Tools for data analyses in Cosmology

- Aula 10 -

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Healpy

Previously on healpy class ... Map \Rightarrow C_{ℓ} [anafast] $C_{\ell} \Rightarrow \text{fits file [write_cl]}$ fits file \Rightarrow C_{ℓ} [read_cl]

$$\ell_{max} = 3 \times N_{side} - 1$$
 e.g.: $N_{side} = 1024 \Rightarrow \ell_{max} = 3071$

healpy.sphtfunc.synfast

healpy.sphtfunc.synfast(cls, nside, lmax=None, mmax=None, alm=False, pol=True, pixwin=False, fwhm=0.0, sigma=None, new=False, verbose=True)

Create a map(s) from cl(s).

$$C_{\ell} \quad \Rightarrow \quad exttt{Map}$$

How to use:

```
In [134]: mapa1 = hp.synfast(Cls,1024, alm=False, pol=False, pixwin=False, fwhm=np.deg2rad(0.))
/home/camila/anaconda3_4p3p1/lib/python3.6/site-packages/healpy/sphtfunc.py:296:
FutureChangeWarning: The order of the input cl's will change in a future release.
Use new=True keyword to start using the new order.
See documentation of healpy.synalm.
    category=FutureChangeWarning)
Sigma is 0.000000 arcmin (0.000000 rad)
-> fwhm is 0.000000 arcmin
```

In [135]: len(mapa1) Out[135]: 12582912

Out[138]: (12582912, 3148795)

How to use:

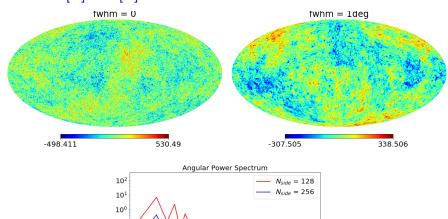
```
In [134]: mapa1 = hp.synfast(Cls.1024, alm=False, pol=False, pixwin=False.
fwhm=np.deg2rad(0.))
/home/camila/anaconda3_4p3p1/lib/python3.6/site-packages/healpy/sphtfunc.py:296:
FutureChangeWarning: The order of the input cl's will change in a future release.
Use new=True keyword to start using the new order.
See documentation of healpy.synalm.
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Sigma is 0.000000 arcmin (0.000000 rad)
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In [135]: len(mapa1)
Out[135]: 12582912
In [136]: mapa1 = hp.synfast(Cls.1024, alm=True, pol=False, pixwin=False,
fwhm=np.deg2rad(0.))
/home/camila/anaconda3 4p3p1/lib/pvthon3.6/site-packages/healpv/sphtfunc.pv:296:
FutureChangeWarning: The order of the input cl's will change in a future release.
Use new=True keyword to start using the new order.
See documentation of healpy.synalm.
  category=FutureChangeWarning)
Sigma is 0.000000 arcmin (0.000000 rad)
-> fwhm is 0 000000 accmin
In [137]: len(mapa1)
Out[137]: 2
In [138]: len(mapa1[0]), len(mapa1[1])
```

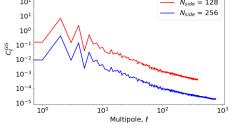
Exercise:

Why???

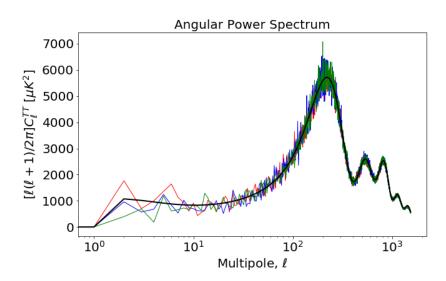
- 1. Generate two CMB maps ($N_{\text{side}} = 512$), with and without smoothing it (fwhm = 0.25 deg). Visualize them and observe their difference.
- 2. Calculate the angular power spectrum from each one. Are they different? Why???
- 3. Generate 3 CMB maps ($N_{\rm side} = 512$) and calculate their angular power spectra. Plot them. Are they different? Are they different from the seed C_ℓ 's?

Spherical harmonic transforms Result: [1.] and [2.]





Result: [3.]



healpy.sphtfunc.map2alm

healpy.sphtfunc.map2alm(maps, Imax=None, mmax=None, iter=3, pol=True, use_weights=False, datapath=None)

Computes the alm of an Healpix map.

