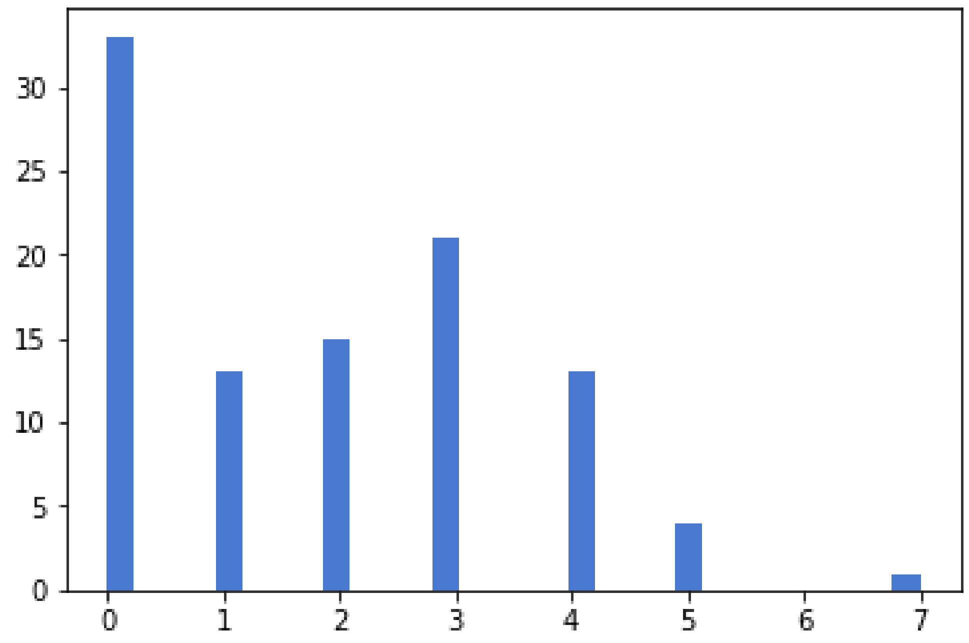


1.2 Zero inflated Poisson model

```
In [16]: lam_params = [0.5, 1.5, 3, 8]
         k = np.arange(0, max(lam_params) * 3)
         for lam in lam_params:
             y = stats.poisson(lam).pmf(k)
             plt.plot(k, y, 'o-', label="$\\lambda$ = {:3.1f}".format(lam))
         plt.legend();
         plt.xlabel('$k$', fontsize=14);
         plt.ylabel('$pmf(k)$', fontsize=14);
```



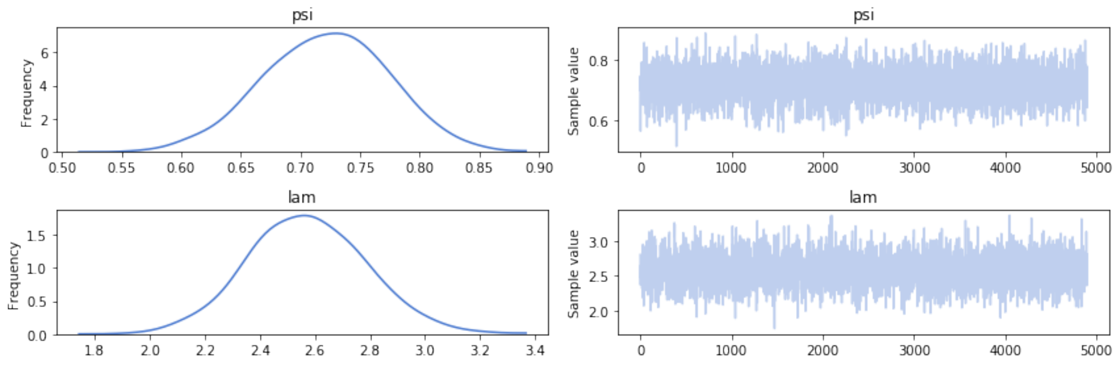
```
In [17]: np.random.seed(42)
         n = 100
         lam_true = 2.5  # Poisson rate
         pi = 0.2  # probability of extra-zeros (pi = 1-psi)

         # Simulate some data
         counts = np.array([(np.random.random() > pi) * np.random.poisson(lam_true) for i in ra

In [18]: plt.hist(counts, bins=30);
```



```
In [19]: with pm.Model() as ZIP:
             psi = pm.Beta('psi', 1, 1)
             lam = pm.Gamma('lam', 2, 0.1)

             y_pred = pm.ZeroInflatedPoisson('y_pred', theta=lam, psi=psi, observed=counts)
             trace_ZIP = pm.sample(5000,chains=1,njobs=1)
```

```
Auto-assigning NUTS sampler...
