Basic stats using `Scipy`

In this example we will go over how to draw samples from various built in probability distributions and define your own custom distributions.

Packages being used

- `scipy` : has all the stats stuff
- `numpy` : has all the array stuff

Relevant documentation

- `scipy.stats` : http://docs.scipy.org/doc/scipy/reference/tutorial/stats.html, http://docs.scipy.org/doc/scipy/reference/generated/scipy.stats.rv_continuous.html#scipy.stats.rv_continuous, http://docs.scipy.org/doc/scipy/reference/stats.html#module-scipy.stats

In [1]:

```
import numpy as np
import scipy.stats as st
# some special functions we will make use of later on
from scipy.special import erfc
from matplotlib import pyplot as plt
from astropy.visualization import hist
import mpl_style
%matplotlib inline
plt.style.use(mpl_style.style1)
```

There are many probability distributions that are already available in `scipy` : http://docs.scipy.org/doc/scipy/reference/stats.html#module-scipy.stats. These classes allow for the evaluations of PDFs, CDFs, PPFs, moments, random draws, and fitting. As an example lets take a look at the normal distribution.

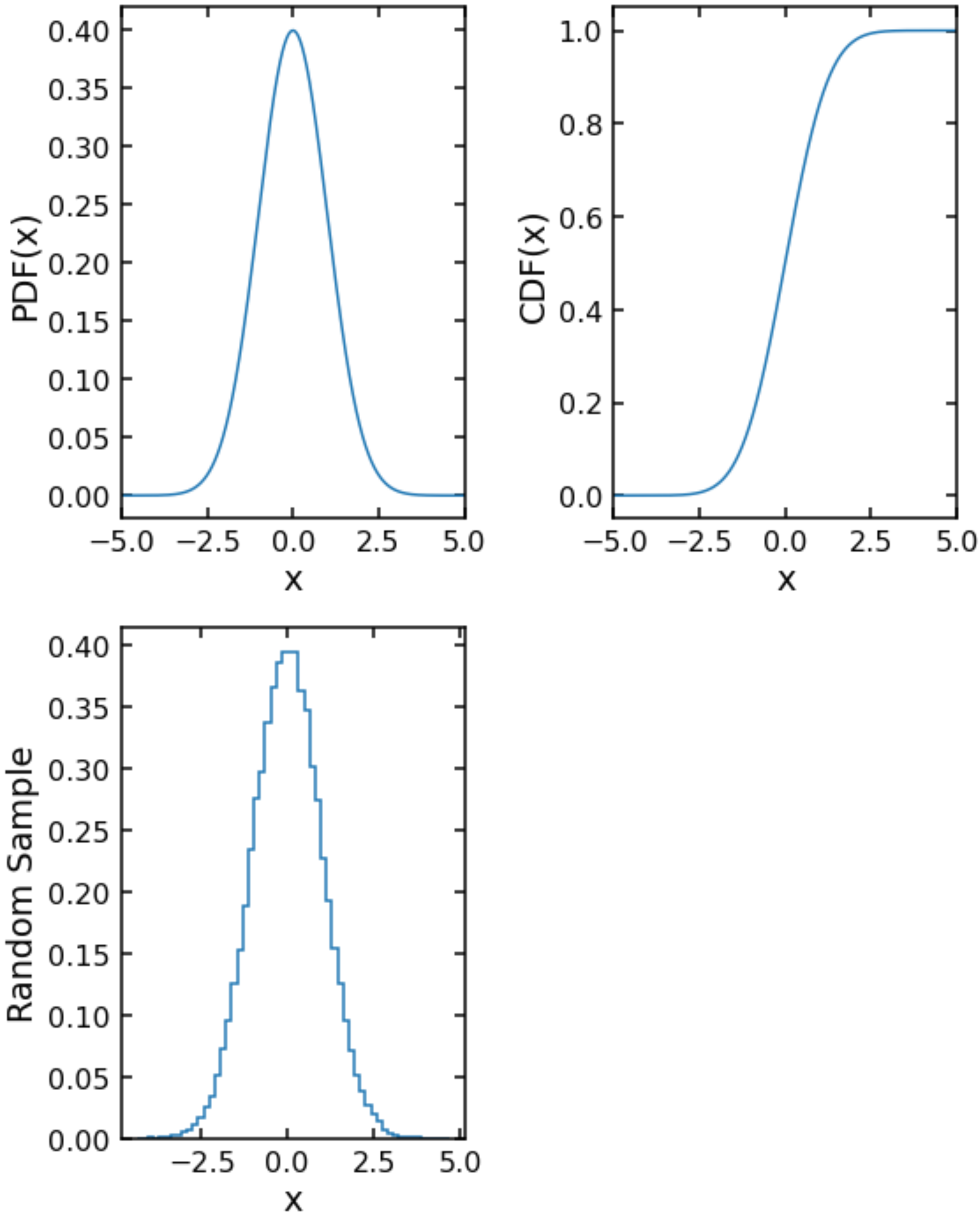
In [2]:

```
norm = st.norm(loc=0, scale=1)
x = np.linspace(-5, 5, 1000)

plt.figure(1, figsize=(8, 10))
plt.subplot2grid((2, 2), (0, 0))
plt.plot(x, norm.pdf(x))
plt.xlabel('x')
plt.ylabel('PDF(x)')
plt.xlim(-5, 5)

plt.subplot2grid((2, 2), (0, 1))
plt.plot(x, norm.cdf(x))
plt.xlabel('x')
plt.ylabel('CDF(x)')
plt.xlim(-5, 5)

plt.subplot2grid((2, 2), (1, 0))
sample_norm = norm.rvs(size=100000)
hist(sample_norm, bins='knuth', histtype='step', lw=1.5, density=True)
plt.xlabel('x')
plt.ylabel('Random Sample')
plt.tight_layout()
```



