Source Detection with *Duchamp* v1.0
A User's Guide

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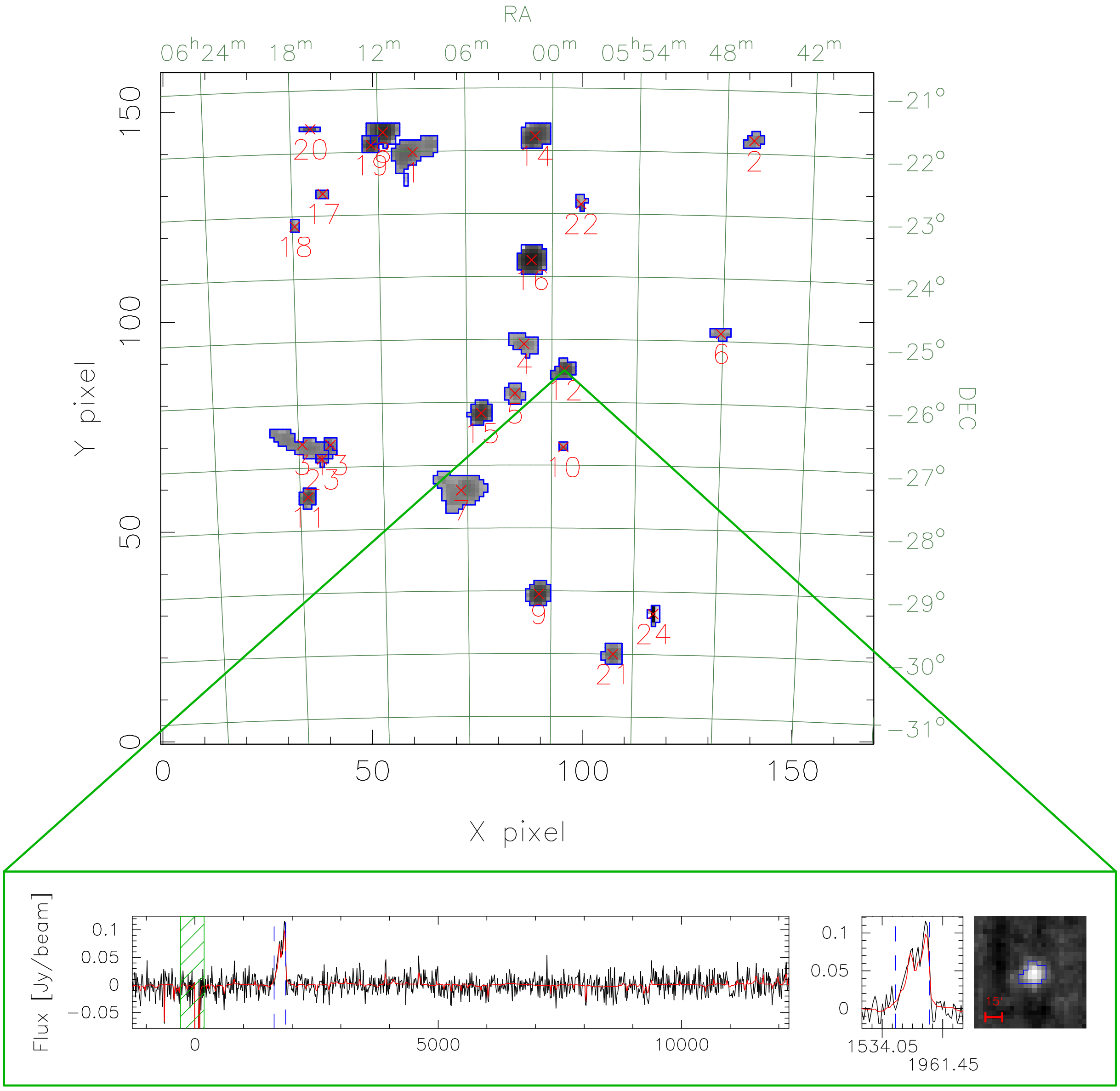

Contents

1 Introduction and getting going quickly

This document provides a user's guide to *Duchamp*, an object-finder for use on spectral-line data cubes. The basic execution of *Duchamp* is to read in a FITS data cube, find sources in the cube, and produce a text file of positions, velocities and fluxes of the detections, as well as a postscript file of the spectra of each detection.

So, you have a FITS cube, and you want to find the sources in it. What do you do? The first step is to make an input file that contains the list of parameters. Brief and detailed examples are shown in Appendix C. This file provides the input file name, the various output files, and defines various parameters that control the execution.

The standard way to run *Duchamp* is by the command

```
Duchamp -p [parameter file]
```

replacing `[parameter file]` with the name of the file listing the parameters. Alternatively, you can use the syntax

```
Duchamp -f [FITS file]
```

where `[FITS file]` is the file you wish to search. In the latter case, all parameters will take their default values detailed in Appendix B. In either case, the program will then work away and give you the list of detections and their spectra. The program execution is summarised below, and detailed in §3. Information on inputs is in §2 and Appendix B, and descriptions of the output is in §4.