Initializing NUTS using jitter+adapt_diag...
Sequential sampling (1 chains in 1 job)
NUTS: [lam, psi]
100%|| 5500/5500 [00:03<00:00, 1652.34it/s]
Only one chain was sampled, this makes it impossible to run some convergence checks
```

```
In [20]: chain_ZIP = trace_ZIP[100:]
         pm.traceplot(chain_ZIP);
```



```
In [21]: pm.summary(chain_ZIP)
```

```
Out[21]:          mean        sd  mc_error   hpd_2.5  hpd_97.5
         psi  0.721471  0.052295  0.000769  0.619399  0.823200
         lam  2.572429  0.214952  0.003234  2.154592  3.001078
```

1.3 Zero inflated Poisson regression

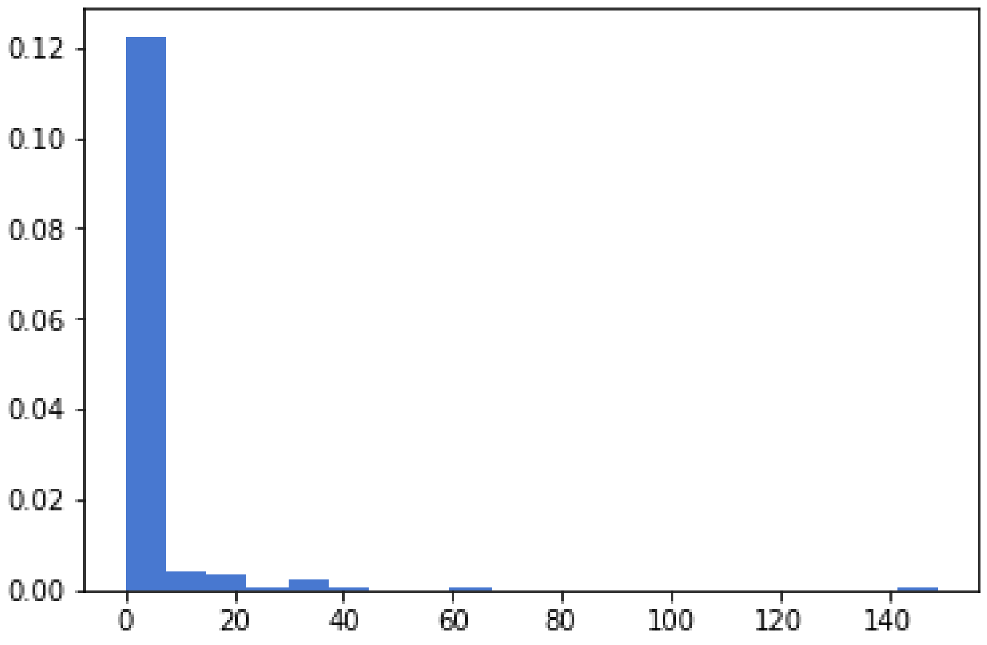
```
In [22]: #Kruschke plot
```

```
In [23]: fish_data = pd.read_csv('fish.csv')
         fish_data.head()
```

```
Out[23]:    nofish  livebait  camper  persons  child        xb        zg  count
         0       1         0       0        1      0 -0.896315  3.050405      0
         1       0         1       1        1      0 -0.558345  1.746149      0
         2       0         1       0        1      0 -0.401731  0.279939      0