You can calculate moments and fit data:

In [3]:
```
for i in range(4):
    print('moment {0}: {1}'.format(i+1, norm.moment(i+1)))

print('best fit: {0}'.format(st.norm.fit(sample_norm)))
```

```
moment 1: 0.0
moment 2: 1.0
moment 3: 0.0
moment 4: 3.0
best fit: (0.0023590267327017016, 1.0016772649523067)
```

Custom probability distributions

Sometimes you need to use obscure PDFs that are not already in `scipy` or `astropy`. When this is the case you can make your own subclass of `st.rv_continuous` and overwrite the `_pdf` or `_cdf` methods. This new sub class will act exactly like the built in distributions.

The methods you can override in the subclass are:

- _rvs: create a random sample drawn from the distribution
- _pdf: calculate the PDF at any point
- _cdf: calculate the CDF at any point
- _sf: survival function, a.k.a. 1-CDF(x)
- _ppf: percent point function, a.k.a. inverse CDF
- _isf: inverse survival function
- _stats: function that calculates the first 4 moments
- _munp: function that calculates the nth moment
- _entropy: differential entropy
- _argcheck: function to check the input arguments are valid (e.g. var>0)

You should override any method you have analytic functions for, otherwise (typically slow) numerical integration, differentiation, and function inversion are used to transform the ones that are specified.

The exponentially modified Gaussian distribution

As and example lets create a class for the EMG distribution (https://en.wikipedia.org/wiki/Exponentially_modified_Gaussian_distribution). This is the distributions resulting from the sum of a Gaussian random variable and an exponential random variable. The PDF and CDF are:

\begin{align} f(x;\mu,\sigma, \lambda) & = \frac{\lambda}{2} \exp{\left(\frac{\lambda}{2} \left[2\mu+\lambda\sigma^{2}-2x \right] \right)} \operatorname{erfc}{\left(\frac{\mu + \lambda \sigma^{2}-x}{\sigma\sqrt{2}} \right)} \\ F(x; \mu, \sigma, \lambda) & = \Phi(u, 0, v) - \Phi(u, v^2, v) \exp{\left(-u + \frac{v^2}{2} \right)} \\ \Phi(x, a, b) & = \frac{1}{2} \left[1 + \operatorname{erf}{\left(\frac{x - a}{b\sqrt{2}} \right)} \right] \\ u & = \lambda(x - \mu) \\ v & = \lambda\sigma \end{align}