1.1 A summary of the execution steps

The basic flow of the program is summarised here – all steps are discussed in more detail in the following sections.

1. If the `-p` option is used, the parameter file given on the command line is read in, and the parameters absorbed.
2. The FITS image is located and read in to memory.
3. If requested, a FITS image with a previously reconstructed array is read in.
4. If requested, blank pixels are trimmed from the edges, and the baseline of each spectrum is removed.
5. If the reconstruction method is requested, and the reconstructed array has not been read in at Step 3 above, the cube is reconstructed using the *à trous* wavelet method.
6. Searching for objects then takes place, using the requested thresholding method.
7. The list of objects is condensed by merging neighbouring objects and removing those deemed unacceptable.
8. The baselines and trimmed pixels are replaced prior to output.
9. The details of the detections are written to screen and to the requested output file.
10. Maps showing the spatial location of the detections are written.

11. The integrated spectra of each detection are written to a postscript file.

12. If requested, the reconstructed array can be written to a new FITS file.

1.2 Guide to terminology

First, a brief note on the use of terminology in this guide. *Duchamp* is designed to work on FITS "cubes". These are FITS[1] image arrays with three dimensions – they are assumed to have the following form: the first two dimensions (referred to as x and y) are spatial directions (that is, relating to the position on the sky), while the third dimension, z, is the spectral direction, which can correspond to frequency, wavelength, or velocity. The three dimensional analogue of pixels are "voxels", or volume cells – a voxel is defined by a unique (x, y, z) location and has a unique flux or intensity value associated with it.

Each spatial pixel (a given (x, y) coordinate) can be said to be a single spectrum, while a slice through the cube perpendicular to the spectral direction at a given z-value is a single channel (the 2-D image is a channel map).

Detection involves locating a contiguous group of voxels with fluxes above a certain threshold. *Duchamp* makes no assumptions as to the size or shape of the detected features, other than having user-selected minimum size criteria.

Features that are detected are assumed to be positive. The user can choose to search for negative features by setting an input parameter – this inverts the cube prior to the search (see §3.5 for details).

Note that it is possible to run *Duchamp* on a two-dimensional image (i.e. one with no frequency or velocity information), or indeed a one-dimensional array, and many of the features of the program will work fine. The focus, however, is on object detection in three dimensions.

1.3 Why *Duchamp*?

Well, it's important for a program to have a name, and the initial working title of *cubefind* was somewhat uninspiring. I wanted to avoid the classic astronomical approach of designing a cute acronym, and since it is designed to work on cubes, I looked at naming it after a cubist. *Picasso*, sadly, was already taken (Minchin 1999), so I settled on naming it after Marcel Duchamp, another cubist, but also one of the first artists to work with "found objects".

2 User Inputs

Input to the program is provided by means of a parameter file. Parameters are listed in the file, followed by the value that should be assigned to them. The syntax used is `paramName value`. Parameter names are not case-sensitive, and lines in the input file that start with `#` are ignored. If a parameter is listed more than once, the latter value is used, but otherwise the order in which the parameters are listed in the input file is arbitrary.

If a parameter is not listed, the default value is assumed. The defaults are chosen to provide a good result (using the reconstruction method), so the user doesn't need to

[1] FITS is the Flexible Image Transport System – see Hanisch et al. (2001) or websites such as http://fits.cv.nrao.edu/FITS.html for details.

specify many new parameters in the input file. Note that the image file **must** be specified! The parameters that can be set are listed in Appendix B, with their default values in parentheses.

The parameters with names starting with `flag` are stored as `bool` variables, and so are either `true = 1` or `false = 0`. *Duchamp* will only read them from the file as integers, and so they should be entered in the file as 0 or 1 (see example file in Appendix C).

3 What *Duchamp* is doing

The execution flow of *Duchamp* is detailed here, indicating the main algorithmic steps that are used. The program is written in C/C++ and makes use of the CFITSIO, WCSLIB and PGPLOT libraries.

3.1 Image input

The cube is read in using basic CFITSIO commands, and stored as an array in a special C++ class. This class keeps track of the list of detected objects, as well as any reconstructed arrays that are made (see §3.3). The World Coordinate System (WCS) information for the cube is also obtained from the FITS header by WCSLIB functions (Calabretta & Greisen 2002; Greisen & Calabretta 2002), and this information, in the form of a `wcsprm` structure, is also stored in the same class.