         3       0         1       1        2      1 -0.956298 -0.601526      0
         4       0         1       0        1      0  0.436891  0.527709      1
```

```
In [24]: plt.hist(fish_data['count'], bins=20, normed=True);
```

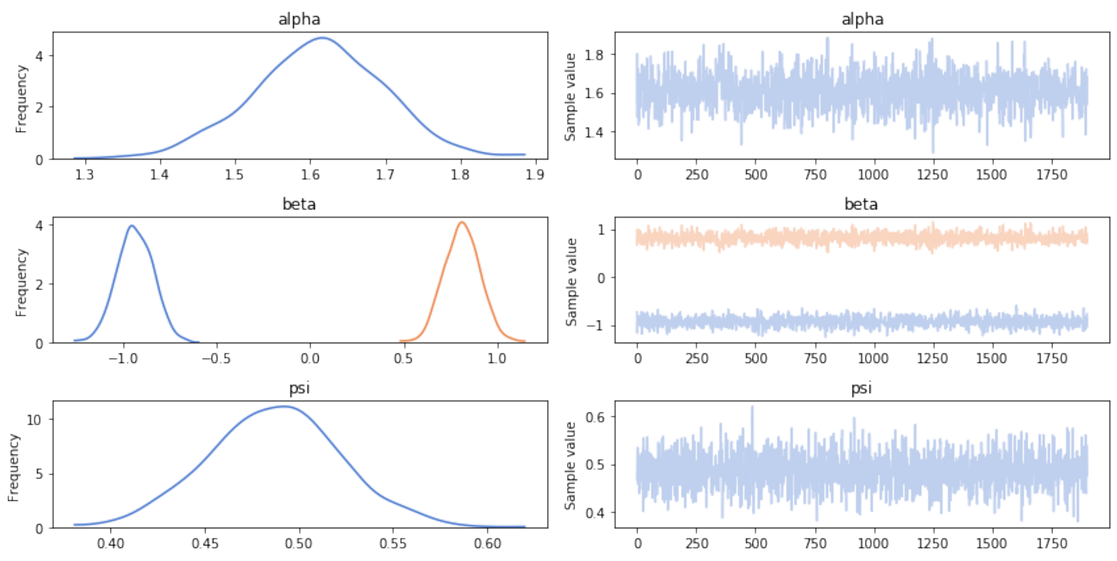
```
/home/damianos/miniconda3/envs/pymc3/lib/python3.7/site-packages/matplotlib/axes/_axes.py:6521
The 'normed' kwarg was deprecated in Matplotlib 2.1 and will be removed in 3.1. Use 'density'
  alternative="'density'", removal="3.1")
```



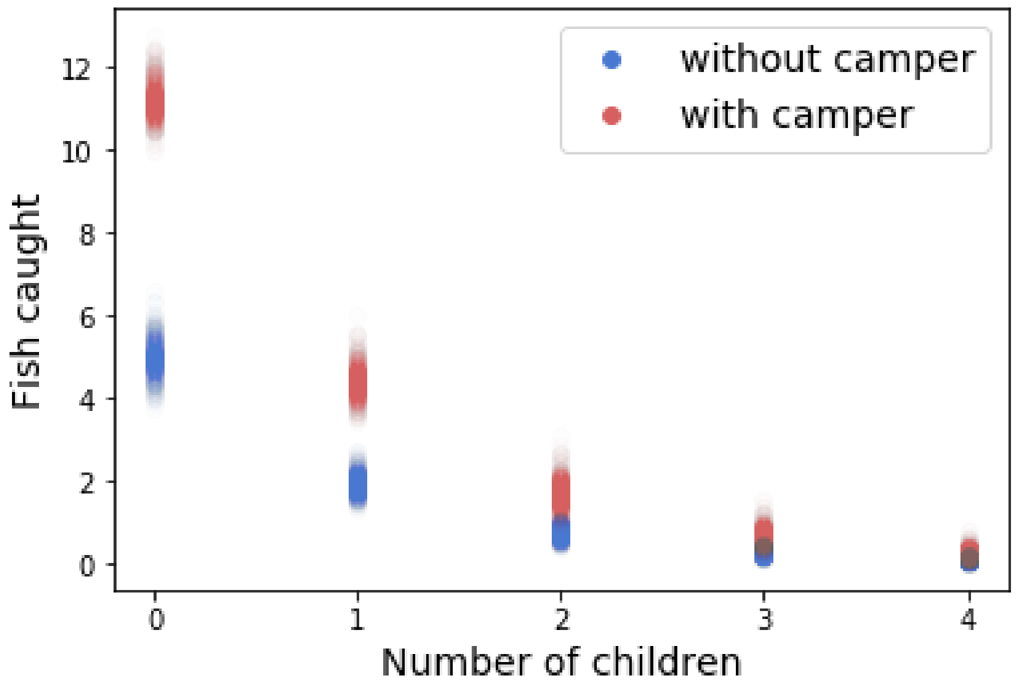
```
In [25]: with pm.Model() as ZIP_reg:
             psi = pm.Beta('psi', 1, 1)

             alpha = pm.Normal('alpha', 0, 10)
             beta = pm.Normal('beta', 0, 10, shape=2)
             lam = pm.math.exp(alpha + beta[0] * fish_data['child'] + beta[1] * fish_data['cam

             y = pm.ZeroInflatedPoisson('y', theta=lam, psi=psi, observed=fish_data['count'])
             trace_ZIP_reg = pm.sample(2000,chains=1,njobs=1)
```

```
Auto-assigning NUTS sampler...