In [4]:

```python
# create a generating class
class EMG_gen1(st.rv_continuous):
    def _pdf(self, x, mu, sig, lam):
        u = 0.5 * lam * (2 * mu + lam * sig**2 - 2 * x)
        v = (mu + lam * sig**2 - x)/(sig * np.sqrt(2))
        return 0.5 * lam * np.exp(u) * erfc(v)
    def _cdf(self, x, mu, sig, lam):
        u = lam * (x - mu)
        v = lam * sig
        phi1 = st.norm.cdf(u, loc=0, scale=v)
        phi2 = st.norm.cdf(u, loc=v**2, scale=v)
        return phi1 - phi2 * np.exp(-u + 0.5 * v**2)
    def _stats(self, mu, sig, lam):
        # reutrn the mean, variance, skewness, and kurtosis
        mean = mu + 1 / lam
        var = sig**2 + 1 / lam**2
        sl = sig * lam
        u = 1 + 1 / sl**2
        skew = (2 / sl**3) * u**(-3 / 2)
        v = 3 * (1 + 2 / sl**2 + 3 / sl**4) / u**2
        kurt = v - 3
        return mean, var, skew, kurt
    def _argcheck(self, mu, sig, lam):
        return np.isfinite(mu) and (sig > 0) and (lam > 0)

class EMG_gen2(EMG_gen1):
    def _ppf(self, q, mu, sig, lam):
        # use linear interpolation to solve this faster (not exact, but much
        # pick range large enough to fit the full cdf
        var = sig**2 + 1 / lam**2
        x = np.arange(mu - 50 * np.sqrt(var), mu + 50 * np.sqrt(var), 0.01)
        y = self.cdf(x, mu, sig, lam)
        return np.interp(q, y, x)

class EMG_gen3(EMG_gen1):
    def _rvs(self, mu, sig, lam):
        # redefine the random sampler to sample based on a normal and exp dis
        return st.norm.rvs(loc=mu, scale=sig, size=self._size) + st.expon.rvs

# use generator to make the new class
EMG1 = EMG_gen1(name='EMG1')
EMG2 = EMG_gen2(name='EMG2')
EMG3 = EMG_gen3(name='EMG3')
```

Lets look at how long it takes to create readom samples for each of these version of the EMG:

In [5]:

```python
%time EMG1.rvs(0, 1, 0.5, size=1000)
print('=========')
%time EMG2.rvs(0, 1, 0.5, size=1000)
print('=========')
%time EMG3.rvs(0, 1, 0.5, size=1000)
print('=========')
```

```
CPU times: user 3.88 s, sys: 7.93 ms, total: 3.88 s
Wall time: 3.87 s
```

```
=========
CPU times: user 3.38 ms, sys: 0 ns, total: 3.38 ms
Wall time: 3.34 ms
=========
CPU times: user 973 µs, sys: 1.62 ms, total: 2.6 ms
Wall time: 20 ms
=========
/mnt/lustre/shared_python_environment/DataLanguages/lib/python3.8/site-packag
es/scipy/stats/_distn_infrastructure.py:1083: VisibleDeprecationWarning: The
signature of <bound method EMG_gen3._rvs of <__main__.EMG_gen3 object at 0x7f
779ee89760>> does not contain a "size" keyword.  Such signatures are deprecat
ed.
  warnings.warn(
```

As you can see, the numerical inversion of the CDF is very slow, the approximation to the inversion is much faster, and defining `_rvs` in terms of the `normal` and `exp` distributions is the fastest.

