healpy tutorial

healpy is a python wrapper for a C++ library called HEALPix (Hierarchical Equal Area isoLatitude Pixelization). It was initially developed with CMB data analysis in mind, but is useful for any situation where you have to handle functions on the sphere (i.e. pretty much all of astronomy and observational cosmology).

Some useful links:

- healpy documentation (very thorough, should be your go-to when you get stuck)
 https://healpy.readthedocs.io/en/latest/ (https://healpy.readthedocs.io/en/latest/)
- original HEALPix documentation https://healpix.jpl.nasa.gov/index.shtml)
- the HEALPix paper (with 2000+ citations!) https://inspirehep.net/record/659804
 (https://inspirehep.net/record/659804)

Basics

Let's start by importing the **healpy** library, along with some other useful things.

```
In [1]: %matplotlib inline
    import healpy as hp
    import numpy as np
    import matplotlib.pyplot as plt

In [2]: plt.rcParams.update({"text.usetex":True})
    plt.rcParams.update({"font.size":20})
```

 ${\tt healpy}$ is, at its heart, an efficient algorithm for tiling the sphere into equal-area "pixels". We control the number of pixels (equivalently, the angular resolution of the map) using the "nside" parameter, which must be an integer power of 2, less than 2^{30} . Shown below are some HEALPix pixelisations for various values of nside.

```
In [3]: from IPython.display import Image
    from IPython.core.display import HTML
    Image(url= "https://healpix.jpl.nasa.gov/images/healpixGridRefinement.jpg")
Out[3]:
```

Let's set a reasonable value of nside.

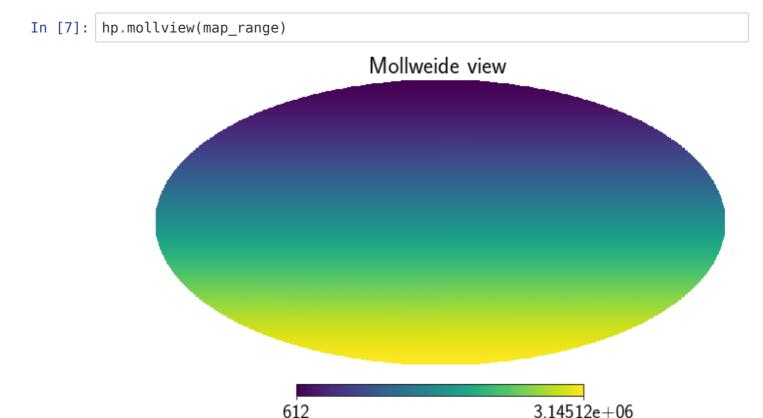
```
In [4]: nside = 2**9
```

healpy provides some useful functions for converting this into the corresponding number of pixels, pixel area, and angular resolution.

Let's create a map. A **healpy** map is just a **numpy** array, with each number in the array corresponding to the value in one pixel.

```
In [6]: map_range = np.arange(npix)
```

In order to visualise this map, we use one of the plotting functions from the module healpy.visufunc. There are lots of different ways to project the sphere S^2 onto the plane \mathbb{R}^2 (like this screen), but let's use the Mollweide projection.

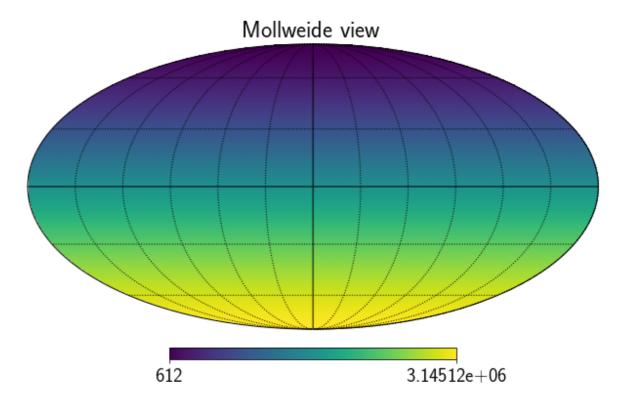


The **healpy.visufunc.graticule** function can be used to add grid lines.