Initializing NUTS using jitter+adapt_diag...
Sequential sampling (1 chains in 1 job)
NUTS: [beta, alpha, psi]
100%|| 2500/2500 [00:05<00:00, 437.66it/s]
Only one chain was sampled, this makes it impossible to run some convergence checks
```

```
In [26]: chain_ZIP_reg = trace_ZIP_reg[100:]
         pm.traceplot(chain_ZIP_reg);
```

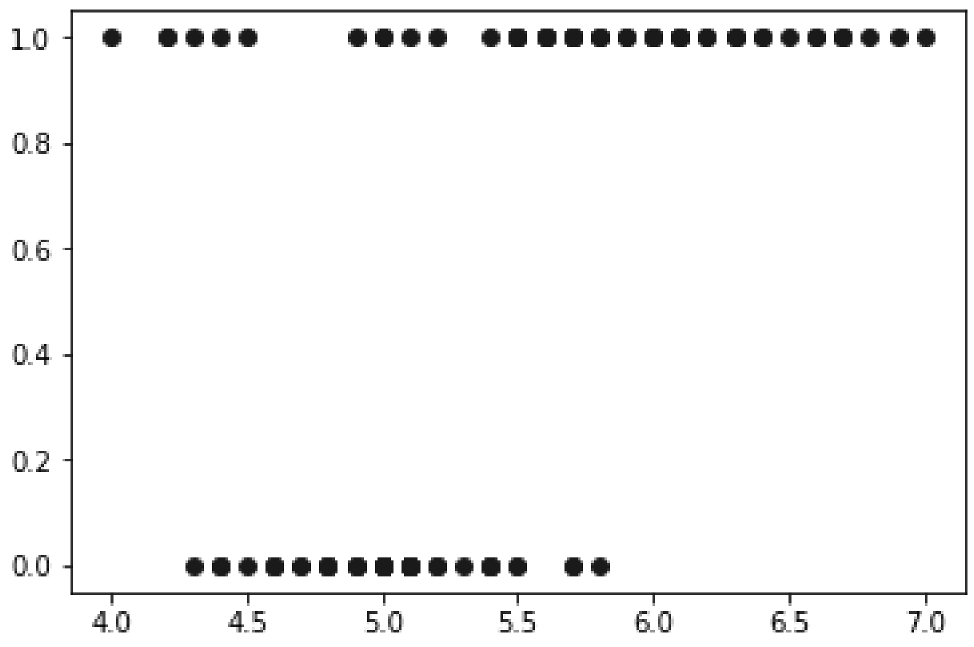


```
In [27]: pm.summary(chain_ZIP_reg)

Out[27]:             mean        sd  mc_error   hpd_2.5  hpd_97.5
         alpha    1.610313  0.088094  0.002596  1.427976  1.771882
         beta__0 -0.936188  0.097573  0.002547 -1.131112 -0.753889
         beta__1  0.810109  0.096980  0.002897  0.621544  0.992202
         psi      0.486522  0.034692  0.000816  0.419652  0.556741

In [28]: children =  [0, 1, 2, 3, 4]
         fish_count_pred_0 = []
         fish_count_pred_1 = []
         thin = 5
         # calculate the expectation lambda with and withour a camper for difference number of
         # note lambda from the model is exp(a+bX)
         for n in children:
             without_camper = chain_ZIP_reg['alpha'][::thin] + chain_ZIP_reg['beta'][:,0][::thi
             with_camper = without_camper + chain_ZIP_reg['beta'][:,1][::thin]
             fish_count_pred_0.append(np.exp(without_camper))
             fish_count_pred_1.append(np.exp(with_camper))

In [29]: plt.plot(children, fish_count_pred_0, 'bo', alpha=0.01)
         plt.plot(children, fish_count_pred_1, 'ro', alpha=0.01)

         plt.xticks(children);
         plt.xlabel('Number of children', fontsize=14)
         plt.ylabel('Fish caught', fontsize=14)
         plt.plot([], 'bo', label='without camper')
         plt.plot([], 'ro', label='with camper')