Lets take a look at the results for `EMG3` :

In [6]:

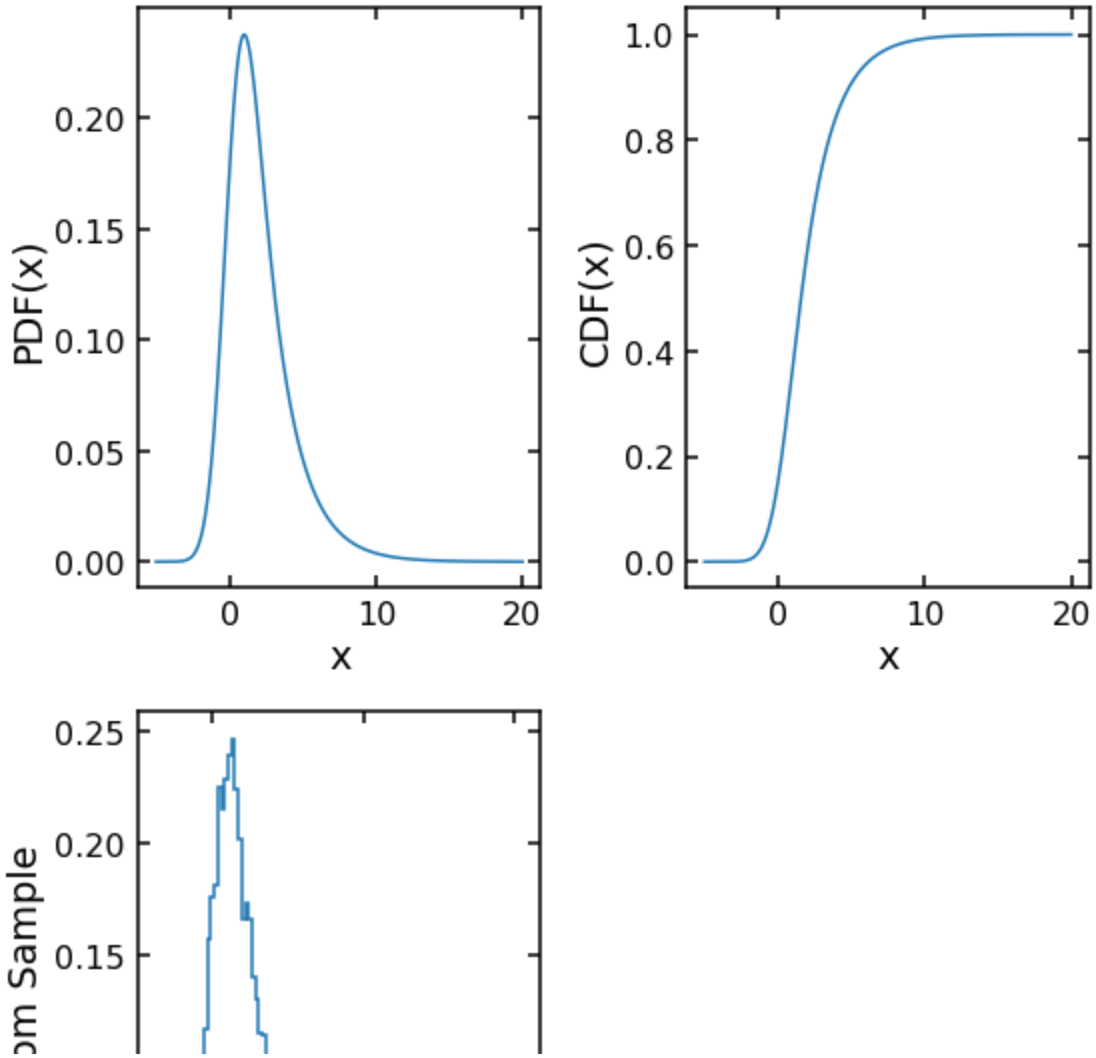
```
dist = EMG3(0, 1, 0.5)
x = np.linspace(-5, 20, 1000)

plt.figure(2, figsize=(8, 10))
plt.subplot2grid((2, 2), (0, 0))
plt.plot(x, dist.pdf(x))
plt.xlabel('x')
plt.ylabel('PDF(x)')

plt.subplot2grid((2, 2), (0, 1))
plt.plot(x, dist.cdf(x))
plt.xlabel('x')
plt.ylabel('CDF(x)')

plt.subplot2grid((2, 2), (1, 0))
sample_emg = dist.rvs(size=10000)
hist(sample_emg, bins='knuth', histtype='step', lw=1.5, density=True)
plt.xlabel('x')
plt.ylabel('Random Sample')
plt.tight_layout()
```

```
/mnt/lustre/shared_python_environment/DataLanguages/lib/python3.8/site-packag
es/scipy/stats/_distn_infrastructure.py:1083: VisibleDeprecationWarning: The
signature of <bound method EMG_gen3._rvs of <__main__.EMG_gen3 object at 0x7f
779ed58520>> does not contain a "size" keyword.  Such signatures are deprecat
ed.
  warnings.warn(
```



As with the built in functions we can calculate moments and do fits to data. **Note** Since we are not using the built in `loc` and `scale` params they are fixed to 0 and 1 in the fit below.