A sub-section of an image can be requested via the `subsection` parameter in the parameter file – this can be a good idea if the cube has very noisy edges, which may produce many spurious detections. The generalised form of the subsection that is used by CFITSIO is `[x1:x2:dx,y1:y2:dy,z1:z2:dz]`, such that the x-coordinates run from `x1` to `x2` (inclusive), with steps of `dx`. The step value can be omitted (so a subsection of the form `[2:50,2:50,10:1000]` is still valid). *Duchamp* does not make use of any step value present in the subsection string, and any that are present are removed before the file is opened.

If one wants the full range of a coordinate then replace the range with an asterisk, e.g. `[2:50,2:50,*]`. If one wants to use a subsection, one must set `flagSubsection = 1`. A complete description of the section syntax can be found at the FITSIO web site [2].

3.2 Image modification

Several modifications to the cube can be made that improve the execution and efficiency of *Duchamp* (these are optional – their use is indicated by the relevant flags set in the input parameter file).

3.2.1 Blank pixel removal

First, the cube is trimmed of any BLANK pixels that pad the image out to a rectangular shape. This is optional, its use determined by the `flagBlankPix` parameter. The value for these pixels is read from the FITS header (using the BLANK, BSCALE and BZERO keywords), but if these are not present then the value can be specified by the user in the parameter file using `blankPixValue`.

[2] http://heasarc.gsfc.nasa.gov/docs/software/fitsio/c/c_user/node90.html

This stage is particularly important for the reconstruction step, as lots of BLANK pixels on the edges will smooth out features in the wavelet calculation stage. The trimming will also reduce the size of the cube's array, speeding up the execution. The amount of trimming is recorded, and these pixels are added back in once the source-detection is completed (so that quoted pixel positions are applicable to the original cube).

Rows and columns are trimmed one at a time until the first non-BLANK pixel is reached, so that the image remains rectangular. In practice, this means that there will be BLANK pixels left in the trimmed image (if the non-BLANK region is non-rectangular). However, these are ignored in all further calculations done on the cube.

3.2.2 Baseline removal

Second, the user may request the removal of baselines from the spectra, via the parameter `flagBaseline`. This may be necessary if there is a strong baseline ripple present, which can result in spurious detections at the high points of the ripple. The baseline is calculated from a wavelet reconstruction procedure (see §3.3) that keeps only the two largest scales. This is done separately for each spatial pixel (i.e. for each spectrum in the cube), and the baselines are stored and added back in before any output is done. In this way the quoted fluxes and displayed spectra are as one would see from the input cube itself – even though the detection (and reconstruction if applicable) is done on the baseline-removed cube.

The presence of very strong signals (for instance, masers at several hundred Jy) can affect the determination of the baseline, leading to a large dip centred on the signal in the baseline-subtracted spectrum. To prevent this, the signal is trimmed prior to the reconstruction process at some standard threshold (at 8σ above the mean). The baseline determined should thus be representative of the true, signal-free baseline. Note that this trimming is only a temporary measure which does not affect the source-detection.

3.2.3 Ignoring bright Milky Way emission

Finally, a single set of contiguous channels can be ignored – these may exhibit very strong emission, such as that from the Milky Way as seen in extragalactic HI cubes (hence the references to "Milky Way" in relation to this task – apologies to Galactic astronomers!). Such dominant channels will produce many detections that are unnecessary, uninteresting (if one is interested in extragalactic HI) and large (in size and hence in memory usage), and so will slow the program down and detract from the interesting detections. The use of this feature is controlled by the `flagMW` parameter, and the exact channels concerned are able to be set by the user (using `maxMW` and `minMW` – these give an inclusive range of channels). When employed, these channels are temporarily blanked out for the searching, and the scaling of the spectral output (see Fig. 1) will not take them into account. They will be present in the reconstructed array, however, and so will be included in the saved FITS file (see §3.4). When the final spectra are plotted, the range of channels covered by these parameters is indicated by a green hashed box.

3.3 Image reconstruction

The user can direct *Duchamp* to reconstruct the data cube using the *à trous* wavelet procedure. A good description of the procedure can be found in Starck & Murtagh (2002). The reconstruction is an effective way of removing a lot of the noise in the image, allowing one to search reliably to fainter levels, and reducing the number of spurious detections.

This is an optional step, but one that greatly enhances the source-detection process, with the payoff that it can be relatively time- and memory-intensive.

3.3.1 Algorithm

The steps in the *à trous* reconstruction are as follows:

1. Set the reconstructed array to 0 everywhere.
2. The input array is discretely convolved with a given filter function. This is determined from the parameter file via the `filterCode` parameter – see Appendix B for details on the filters available.
3. The wavelet coefficients are calculated by taking the difference between the convolved array and the input array.
4. If the wavelet coefficients at a given point are above the requested threshold (given by `snrRecon` as the number of σ above the mean and adjusted to the current scale – see Appendix H), add these to the reconstructed array.
5. The separation of the filter coefficients is doubled. (Note that this step provides the name of the procedure[3], as gaps or holes are created in the filter coverage.)
6. The procedure is repeated from step 2, using the convolved array as the input array.
7. Continue until the required maximum number of scales is reached.
8. Add the final smoothed (i.e. convolved) array to the reconstructed array. This provides the "DC offset", as each of the wavelet coefficient arrays will have zero mean.

