HEALPix Demonstration file
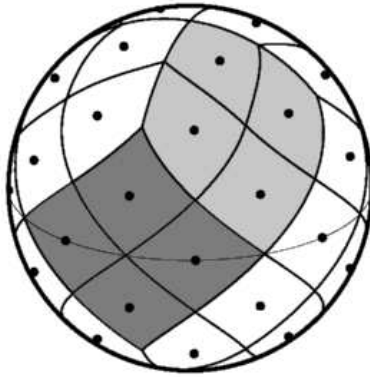
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Abstract: Test document

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Synneed

Location in HEALPix directory tree: src/f90/NeedATool/synneed_dr.f90

It computes the needlet coefficients of a given temperature map in the **HEALPix** format.

synneed is directly adapted from the NEEDATOOL code described in Pietrobon et al, SApJ, , (2010).

The scaling is dominated by the spherical harmonic decomposition as implemented in alm2map and map2alm_iterative. Needlet specifics and mask can be selected by the user.

FORMAT

% synneed [parameter_file]

QUALIFIERS

healpix_dir =	Defines the path of the **HEALPix** software package.
mapfile =	Defines the input scalar field defined on a pixelized sphere, (default= HEALPIX/test/temp_map.fits).
mapnside =	Defines the resolution of the input map, (default= 256).
l_max =	Defines the maximum ℓ value at which the needlet analysis is carried out. (default= 500)
B =	Defines the shape in harmonic domain of the filter function $b(\cdot)$. (default= 2.)
compute_needlets =	Sets the needlet coefficients computation. If "F" only filter functions b_ℓ^2 are computed (default= T)
maskfile =	Defines the FITS file describing the sky cut applied to the input temperature map. (default='')
bl2_root =	Defines the tag attached to the file where filters are saved. (default= test_bl2)
need_root =	Defines the tag attached to the file where needlet coefficients are saved. (default= test_needlet_coefficients)
nside_boost =	Necessary to determine the needlet coefficient resolution according to $\ell \leq$ nside_boost $* N_{\mathrm{side}}$. (default= 2)

DESCRIPTION

Needlet filters in harmonic domain are computed according to the procedure described in Pietrobon et al. SApJ , , (2010). These functions are defined in the interval $x \in [1/B, B]$, where $x \equiv \ell/B^j$ with j integer number which defines the needlet scale. The parameter B (must be greater than 1.) is chosen by the user according to the properties of the field analyzed. B, that must get values larger than one, can be varied by the user according to the scale analysis of interest. Needlet coefficients are univocally specified by the resolution j and the their positions are defined in the **HEALPix** pixelization scheme. The resolution of the needlet coefficients is set by the code by means of the function `set_nside`. For each resolution j the coefficients are stored in a **HEALPix** map format.

DATASETS

The following datasets are involved in the **Synneed** processing.

Dataset	Description
/data/pixel_window_nxxxx.fits	Files containing pixel windows for various nsmax.

SUPPORT

This section lists those routines and facilities (including those *external* to the HEALPix distribution) which can assist in the utilisation of **Synneed**.

read_fits_map	This **HEALPix** IDL facility can be used to read the output needlet coefficients.
synfast	This **HEALPix** Fortran facility can create a **HEALPix** map suitable to be decomposed onto needlet frame.
ananeed	This **HEALPix** Fortran facility can reconstruct a **HEALPix** map given needlet coefficients.

EXAMPLES: #1

synneed

`synneed` runs in interactive mode, self-explanatory.

EXAMPLES: #2

`synneed filename`

> When 'filename' is present, `synneed` enters the non-interactive mode and parses its inputs from the file 'filename'. This has the following structure: the first entry is a qualifier which announces to the parser which input immediately follows. If this input is omitted in the input file, the parser assumes the default value. If the equality sign is omitted, then the parser ignores the entry. In this way comments may also be included in the file. In this example, the file contains the following qualifiers:
>
> `healpix_dir = /usr/local/Healpix_2.14/`
> `l_max = 500`
> `B = 2.0`
> `compute_needlets = T`
> `mapfile = temp_map.fits`
> `mapnside = 256`
> `bl2_root = test_bl2`
> `need_root = test_needlet_coefficients`
> `nside_boost = 2`
>
> `synneed` reads in the map in 'temp_map.fits', and produces the needlet filter functions 'test_bl2_B2.00_Nj008_j.dat', where $j = 1, \ldots, j_{max}$, and coefficients 'test_needlet_coefficients_B2.00_Nj008.fits'. Needlet coefficients are j_{max} maps in the **HEALPix** format.