In [7]:

```
for i in range(4):
    print('moment {0}: {1}'.format(i+1, dist.moment(i+1)))

print('best fit: {0}'.format(EMG3.fit(sample_emg, floc=0, fscale=1)))
```

```
moment 1: 2.0
moment 2: 9.0
moment 3: 54.0
moment 4: 435.0
best fit: (-0.02693863999005528, 1.0210387739316098, 0.49836860851157133, 0,
1)
```

For reference here is how `scipy` defines this distribution (found under the name `exponnorm`):

In [8]:

```
import scipy.stats._continuous_distns as cd
np.source(cd.exponnorm_gen)
```

```
In file: /mnt/lustre/shared_python_environment/DataLanguages/lib/python3.8/si
te-packages/scipy/stats/_continuous_distns.py
```

```
class exponnorm_gen(rv_continuous):
    r"""An exponentially modified Normal continuous random variable.

    Also known as the exponentially modified Gaussian distribution [1]_.

    %(before_notes)s

    Notes
    -----
    The probability density function for `exponnorm` is:

    .. math::

        f(x, K) = \frac{1}{2K} \exp\left(\frac{1}{2 K^2} - x / K \right)
                  \text{erfc}\left(-\frac{x - 1/K}{\sqrt{2}}\right)

    where :math:`x` is a real number and :math:`K > 0`.

    It can be thought of as the sum of a standard normal random variable
    and an independent exponentially distributed random variable with rate
    ``1/K``.

    %(after_notes)s

    An alternative parameterization of this distribution (for example, in
    the Wikpedia article [1]_) involves three parameters, :math:`\mu`,
    :math:`\lambda` and :math:`\sigma`.

    In the present parameterization this corresponds to having ``loc`` and
    ``scale`` equal to :math:`\mu` and :math:`\sigma`, respectively, and
    shape parameter :math:`K = 1/(\sigma\lambda)`.

    .. versionadded:: 0.16.0

    References
    ----------
    .. [1] Exponentially modified Gaussian distribution, Wikipedia,
           https://en.wikipedia.org/wiki/Exponentially_modified_Gaussian_dist
ribution

    %(example)s

    """
    def _rvs(self, K, size=None, random_state=None):
        expval = random_state.standard_exponential(size) * K
        gval = random_state.standard_normal(size)
        return expval + gval

    def _pdf(self, x, K):
        return np.exp(self._logpdf(x, K))

    def _logpdf(self, x, K):
        invK = 1.0 / K
        exparg = invK * (0.5 * invK - x)
        return exparg + _norm_logcdf(x - invK) - np.log(K)

    def _cdf(self, x, K):
        invK = 1.0 / K
        expval = invK * (0.5 * invK - x)
        logprod = expval + _norm_logcdf(x - invK)
```

```python
        return _norm_cdf(x) - np.exp(logprod)

    def _sf(self, x, K):
        invK = 1.0 / K
        expval = invK * (0.5 * invK - x)
        logprod = expval + _norm_logcdf(x - invK)
        return _norm_cdf(-x) + np.exp(logprod)

    def _stats(self, K):
        K2 = K * K
        opK2 = 1.0 + K2
        skw = 2 * K**3 * opK2**(-1.5)
        krt = 6.0 * K2 * K2 * opK2**(-2)
        return K, opK2, skw, krt
```

In [9]:

```python
%time st.exponnorm.rvs(0.5, size=1000)
print('=========')
```

```
CPU times: user 868 µs, sys: 0 ns, total: 868 µs
Wall time: 576 µs
=========
```

In [ ]:

```python

```