The reconstruction has at least two iterations. The first iteration makes a first pass at the wavelet reconstruction (the process outlined in the 8 stages above), but the residual array will inevitably have some structure still in it, so the wavelet filtering is done on the residual, and any significant wavelet terms are added to the final reconstruction. This step is repeated until the change in the σ of the background is less than some fiducial amount.

It is important to note that the *à trous* decomposition is an example of a "redundant" transformation. If no thresholding is performed, the sum of all the wavelet coefficient arrays and the final smoothed array is identical to the input array. The thresholding thus removes only the unwanted structure in the array.

Note that any BLANK pixels that are still in the cube will not be altered by the reconstruction – they will be left as BLANK so that the shape of the valid part of the cube is preserved.

3.3.2 Note on Statistics

The correct calculation of the reconstructed array needs good estimation of the underlying mean and standard deviation of the background noise distribution. These statistics are estimated using robust methods, to avoid corruption by strong outlying points. The mean of the distribution is actually estimated by the median, while the median absolute deviation from the median (MADFM) is calculated and corrected assuming Gaussianity to

[3] *à trous* means "with holes" in French.

estimate the underlying standard deviation σ. The Gaussianity (or Normality) assumption is critical, as the MADFM does not give the same value as the usual rms or standard deviation value – for a normal distribution $N(\mu, \sigma)$ we find MADFM$= 0.6744888\sigma$. The difference between the MADFM and σ is corrected for, so the user need only think in the usual multiples of σ when setting `snrRecon`. See Appendix G for a derivation of this value.

When thresholding the different wavelet scales, the value of σ as measured from the wavelet array needs to be scaled to account for the increased amount of correlation between neighbouring pixels (due to the convolution). See Appendix H for details on this scaling.

3.3.3 User control of reconstruction parameters

The most important parameter for the user to select in relation to the reconstruction is the threshold for each wavelet array. This is set using the `snrRecon` parameter, and is given as a multiple of the rms (estimated by the MADFM) above the mean (which for the wavelet arrays should be approximately zero). There are several other parameters that can be altered as well that affect the outcome of the reconstruction.

By default, the cube is reconstructed in three dimensions, using a 3-dimensional filter and 3-dimensional convolution. This can be altered, however, using the parameter `reconDim`. If set to 1, this means the cube is reconstructed by considering each spectrum separately, whereas `reconDim=2` will mean the cube is reconstructed by doing each channel map separately. The merits of these choices are discussed in §5, but it should be noted that a 2-dimensional reconstruction can be susceptible to edge effects if the spatial shape is not rectangular.

The user can also select the minimum scale to be used in the reconstruction – the first scale exhibits the highest frequency variations, and so ignoring this one can sometimes be beneficial in removing excess noise. The default, however, is to use all scales (`minscale = 1`).

Finally, the filter that is used for the convolution can be selected by using `filterCode` and the relevant code number – the choices are listed in Appendix B. A larger filter will give a better reconstruction, but take longer and use more memory when executing. When multi-dimensional reconstruction is selected, this filter is used to construct a 2- or 3-dimensional equivalent.

3.4 Reconstruction I/O

The reconstruction stage can be relatively time-consuming, particularly for large cubes and reconstructions in 3-D. To get around this, *Duchamp* provides a shortcut to allow users to perform multiple searches (e.g. with different thresholds) on the same reconstruction without calculating the reconstruction each time.

The first step is to choose to save the reconstructed array as a FITS file by setting `flagOutputRecon = true`. The file will be saved in the same directory as the input image, so the user needs to have write permissions for that directory.

The filename will be derived from the input filename, with extra information detailing the reconstruction that has been done. For example, suppose `image.fits` has been reconstructed using a 3-dimensional reconstruction with filter 2, thresholded at 4σ using all scales. The output filename will then be `image.RECON-3-2-4-1.fits` (i.e. it uses the four parameters relevant for the *à trous* reconstruction as listed in Appendix B).

The new FITS file will also have these parameters as header keywords. If a subsection of the input image has been used (see §3.1), the format of the output filename will be `image.sub.RECON-3-2-4-1.fits`, and the subsection that has been used is also stored in the FITS header.

Likewise, the residual image, defined as the difference between the input and reconstructed arrays, can also be saved in the same manner by setting `flagOutputResid = true`. Its filename will be the same as above, with RESID replacing RECON.