         plt.legend(fontsize=14);
```



1.4 Robust logistic Regression

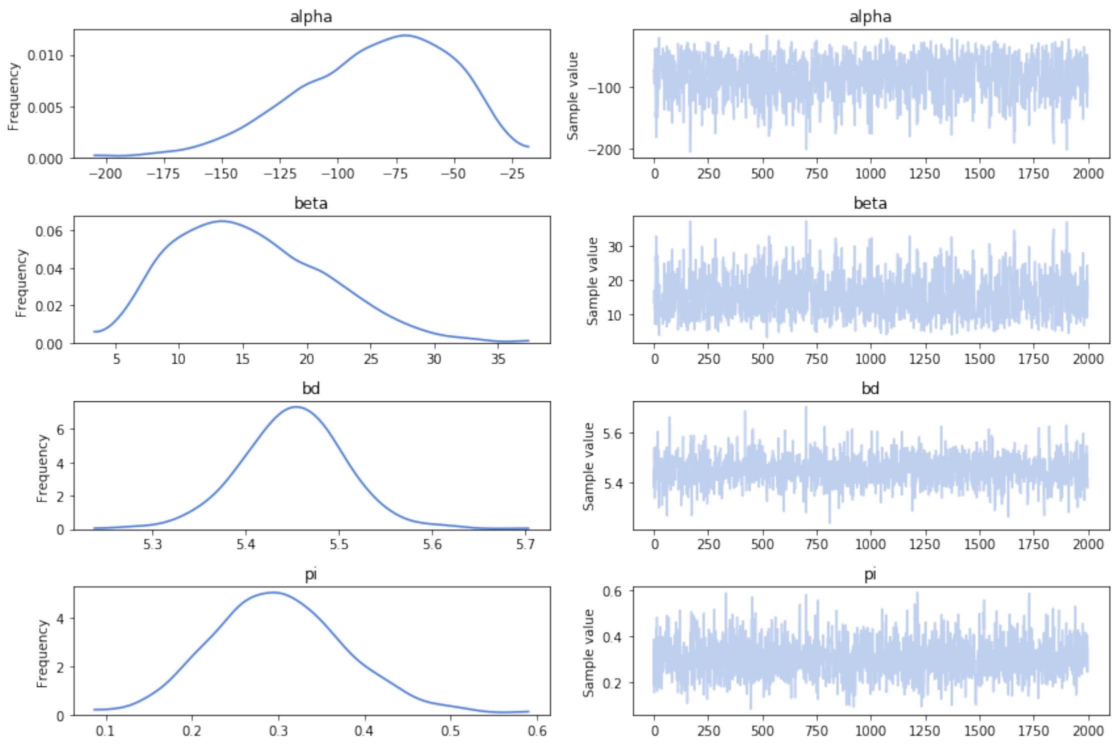
```
In [30]: iris = sns.load_dataset("iris")
         df = iris.query("species == ('setosa', 'versicolor')")
         y_0 = pd.Categorical(df['species']).codes
         x_n = 'sepal_length'
         x_0 = df[x_n].values
         # contaminate our set with ones with unusually small sepal length
         y_0 = np.concatenate((y_0, np.ones(6)))
         x_0 = np.concatenate((x_0, [4.2, 4.5, 4.0, 4.3, 4.2, 4.4]))
         x_0_m = x_0 - x_0.mean()
         plt.plot(x_0, y_0, 'o', color='k');
```



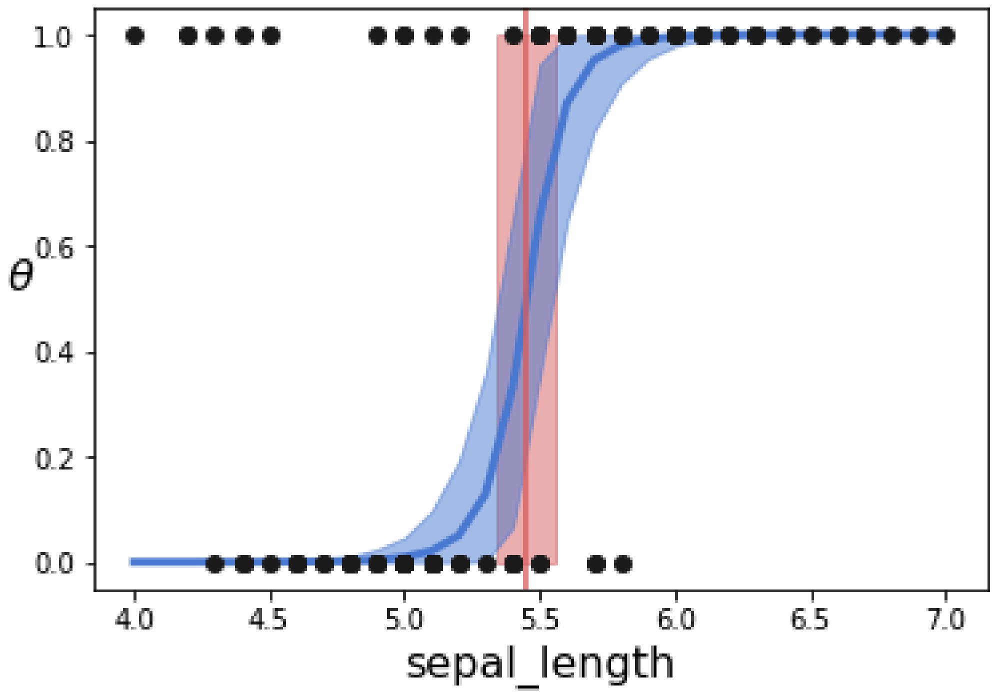
```
In [31]: with pm.Model() as model_rlg:
             alpha_tmp = pm.Normal('alpha_tmp', mu=0, sd=100)
             beta = pm.Normal('beta', mu=0, sd=10)

             mu = alpha_tmp + beta * x_0_m
             theta = pm.Deterministic('theta', 1 / (1 + pm.math.exp(-mu)))
             # add the mixture here as a combination of the logistic derived theta
             # and a random pi from a Beta distribution
             pi = pm.Beta('pi', 1, 1)
             p = pi * 0.5 + (1 - pi) * theta
             # correct alpha from centering
             alpha = pm.Deterministic('alpha', alpha_tmp - beta * x_0.mean())
             bd = pm.Deterministic('bd', -alpha/beta)

             yl = pm.Bernoulli('yl', p=p, observed=y_0)

             trace_rlg = pm.sample(2000, njobs=1,chains=1)
```

```
Auto-assigning NUTS sampler...
Initializing NUTS using jitter+adapt_diag...
Sequential sampling (1 chains in 1 job)
NUTS: [pi, beta, alpha_tmp]
100%|| 2500/2500 [00:02<00:00, 1131.39it/s]
There were 3 divergences after tuning. Increase `target_accept` or reparameterize.