0.0 180.0 -180.0 180.0

The interval between parallels is 30 deg -0.00'. The interval between meridians is 30 deg -0.00'.

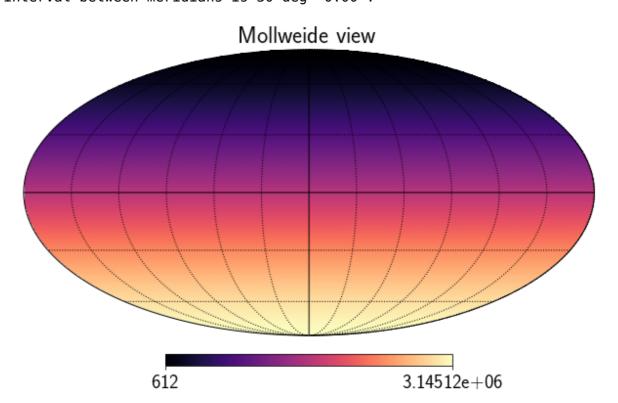


We can also use the **cmap** argument to change the colourmap (the default is "viridis"; see https://matplotlib.org/tutorials/colors/colormaps.html) for a full list).

```
In [9]: hp.mollview(map_range, cmap="magma")
hp.graticule()

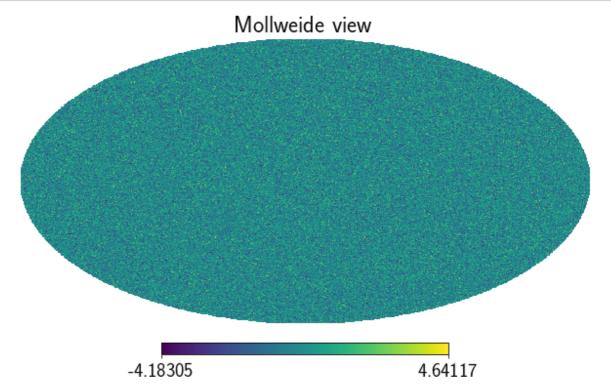
0.0 180.0 -180.0 180.0
```

The interval between parallels is 30 deg -0.00'. The interval between meridians is 30 deg -0.00'.



This map is pretty artificial-looking. Let's simulate a Gaussian random noise map using **numpy**'s random number generator.

```
In [10]: map_gauss = np.random.normal(size=npix)
hp.mollview(map_gauss)
```



healpy provides some useful functions for converting between a given pixel's index within the map array, its angular coordinates, and the unit vector pointing in its direction. Let's find the index of the pixel with coordinates $\theta=\pi/4$, $\phi=\pi/2$, then convert this to a vector and check it has unit length.

```
In [11]: pix = hp.ang2pix(nside, np.pi/4.0, np.pi/2.0)
    print("the pixel index for coordinates theta=pi/4, phi=pi/2 is {}".format(p ix))

    vec = hp.pix2vec(nside, pix)
    print("the unit vector pointing to this pixel is {}".format(vec))

    vec = hp.ang2vec(np.pi/4.0, np.pi/2.0)
    print("the unit vector point to those coordinates is {}".format(vec))
    print("this vector has length {}".format(vec.dot(vec)))

    the pixel index for coordinates theta=pi/4, phi=pi/2 is 460320
    the unit vector pointing to this pixel is (-0.0011571238232320875, 0.7071813 576359993, 0.70703125)
    the unit vector point to those coordinates is [4.32978028e-17 7.07106781e-01 7.07106781e-01]
    this vector has length 1.0
```

Note that the outputs of pix2vec and ang2vec are slightly different---this is because pix2vec returns a vector pointing toward the centre of the pixel, which is slightly offset from our original coordinates.

Also, notice that functions which depend on the pixelisation scheme must take **nside** as an argument.