RELEASE NOTES

Revision 1: Initial release (**HEALPix** 2.15)

Ananeed

Location in HEALPix directory tree: src/f90/NeedATool/ananeed_dr.f90

It reads in the needlet coefficients of a given scalar field and reconstructs the original map in the **HEALPix** format.

ananeed is directly adapted from the NEEDATOOL code described in Pietrobon et al, SApJ, , (2010).

The scaling is dominated by the spherical harmonic decomposition as implemented in alm2map and map2alm_iterative. The needlet coefficients and specifics and mask can be selected by the user.

FORMAT
% ananeed [parameter_file]

QUALIFIERS

healpix_dir =	Defines the path of the **HEALPix** software package.
mapfile =	Defines the input needlet coefficients defined on a pixelized sphere, (default= HEALPIX/test/temp_needlet_coefficients.fits).
mapnside =	Defines the resolution of the input needlet coefficinets, (default= 256).
l_max =	Defines the maximum ℓ value at which the needlet analysis is carried out. (default= 500)
B =	Defines the shape in harmonic domain of the filter function $b(\cdot)$. (default= 2.)
need_maskfile =	Defines the FITS file describing the sky cut applied to the input needlet coefficients. (default='')
need_root =	Defines the tag attached to the file where recovered map is saved. (default= test_recmap)
nside_boost =	Necessary to determine the needlet coefficient resolution according to $\ell \leq$ nside_boost $* N_{\text{side}}$. (default= 2)

DESCRIPTION

Needlet coefficients are read in and needlet filters in harmonic domain are computed according to the procedure described in Pietrobon et al. SApJ , , (2010). These functions are defined in the interval $x \in [1/B, B]$, where $x \equiv \ell/B^j$ with j integer number which defines the needlet scale. The parameter B (must be greater than 1.) is chosen by the user according to the properties of the field analyzed. The value of B must match the value used to create needlet coefficients. Needlet filters are necessary to properly sum up the needlet coefficients and reconstruct the input map.

DATASETS

The following datasets are involved in the **Ananeed** processing.

Dataset	Description
/data/pixel_window_nxxxx.fits	Files containing pixel windows for various nsmax.

SUPPORT

This section lists those routines and facilities (including those *external* to the HEALPix distribution) which can assist in the utilisation of **Ananeed**.

read_fits_map	This **HEALPix** IDL facility can be used to read the output recovered map as well as the input needlet coefficients.
anafast	This **HEALPix** Fortran facility analyzes a **HEALPix** map.
synneed	This **HEALPix** Fortran facility decomposed a **HEALPix** map onto needlet frame.

EXAMPLES: #1

```
ananeed
```

ananeed runs in interactive mode, self-explanatory.

EXAMPLES: #2

`ananeed filename`

When 'filename' is present, `ananeed` enters the non-interactive mode and parses its inputs from the file 'filename'. This has the following structure: the first entry is a qualifier which announces to the parser which input immediately follows. If this input is omitted in the input file, the parser assumes the default value. If the equality sign is omitted, then the parser ignores the entry. In this way comments may also be included in the file. In this example, the file contains the following qualifiers:

`healpix_dir = /usr/local/Healpix_2.14/`
`l_max = 500`
`B = 2.0`
`mapfile = temp_needlet_coefficients.fits`
`mapnside = 256`
`need_maskfile = ''`
`need_root = test_recmap`
`nside_boost = 2`

`ananeed` reads in the needlet coefficients in 'temp_needlets.fits', and reconstructs the original scalar field map.

RELEASE NOTES

Revision 1: Initial release (**HEALPix** 2.15)

bj_of_l*

Location in HEALPix directory tree: src/f90/mod/needlets_mod.f90

This function computes the needlet filters in harmonic domain. Filters span the interval $x \in [1/B, B]$ where $x = \ell/B^j$, for $j = 1, \ldots, j_{max}$. j_{max} is set according to ℓ_{max} and B by the subroutine `set_needlet_environment`.

EXAMPLE:

```
use needlet_variables
use needlets_mod, only:  bj_of_l, set_needlet_environment, set_input
...
call set_input
call set_needlet_environment
call bj_of_l
```

Outputs in `bl2` the squared of the needlet filter in harmonic space normalized to 1

MODULES & ROUTINES

This section lists the modules and routines used by **bj_of_l***.

needlet_variables module which loads the basic needlet variable required by the package.

RELATED ROUTINES

This section lists the routines related to **bj_of_l***.

set_input   ask the user for the needlet variables
set_needlet_environment   set the needlet variables

build_needlet

Location in HEALPix directory tree: src/f90/mod/needlets_mod.f90

This subroutine returns the needlet coefficients for a given needlet scale. The $a_{\ell m}$ of the map are required as input. Needlet variable need to be initialized before.