Only one chain was sampled, this makes it impossible to run some convergence checks
```

```
In [32]: varnames = ['alpha', 'beta', 'bd', 'pi']
         pm.traceplot(trace_rlg, varnames);
```



```
In [33]: pm.summary(trace_rlg, varnames)

Out[33]:              mean         sd  mc_error     hpd_2.5   hpd_97.5
         alpha -84.752824  32.430609  1.204960 -145.679729 -28.152112
         beta   15.543885   5.935414  0.219442    5.178316  26.580590
         bd      5.450754   0.055642  0.001486    5.337383   5.553501
         pi      0.300910   0.079280  0.002478    0.145793   0.453829

In [34]: theta = trace_rlg['theta'].mean(axis=0)
         idx = np.argsort(x_0)
         plt.plot(x_0[idx], theta[idx], color='b', lw=3);
         plt.axvline(trace_rlg['bd'].mean(), ymax=1, color='r')
         bd_hpd = pm.hpd(trace_rlg['bd'])
         plt.fill_betweenx([0, 1], bd_hpd[0], bd_hpd[1], color='r', alpha=0.5)

         plt.plot(x_0, y_0, 'o', color='k');
         theta_hpd = pm.hpd(trace_rlg['theta'])[idx]
         plt.fill_between(x_0[idx], theta_hpd[:,0], theta_hpd[:,1], color='b', alpha=0.5);

         plt.xlabel(x_n, fontsize=16);
         plt.ylabel('$\\theta$', rotation=0, fontsize=16);
```



```
In [35]: import sys, IPython, scipy, matplotlib, platform
         print("This notebook was created on a %s computer running %s and using:\nPython %s\nIP
```

```
This notebook was created on a x86_64 computer running debian buster/sid and using:
Python 3.7.2
IPython 7.2.0
PyMC3 3.6
NumPy 1.16.0
SciPy 1.2.0
Matplotlib 3.0.2
Seaborn 0.9.0
Pandas 0.23.4


/home/damianos/miniconda3/envs/pymc3/lib/python3.7/site-packages/ipykernel_launcher.py:2: Depre
```