Exercise 1: Find the angle between the minimum and maximum values of the Gaussian map we've created.

```
In [12]: vec_max = np.array(hp.pix2vec(nside, map_gauss.argmax()))
    vec_min = np.array(hp.pix2vec(nside, map_gauss.argmin()))
    ang_sep = np.arccos(vec_max.dot(vec_min))
    print("the maximum and minimum points are separated by an angle of {0:.3} r
    adians".format(ang_sep))
```

the maximum and minimum points are separated by an angle of 1.32 radians

Fun with LIGO/Virgo alerts

INDXSCHM = IMPLICIT

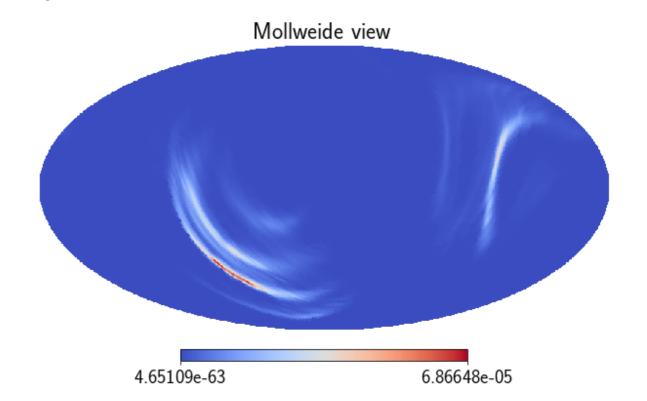
Ordering converted to RING

Now for a fun example with some actual data. Let's download the publicly-available skymap for GW190425, a recent binary neutron star signal detected by LIGO/Virgo. This is just a HEALPix map of the probability distribution of the source's sky location.

The map is stored in a .fits file, which is a special file format often used in astronomy and cosmology for full-sky maps. We can read it into python using the healpy.read_map function, which will automatically determine the correct nside to use.

```
In [13]: #! wget -v https://gracedb.ligo.org/api/superevents/S190425z/files/LALInfer
ence.fits.gz
map_gw = hp.read_map("LALInference.fits.gz")
nside = hp.get_nside(map_gw)
hp.mollview(map_gw, cmap="coolwarm")

NSIDE = 256
ORDERING = NESTED in fits file
```



We can check that the pixel values sum to unity, as they should for a probability distribution.

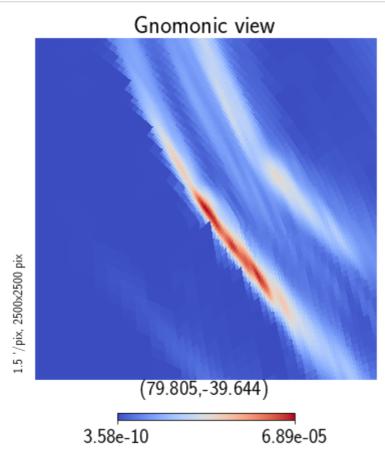
```
In [14]: print np.sum(map_gw)
```

1.00000000000000000

Clearly the probability distribution is peaked in a relatively small area. We might want to zoom in on this area. To do so, we can use a gnomonic projection around a given point, using **healpy.gnomview**.

In the cell below we'll find the angular coordinates of the maximum-probability pixel, and zoom in to a 1000-by-1000 pixel area centred on that point. (Note the use of the "lonlat" argument, which ensures the angular coordinates are in the right format for gnomview.)

```
In [15]: ang_max = hp.pix2ang(nside, map_gw.argmax(), lonlat=True)
hp.gnomview(map_gw, rot=ang_max, xsize=2500, ysize=2500, cmap="coolwarm")
```