FORMAT   call build_needlet(j, alms, nlmax, nmmax, need_nside, needlet)

ARGUMENTS

name & dimensionality	kind	in/out	description
j	I4B	IN	The needlet scale which determines the range f multipoles ($\ell \in [B^{j-1}, B^{j+1}]$).
alms(1:nmap, 0:nlmax, 0:nmmax)	DPC	IN	$a_{\ell m}$ of the map to be decomposed.
nmap	I4B	IN	number of maps in the $a_{\ell m}$ array.
nlmax	I4B	IN	The maximum ℓ value for the analysis.
nmmax	I4B	IN	The maximum m value for the analysis.
need_side	I4B	IN	The N_{side} value of the needlet coefficients.
needlet(0:)	DP	OUT	Needlet coefficients.

EXAMPLE:

```
use needlets_mod
integer(i4b) ::  j, nlmax, nmmax, nside
complex(dp), dimension(1:p,0:nlmax, 0:nmmax)
real(dp), dimension(:), allocatable ::  needlet
call set_input
call set_needlet_environment
```

```
nlmax = lmax
nmmax = nlmax
p = 1
nside = 256
npix = 12*nside**2
allocate( needlet(0:npix-1) )
call build_needlet(j,alms, nlmax, nmmax, nside, needlet)
```

This computes needlet coefficients for the chosen scale j given the $a_{\ell m}$ of the map.

MODULES & ROUTINES
This section lists the modules and routines used by **build_needlet**.

alm_tools	module, containing:
alm2map	which build a **HEALPix** map given a set of spherical harmonic coefficients.

RELATED ROUTINES
This section lists the routines related to **build_needlet**.

set_input	asks for input needlet parameters.
set_needlet_environment	initializes the needlet variables.
parsing_hpx	asks for global needlet parameters.

set_input

Location in HEALPix directory tree: src/f90/mod/needlets_mod.f90

This subroutine asks for the necessary input needlet parameters [lmax, B, nside_boost]. `lmax` sets the maximum multipole value at which the analysis is performed. `B` is the fundamental needlet parameter which defines the multipole range for each needlet scale j. `nside_boost`$\in [1, 4]$ is used to set the resolution of the needlet coefficients N_{side} given ℓ, according to the relation $\ell_{\max} \leq$ `nside_boost` $* N_{\mathrm{side}}$.

FORMAT

call set_input()

ARGUMENTS

No arguments required.

EXAMPLE:

```
use needlets_mod

call set_input
call set_needlet_environment
```
⋮

This sets needlet variables and initializes arrays.

RELATED ROUTINES

This section lists the routines related to **set_input**.

set_input	asks for input needlet parameters.
set_needlet_environment	initializes the needlet variables.
parsing_hpx	asks for global needlet parameters.

set_needlet_environment

Location in HEALPix directory tree: src/f90/mod/needlets_mod.f90

This subroutine initializes needlet variables and arrays given the input needlet parameters [lmax, B, nside_boost]. It calls `bj_of_l` which computes the needlet filters and provides information on the needlet sets generated.

FORMAT

call set_needlet_environment(voice)

ARGUMENTS

name & dimensionality	kind	in/out	description
voice OPTIONAL	LGT	INOUT	If .true. displays ℓ range for each j and other information.

EXAMPLE:

```
use needlets_mod
logical ::  voice = .true.
call set_input
call set_needlet_environment(voice)
⋮
```

This sets needlet variables and initializes arrays.

RELATED ROUTINES

This section lists the routines related to **set_needlet_environment**.

set_input	asks for input needlet parameters.
bj_of_l	computes needlet filters in harmonic domain.
write_bl2_l	writes into formatted files the needlet filters $b^2(\ell/B^j)$.

write_bl2

Location in HEALPix directory tree: src/f90/mod/needlets_mod.f90
> This subroutine writes into formatted files the needlet filters defined in harmonic domain.

FORMAT

> call write_bl2(in_root)

ARGUMENTS

name & dimensionality	kind	in/out	description
in_root	CHR(len=filenamelen)	IN	The prefix of the output files.

EXAMPLE:

```
use needlets_mod
character(len=filenamelen) ::  in_root

in_root = 'bl2'
call set_input
call set_needlet_environment(voice)
call write_bl2(in_root)
```

> After setting needlet variables and computing the filters $b^2(\ell/B^j)$ (wrapped in `set_needlet_environment`), this writes them into formatted files 'in_root_B2.00_Nj009_j.dat', where j runs from 1 to j_{max} and 2. 00 and 009 are defined internally by the code according to the B parameter set by the user and the number of resolutions required.

RELATED ROUTINES

This section lists the routines related to **write_bl2**.

> set_input   asks for input needlet parameters.

bj_of_l	computes needlet filters in harmonic domain.
set_needlet_environment	initializes the needlet variables.