If a reconstructed image has been saved, it can be read in and used instead of redoing the reconstruction. To do so, the user should set `flagReconExists = true`. The user can indicate the name of the reconstructed FITS file using the `reconFile` parameter, or, if this is not specified, *Duchamp* searches for the file with the name as defined above. If the file is not found, the reconstruction is performed as normal. Note that to do this, the user needs to set `flagAtrous = true` (obviously, if this is `false`, the reconstruction is not needed).

3.5 Searching the image

The image is searched for detections in two ways: spectrally (a 1-dimensional search in the spectrum in each spatial pixel), and spatially (a 2-dimensional search in the spatial image in each channel). In both cases, the algorithm finds connected pixels that are above the user-specified threshold. In the case of the spatial image search, the algorithm of Lutz (1980) is used to raster scan through the image and connect groups of pixels on neighbouring rows.

Note that this algorithm cannot be applied directly to a 3-dimensional case, as it requires that objects are completely nested in a row: that is, if you are scanning along a row, and one object finishes and another starts, you know that you will not get back to the first one (if at all) until the second is completely finished for that row. Three-dimensional data does not have this property, which is why we break up the searching into 1- and 2-dimensional cases.

The determination of the threshold is done in one of two ways. The first way is a simple sigma-clipping, where a threshold is set at a fixed number n of standard deviations above the mean, and pixels above this threshold are flagged as detected. The value of n is set with the parameter `snrCut`. As before, the value of the standard deviation is estimated by the MADFM, and corrected by the ratio derived in Appendix G.

The second method uses the False Discovery Rate (FDR) technique (Hopkins et al. 2002; Miller et al. 2001), whose basis we briefly detail here. The false discovery rate (given by the number of false detections divided by the total number of detections) is fixed at a certain value α (e.g. $\alpha = 0.05$ implies 5% of detections are false positives). In practice, an α value is chosen, and the ensemble average FDR (i.e. $\langle FDR \rangle$) when the method is used will be less than α. One calculates p – the probability, assuming the null hypothesis is true, of obtaining a test statistic as extreme as the pixel value (the observed test statistic) – for each pixel, and sorts them in increasing order. One then calculates d where

$$d = \max_j \left\{ j : P_j < \frac{j\alpha}{c_N N} \right\},$$

and then rejects all hypotheses whose p-values are less than or equal to P_d. (So a $P_i < P_d$ will be rejected even if $P_i \geq j\alpha/c_N N$.) Note that "reject hypothesis" here means "accept the pixel as an object pixel" (i.e. we are rejecting the null hypothesis that the pixel belongs to the background).

The c_N values here are normalisation constants that depend on the correlated nature of the pixel values. If all the pixels are uncorrelated, then $c_N = 1$. If N pixels are correlated, then their tests will be dependent on each other, and so $c_N = \sum_{i=1}^{N} i^{-1}$. Hopkins et al. (2002) consider real radio data, where the pixels are correlated over the beam. In this case the sum is made over the N pixels that make up the beam. The value of N is calculated from the FITS header (if the correct keywords – BMAJ, BMIN – are not present, a default value of 10 pixels is assumed).

The theory behind the FDR method implies a direct connection between the choice of α and the fraction of detections that will be false positives. However, due to the merging process, this direct connection is lost when looking at the final number of detections – see discussion in §5. The effect is that the number of false detections will be less than indicated by the α value used.

If a reconstruction has been made, the residuals (defined as original − reconstruction) are used to estimate the noise parameters of the cube. Otherwise they are estimated directly from the cube itself. In both cases, robust estimators are used as described above.

Detections must have a minimum number of pixels to be counted. This minimum number is given by the input parameters `minPix` (for 2-dimensional searches) and `minChannels` (for 1-dimensional searches).

The search only looks for positive features. If one is interested instead in negative features (such as absorption lines), set the parameter `flagNegative = true`. This will invert the cube (i.e. multiply all pixels by -1) prior to the search, and then re-invert the cube (and the fluxes of any detections) after searching is complete. All outputs are done in the same manner as normal, so that fluxes of detections will be negative.

3.6 Merging detected objects

The searching step produces a list of detected objects that will have many repeated detections of a given object – for instance, spectral detections in adjacent pixels of the same object and/or spatial detections in neighbouring channels. These are then combined in an algorithm that matches all objects judged to be "close". This determination is made in one of two ways.

One way is to define two thresholds – one spatial and one in velocity – and say that two objects should be merged if there is at least one pair of pixels that lie within these threshold distances of each other. These thresholds are specified by the parameters `threshSpatial` and `threshVelocity` (in units of pixels and channels respectively).

Alternatively, the spatial requirement can be changed to say that there must be a pair of pixels that are *adjacent* – a stricter, but perhaps more realistic requirement, particularly when the spatial pixels have a large angular size (as is the case for HI surveys). This method can be selected by setting the parameter `flagAdjacent` to 1 (i.e. `true`) in the parameter file. The velocity thresholding is done in the same way as the first option.