Exercise 2: Estimate the size in steradians of the 90% confidence region---i.e. the smallest possible region of the sky which contains 90% of the total probability.

```
In [16]: cum_prob = 0.0
    pixel_count = 0
    map_sort = list(np.sort(map_gw))

while cum_prob < 0.9:
        cum_prob += map_sort.pop()
        pixel_count += 1

pixarea = hp.nside2pixarea(nside)

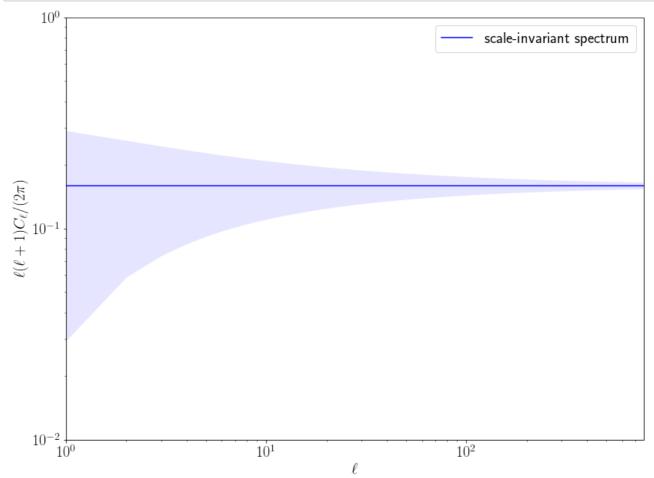
print("the 90% confidence region is roughly {:.3} steradians".format(pixel_count*pixarea))</pre>
```

the 90% confidence region is roughly 2.27 steradians

Spherical harmonics and angular power spectra

Let's start by defining a scale-invariant angular power spectrum. Note that the maximum ℓ we can use is set by the resolution of the maps we'll be working with, and is limited to $\ell_{\max}=3\times \mathtt{nside}-1$.

```
In [17]:
         lmax = 3*nside-1
         ell = np.arange(lmax+1)
         C ell = np.array([np.power((l+1.0)*np.max([l,1.0]),-1.0) for l in ell])
         sigma = np.array([np.sqrt(2.0*np.power(2.0*l+1.0,-1.0)) for l in ell])
         D ell = np.array([0.5*l*(l+1.0)*C ell[l]/np.pi for l in ell])
         D_ell_plus_sigma = np.array([D_ell[l]*(1.0+sigma[l]) for l in ell])
         D_ell_minus_sigma = np.array([D_ell[l]*(1.0-sigma[l]) for l in ell])
         fig = plt.figure()
         fig.set_size_inches(12, 9)
         plt.xlabel(r"$\ell$")
         plt.ylabel(r"$\ell(\ell+1)C_\ell/(2\pi)$")
         plt.loglog(ell, D_ell, "b", label=r"scale-invariant spectrum")
         plt.fill between(ell, D ell plus sigma,
                               D_ell_minus_sigma,
                               where=D_ell_plus_sigma>=D_ell_minus_sigma,
                               facecolor="b", alpha=0.1)
         plt.xlim(1, lmax)
         plt.ylim(0.01, 1.0)
         plt.legend(loc=0)
         fig.tight layout()
```

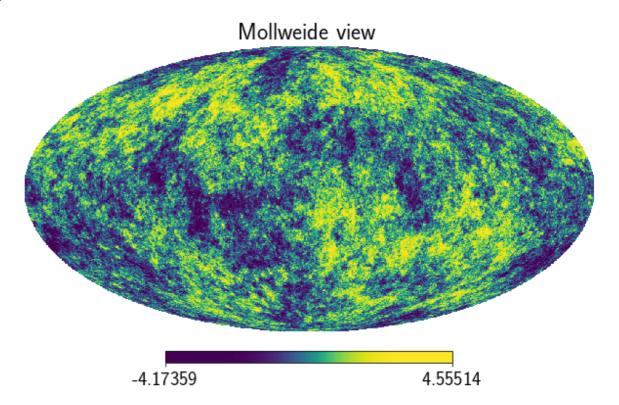


One of the most common things you'll want to do with **healpy** is to generate a map from a given spectrum. This is done using the function **healpy.synfast** (where the "syn" stands for "synthesise").

What we are doing here is effectively drawing each $a_{\ell m}$ from a Gaussian distribution with variance C_{ℓ} . Since this is a random process, notice that rerunning this cell leads to a different map each time.