Map
$$\Rightarrow$$
 $a_{\ell m}$

In [37]: mapa = hp.synfast(Cls,512, alm=True)

How to use:

...: mapa1 = mapa[0]

```
...: alm1 = mapa[1]
...:
...: alm2 = hp.map2alm(mapa1)
...:
/home/camila/anaconda3_4p3p1/lib/python3.6/site-packages/healpy/sphtfunc.py:296:
FutureChangeWarning: The order of the input cl's will change in a future release
Use new=True keyword to start using the new order.
See documentation of healpy.synalm.
category=FutureChangeWarning)
```

```
Category=Futurechangewarning)
Sigma is 0.000000 arcmin (0.000000 rad)
-> fwhm is 0.000000 arcmin
In [38]: alm1
```

healpy.sphtfunc.alm2map

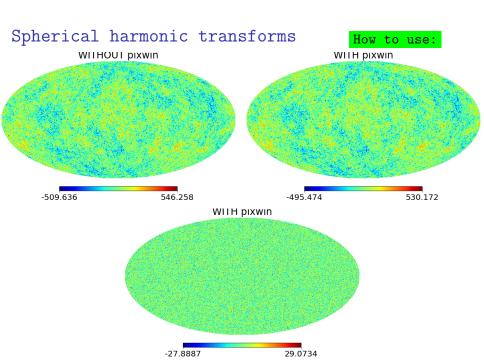
healpy.sphtfunc.alm2map(alms, nside, Imax=None, mmax=None, pixwin=False, fwhm=0.0, sigma=None, pol=True, inplace=False, verbose=True)

Computes an Healpix map given the alm.

$$a_{\ell m} \Rightarrow \operatorname{Map} \hookrightarrow \operatorname{complex\ array}$$

How to use:

Python x IDL: the "seed"!



healpy.sphtfunc.alm2map_der1

healpy.sphtfunc.alm2map_der1(alm, nside, lmax=None, mmax=None)

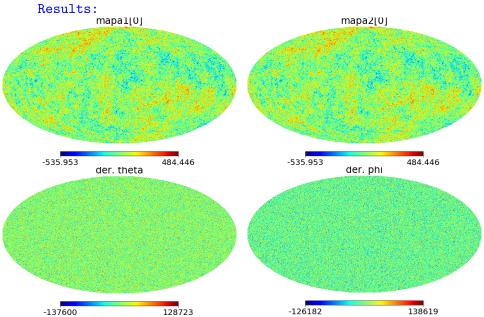
Computes an Healpix map and its first derivatives given the alm.

 \searrow Less parameters.

 $a_{\ell m} \Rightarrow \text{Map} + \text{its 1st derivatives}$

Exercise:

- 1. From the Planck best-fit C_ℓ 's, generate a map and the corresponding $a_{\ell m}$.
- 2. Use this $a_{\ell m}$ set to generate back the CMB map, besides its first derivatives.
- 3. Compare the CMB maps from [1.] and [2.] and visualize the derivatives.



healpy.fitsfunc.write_alm

 $\textbf{healpy.fitsfunc.write_alm} (\textit{filename}, \textit{alms}, \textit{out_dtype=None}, \textit{lmax=-1}, \textit{mmax=-1}, \textit{mmax_in=-1}) \text{ } \% \\$

Write alms to a fits file.

healpy.fitsfunc.read_alm

healpy.fitsfunc.read_alm(filename, hdu=1, return_mmax=False)

Read alm from a fits file.

Exercise:

- 1. Generate the $a_{\ell m}$ from a map (you already have it) and write it to a fits file.
- 2. Read the fits file you just save to verify if it was correctly written.

Obs.:

```
In [59]: alms1
Out[59]:
array([ 0.0000000+0.j , 0.00000000+0.j , -24.37779492+0.j , ..., 0.05781267+0.00217739j,
        -0.04033944-0.03193015j, -0.03127322-0.00663547j])
In [59]:
In [60]: alms2
Out[60]:
(array([ 0.00000000+0.j , 0.00000000+0.j
      -24.37779492+0.j , ..., 0.05781267+0.00217739j,
        -0.04033944-0.03193015j, -0.03127322-0.00663547j]),
1535) <---
```