Once the detections have been merged, they may be "grown". This is a process of increasing the size of the detection by adding adjacent pixels that are above some secondary threshold. This threshold is lower than the one used for the initial detection, but above the noise level, so that faint pixels are only detected when they are close to a bright pixel. The value of this threshold is a possible input parameter (`growthCut`), with a default value of 1.5σ. The use of the growth algorithm is controlled by the `flagGrowth` parameter –

the default value of which is `false`. If the detections are grown, they are sent through the merging algorithm a second time, to pick up any detections that now overlap or have grown over each other.

Finally, to be accepted, the detections must span *both* a minimum number of channels (to remove any spurious single-channel spikes that may be present), and a minimum number of spatial pixels. These numbers, as for the original detection step, are set with the `minChannels` and `minPix` parameters. The channel requirement means there must be at least one set of `minChannels` consecutive channels in the source for it to be accepted.

4 Outputs

4.1 During execution

Duchamp provides the user with feedback whilst it is running, to keep the user informed on the progress of the analysis. Most of this consists of self-explanatory messages about the particular stage the program is up to. The relevant parameters are printed to the screen at the start (once the file has been successfully read in), so the user is able to make a quick check that the setup is correct (see Appendix app-input for an example).

If the cube is being trimmed (§3.2), the resulting dimensions are printed to indicate how much has been trimmed. If a reconstruction is being done, a continually updating message shows either the current iteration and scale, compared to the maximum scale (when `reconDim=3`), or a progress bar showing the amount of the cube that has been reconstructed (for smaller values of `reconDim`).

During the searching algorithms, the progress through the 1D and 2D searches are shown. When the searches have completed, the number of objects found in both the 1D and 2D searches are reported (see §3.5 for details).

In the merging process (where multiple detections of the same object are combined – see §3.6), two stages of output occur. The first is when each object in the list is compared with all others. The output shows two numbers: the first being how far through the list the current object is, and the second being the length of the list. As the algorithm proceeds, the first number should increase and the second should decrease (as objects are combined). When the numbers meet (i.e. the whole list has been compared), the second phase begins, in which multiply-appearing pixels in each object are removed, as are objects not meeting the minimum channels requirement. During this phase, the total number of accepted objects is shown, which should steadily increase until all have been accepted or rejected. Note that these steps can be very quick for small numbers of detections.

Since this continual printing to screen has some overhead of time and CPU involved, the user can elect to not print this information by setting the parameter `verbose = 0`. In this case, the user is still informed as to the steps being undertaken, but the details of the progress are not shown.

4.2 Results

4.2.1 Table of Results

Finally, we get to the results – the reason for running *Duchamp* in the first place. Once the detection list is finalised, it is sorted by the mean velocity of the detections (or, if there is no good WCS associated with the cube, by the mean Z-pixel position). The results are then printed to the screen and to the output file, given by the `OutFile` parameter. The results list, an example of which can be seen in Appendix D, contains the following columns (note that the title of the columns depending on WCS information will depend on the projection of the WCS):

Obj#: The ID number of the detection (simply the sequential count for the list, which is ordered by increasing velocity).

Name: The IAU-format name of the detection (derived from the WCS projection).

X: The average X-pixel position.

Y: The average Y-pixel position.

Z: The average Z-pixel position.

RA/GLON: The Right Ascension or Galactic Longitude of the centre of the object.

DEC/GLAT: The Declination or Galactic Latitude of the centre of the object.

VEL: The mean velocity of the object [units given by the `spectralUnits` parameter].

w_RA/w_GLON: The width of the object in Right Ascension or Galactic Longitude [arcmin].

w_DEC/w_GLAT: The width of the object in Declination Galactic Latitude [arcmin].

w_VEL: The full velocity width of the detection (max channel − min channel, in velocity units [see note below]).

F_int: The integrated flux over the object, in the units of flux times velocity, corrected for the beam if necessary.

F_peak: The peak flux over the object, in the units of flux.

X1, X2: The minimum and maximum X-pixel coordinates.

Y1, Y2: The minimum and maximum Y-pixel coordinates.

Z1, Z2: The minimum and maximum Z-pixel coordinates.

Npix: The number of voxels (i.e. distinct (x, y, z) coordinates) in the detection.

Flag: Whether the detection has any warning flags (see below).

The Name is derived from the WCS position. For instance, a source centred on the RA,Dec position $12^h53^m45^s$, -36°24′12″ will be called J125345−362412 (if the epoch is J2000) or B125345−362412 (if B1950). An alternative form is used for Galactic coordinates: a source centred on the position (l,b) = (323.1245, 5.4567) will be called G323.124+05.457. If the WCS is not valid (i.e. is not present or does not have all the necessary information), the Name, RA, DEC, VEL and related columns are not printed, but the pixel coordinates are still provided.