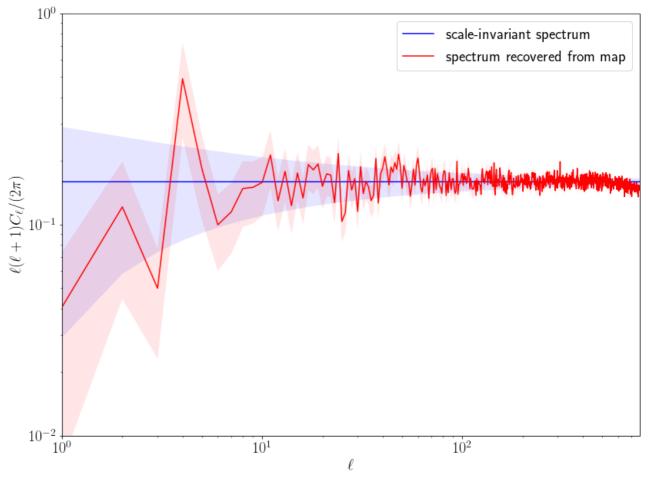
```
In [18]: map_scale_inv = hp.synfast(C_ell, nside, new=True, verbose=False)
    fig = plt.figure()
    fig.set_size_inches(16, 9)
    hp.mollview(map_scale_inv, norm="hist")
```

<Figure size 1152x648 with 0 Axes>



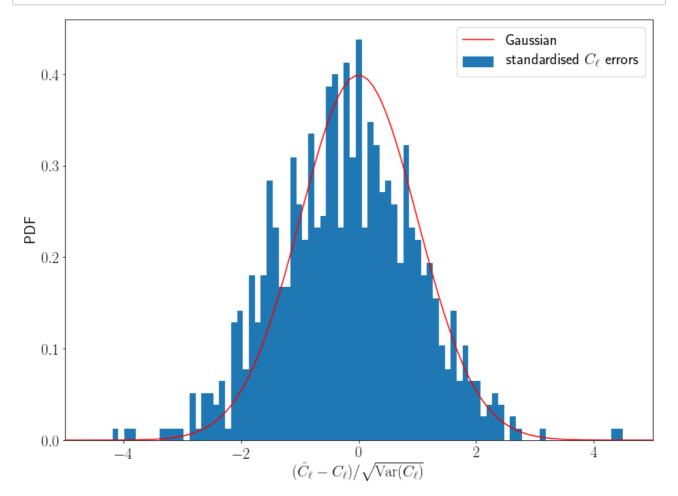
We'll also often want to do the reverse process: analyse a given map to find its spectrum. We do this with healpy.anafast.

```
In [19]: C ell ana = hp.anafast(map scale inv)
         D ell ana = np.array([0.5*l*(l+1.0)*C ell ana[l]/np.pi for l in ell])
         D_ell_ana_plus_sigma = np.array([D_ell_ana[l]*(1.0+sigma[l]) for l in ell
         D_{ell\_ana\_minus\_sigma} = np.array([D_{ell\_ana[l]}*(1.0-sigma[l])) for l in ell
         fig = plt.figure()
         fig.set size inches(12, 9)
         plt.xlabel(r"$\ell$")
         plt.ylabel(r"\$\ell(\ell+1)C_\ell/(2\pi)\$")
         plt.loglog(ell, D_ell, "b", label=r"scale-invariant spectrum")
         plt.fill between(ell, D ell plus sigma,
                                D ell minus sigma,
                                where=D_ell_plus_sigma>=D_ell_minus sigma,
                                facecolor="b", alpha=0.1)
         plt.loglog(ell, D_ell_ana, "r", label=r"spectrum recovered from map")
         plt.fill_between(ell, D_ell_ana_plus_sigma,
                                D_ell_ana_minus_sigma,
                                where=D ell ana plus sigma>=D ell ana minus sigma,
                                facecolor="r", alpha=0.1)
         plt.xlim(1, lmax)
         plt.ylim(0.01, 1.0)
         plt.legend(loc=0)
         fig.tight layout()
```