The velocity units can be specified by the user, using the parameter `spectralUnits` (enter it as a single string). The default value is km/s, which should be suitable for most users. These units are also used to give the units of integrated flux.

The last column contains any warning flags about the detection. There are currently two options here. An 'E' is printed if the detection is next to the edge of the image, meaning either the limit of the pixels, or the limit of the non-BLANK pixel region. An

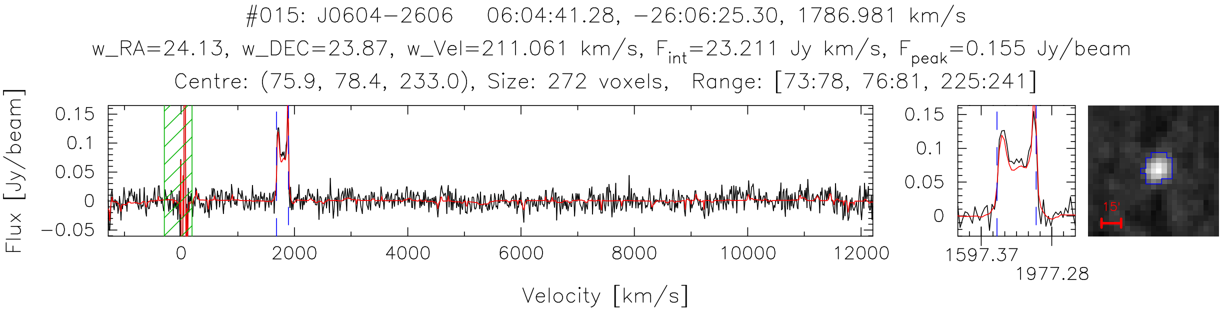

Figure 1: An example of the spectrum output. Note several of the features discussed in the text: the red lines indicating the reconstructed spectrum; the blue dashed lines indicating the spectral extent of the detection; the green hashed area indicating the Milky Way channels that are ignored by the searching algorithm; the blue border showing its spatial extent on the 0th moment map; and the 15 arcmin-long scale bar.

'N' is printed if the total flux, summed over all the (non-BLANK) pixels in the smallest box that completely encloses the detection, is negative. Note that this sum is likely to include non-detected pixels. It is of use in pointing out detections that lie next to strongly negative pixels, such as might arise due to interference – the detected pixels might then also be due to the interference, so caution is advised.

4.2.2 Other results lists

Two alternative results files can also be requested. One option is a VOTable-format XML file, containing just the RA, Dec, Velocity and the corresponding widths of the detections, as well as the fluxes. The user should set `flagVOT = 1`, and put the desired filename in the parameter `votFile` – note that the default is for it not to be produced. This file should be compatible with all Virtual Observatory tools (such as Aladin[4]). The second option is an annotation file for use with the Karma toolkit of visualisation tools (in particular, with `kvis`). This will draw a circle at the position of each detection, and number it according to the Obj# given above. To make use of this option, the user should set `flagKarma = 1`, and put the desired filename in the parameter `karmaFile` – again, the default is for it not to be produced.

As the program is running, it also (optionally) records the detections made in each individual spectrum or channel (see §3.5 for details on this process). This is recorded in the file given by the parameter `LogFile`. This file does not include the columns `Name, RA, DEC, w_RA, w_DEC, VEL, w_VEL`. This file is designed primarily for diagnostic purposes: e.g. to see if a given set of pixels is detected in, say, one channel image, but does not survive the merging process. The list of pixels (and their fluxes) in the final detection list are also printed to this file, again for diagnostic purposes. This feature can be turned off by setting `flagLog = false`. (This may be a good idea if you are not interested in its contents, as it can be a large file.)

4.2.3 Graphical output – spectra

As well as the output data file, a postscript file is created that shows the spectrum for each detection, together with a small cutout image (the 0th moment) and basic information