Notice that the recovered spectrum is *not* the same as the one we injected, due to cosmic variance. We should expect the points on the red line to be randomly distributed around the points on the blue line, with variance equal to $2C_\ell^2/(2\ell+1)$. Let's check this by creating a histogram.

```
In [20]:
         std_errors = np.array([(C_ell_ana[l]-C_ell[l])/(C_ell[l]*sigma[l]) for l in
         ell])
         bins = np.linspace(-5.0, +5.0, num=100)
         gaussian = np.array([np.power(2.0*np.pi, -0.5)*np.exp(-0.5*bins[x]**2.0)) for
         x in xrange(100)])
         fig = plt.figure()
         fig.set size inches(12, 9)
         plt.xlabel(r"$(\hat{C} \ell-C \ell)/\sqrt{\mathrm{Var}(C \ell)}$")
         plt.ylabel("PDF")
         n, bins, patches = plt.hist(std_errors, bins=bins, density=True, label=r"st
         andardised $C_\ell$ errors")
         plt.plot(bins, gaussian, "r", label="Gaussian")
         plt.xlim(-5.0, +5.0)
         plt.legend(loc=0)
         fig.tight_layout()
```

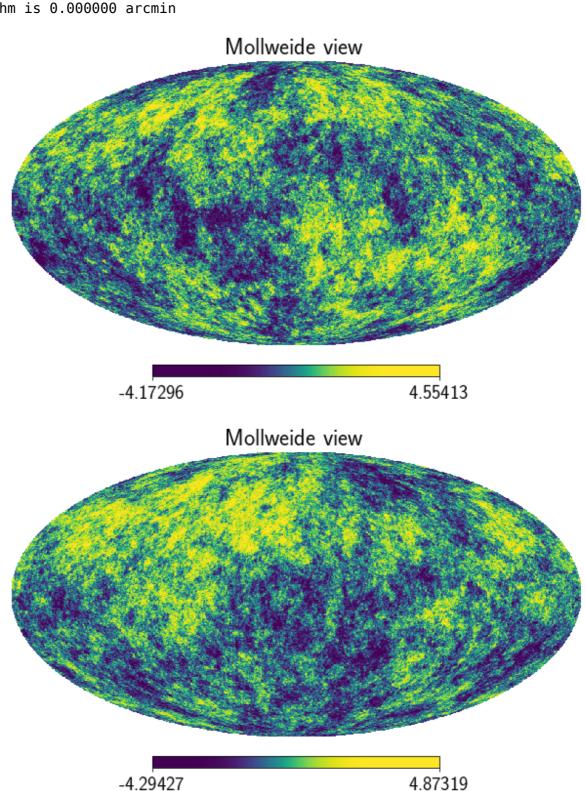


We may also want to work in terms of the $a_{\ell m}$'s. There are two ways to do this: either use **healpy.map2alm** to calculate the $a_{\ell m}$'s of a given map, or use **healpy.synalm** to randomly generate a set of $a_{\ell m}$'s from a given spectrum. The conversion from $a_{\ell m}$'s back to a map or a spectrum are achieved with **healpy.alm2map** and **healpy.alm2cl** respectively.

```
In [21]: alm_map = hp.map2alm(map_scale_inv)
alm_syn = hp.synalm(C_ell, new=True)

hp.mollview(hp.alm2map(alm_map, nside), norm="hist")
hp.mollview(hp.alm2map(alm_syn, nside), norm="hist")
```

Sigma is 0.000000 arcmin (0.000000 rad)
-> fwhm is 0.000000 arcmin
Sigma is 0.000000 arcmin (0.000000 rad)
-> fwhm is 0.000000 arcmin



Both alm_map and alm_syn in the previous cell are numpy arrays, with each element corresponding to a particular (ℓ, m) . However, the order that healpy puts these in within the array is pretty counter-intuitive, which can be annoying when you want to access a particular $a_{\ell m}$ from the array.

Luckily, healpy provides a couple of functions for this: healpy.Alm.getidx tells you the index in the array of a particular (ℓ, m) , while healpy.Alm.getlm does the converse. Both require ℓ_{\max} as an argument, as this determines the order in which the $a_{\ell m}$'s are stored. You can find out the ℓ_{\max} of a given array using healpy.Alm.getlmax.

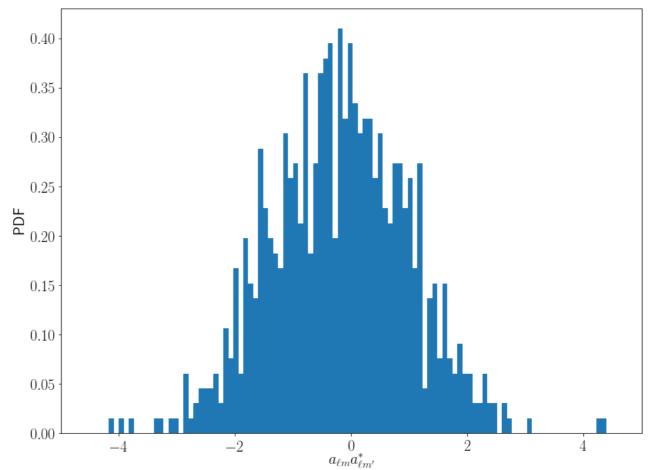
```
In [22]: lmax = hp.Alm.getlmax(len(alm_syn))
    idx = hp.Alm.getidx(lmax, 100, 50)
    (l, m) = hp.Alm.getlm(lmax, 120839)

print("we have l_max={}".format(lmax))
print("the l=100, m=50 mode is stored at index={}".format(idx))
print("index 120839 contains the l={0}, m={1} mode".format(l, m))

we have l_max=767
    the l=100, m=50 mode is stored at index=37225
    index 120839 contains the l=656, m=177 mode
```

Exercise 3: For $\ell=1500$, confirm that different m-modes are uncorrelated; i.e. check that for $m\neq m'$ the product $a_{\ell m}a_{\ell m'}^*$ is distributed around zero.

```
In [23]:
         ell = 1500
         asq = []
         for m1 in range(ell+1):
             for m2 in range(m1):
                  idx1 = hp.Alm.getidx(lmax, l, m1)
                 idx2 = hp.Alm.getidx(lmax, l, m2)
                 alm1 = alm syn[idx1]
                 alm2 = alm_syn[idx2]
                 asq.append(alm1*alm2.conj())
         fig = plt.figure()
         fig.set_size_inches(12, 9)
         plt.xlabel(r"$a {\ell m}a^* {\ell m'}$")
         plt.ylabel("PDF")
         plt.hist(std errors, bins=100, density=True)
         plt.xlim(-5.0, +5.0)
         fig.tight_layout()
```



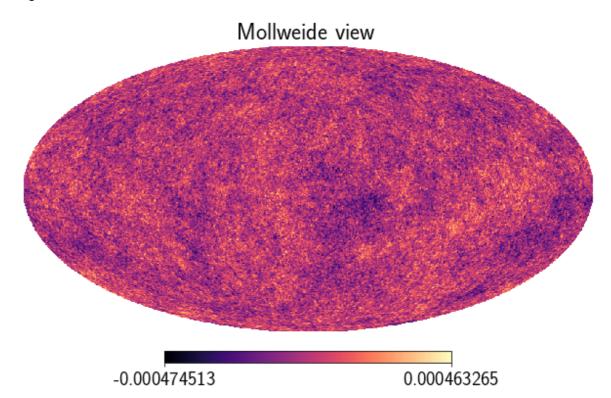
The real deal: Planck CMB maps

Let's download one of the Planck temperature maps and compute its spectrum. This map has a very high resolution (${\tt nside}=2^{11}$), so this may take a little while.

NSIDE = 2048
ORDERING = NESTED in fits file
INDXSCHM = IMPLICIT

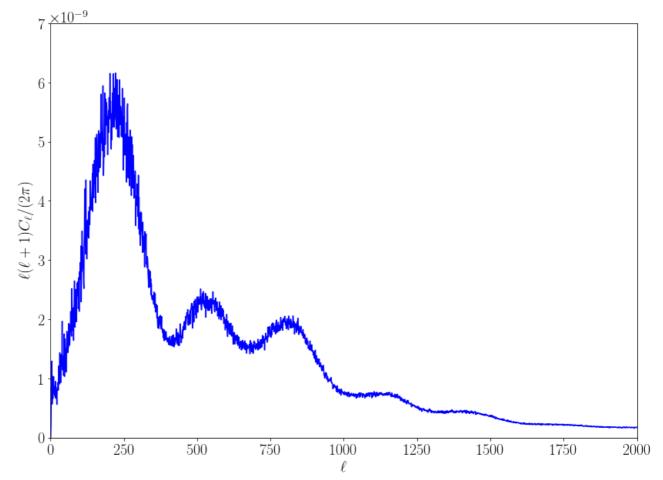
/home/alex/.local/lib/python2.7/site-packages/healpy/fitsfunc.py:372: UserWa
rning: No INDXSCHM keyword in header file : assume IMPLICIT
 warnings.warn("No INDXSCHM keyword in header file : " "assume {}".format(s
chm))

Ordering converted to RING



```
In [25]: C_ell = hp.anafast(map_cmb, lmax=2000)
    ell = np.arange(len(C_ell))
    D_ell = np.array([0.5*l*(l+1.0)*C_ell[l]/np.pi for l in ell])

fig = plt.figure()
    fig.set_size_inches(12, 9)
    plt.xlabel(r"$\ell$")
    plt.ylabel(r"$\ell(\ell+1)C_\ell/(2\pi)$")
    plt.plot(ell, D_ell, "b")
    plt.xlim(0, 2000)
    plt.ylim(0.0, 7.0e-9)
    fig.tight_layout()
```

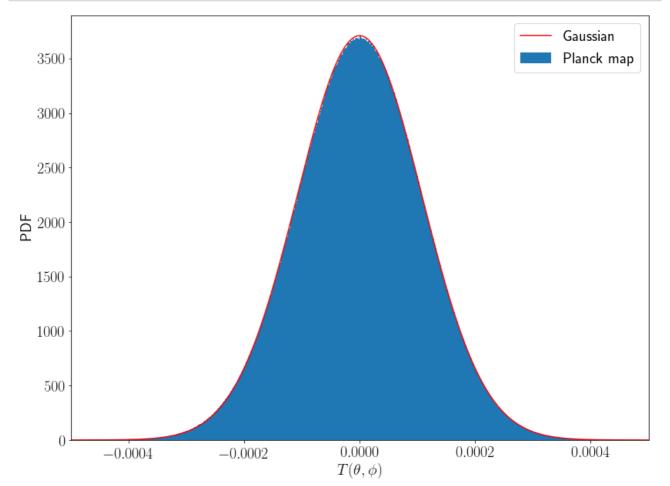


Exercise 4: Plot a histogram of the pixel values to check that the CMB is Gaussian-distributed with zero mean and variance equal to $\sum_\ell (2\ell+1)C_\ell/(4\pi)$.

```
In [26]: var = np.sum([0.25*(2.0*l+1.0)*C_ell[l]/np.pi for l in ell])

bins = np.linspace(-5.0e-4, +5.0e-4, num=1000)
gaussian = np.array([np.power(2.0*np.pi*var,-0.5)*np.exp(-0.5*bins[x]**2.0/var) for x in xrange(1000)])

fig = plt.figure()
fig.set_size_inches(12, 9)
plt.xlabel(r"$T(\theta,\phi)$")
plt.ylabel("PDF")
n, bins, patches = plt.hist(map_cmb, bins=bins, density=True, label="Planck map")
plt.plot(bins, gaussian, "r", label="Gaussian")
plt.xlim(-5.0e-4, +5.0e-4)
plt.legend(loc=0)
fig.tight_layout()
```



Exercise 5: Let's modify the Planck spectrum, and see how it changes the map. Add a new peak centred on $\ell=500$, with a Gaussian profile with variance $\sigma_\ell=500$, and height 1×10^{-13} .