[4] Aladin can be found on the web at http://aladin.u-strasbg.fr/

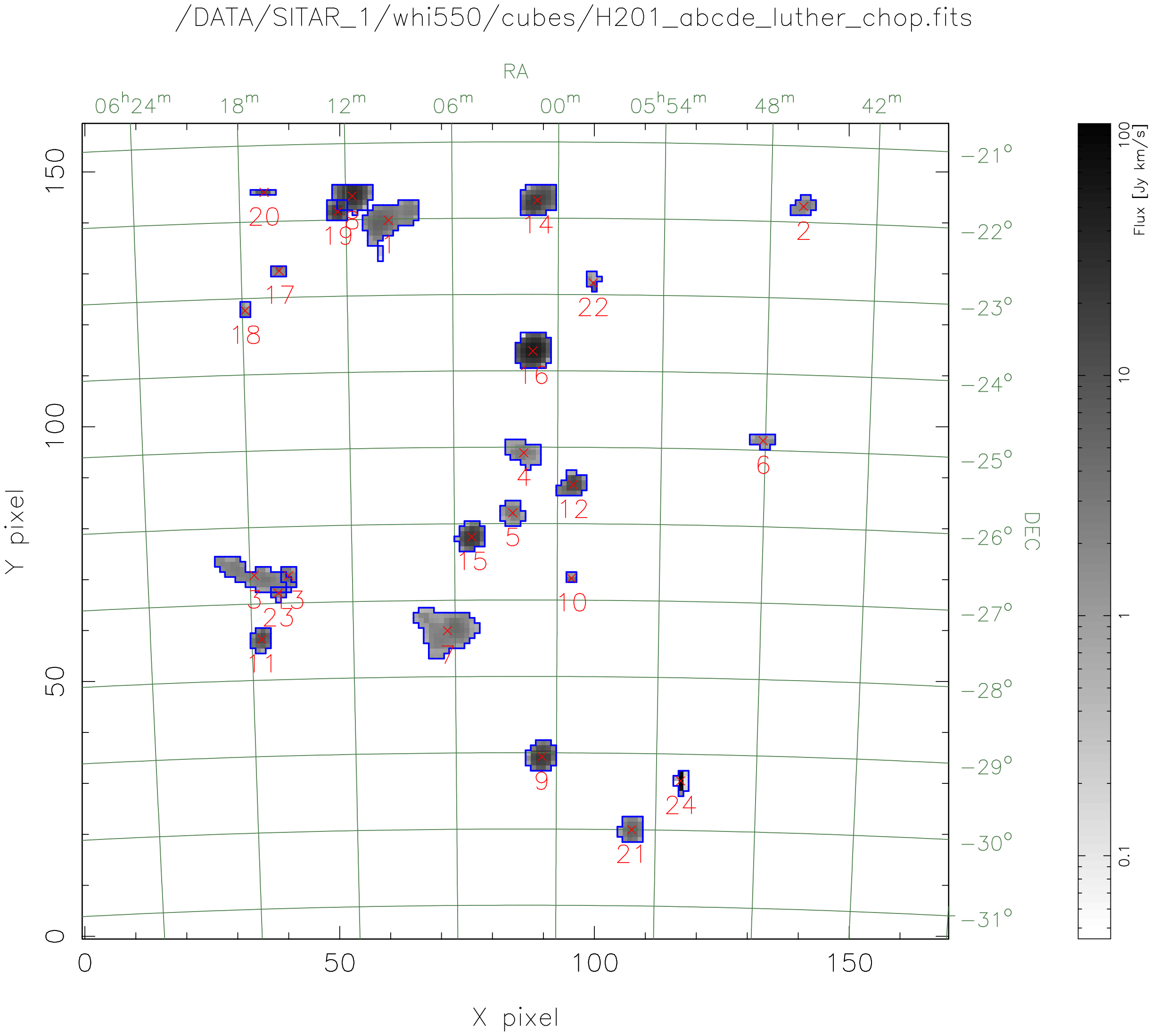

Figure 2: An example of the moment map created by *Duchamp*. The full extent of the cube is covered, and the 0th moment of each object is shown (integrated individually over all the detected channels).

about the detection (note that any flags are printed after the name of the detection, in the format `[E]`). If the cube was reconstructed, the spectrum from the reconstruction is shown in red, over the top of the original spectrum. The spectral extent of the detected object is indicated by two dashed blue lines, and the region covered by the "Milky Way" channels is shown by a green hashed box.

The spectrum that is plotted is governed by the `spectralMethod` parameter. It can be either `peak`, where the spectrum is from the spatial pixel containing the detection's peak flux; or `sum`, where the spectrum is summed over all spatial pixels, and then corrected for the beam size.

The spectral extent of the detection is indicated with blue lines, and a zoom is shown in a separate window. The cutout image can optionally include a border around the spatial pixels that are in the detection (turned on and off by the parameter `drawBorders` – the default is `true`). It also includes a scale bar in the bottom left corner to indicate size – it is 15 arcmin long (note that due to projection effects it may be a slightly different physical length from object to object). An example detection can be seen below in Fig. 1.

4.2.4 Graphical output – maps

Finally, a couple of images are optionally produced: a 0th moment map of the cube, combining just the detected channels in each object, showing the integrated flux in grey-scale; and a "detection image", a grey-scale image where the pixel values are the number of channels that spatial pixel is detected in. In both cases, if `drawBorders = true`, a border is drawn around the spatial extent of each detection. An example moment map is shown in Fig. 2. The production or otherwise of these images is governed by the `flagMaps` parameter.

The purpose of these images are to provide a visual guide to where the detections have been made, and, particularly in the case of the moment map, to provide an indication of the strength of the source. In both cases, the detections are numbered (in the same sense as the output list), and the spatial borders are marked out as for the cutout images in the spectra file. Both these images are saved as postscript files (given by the parameters `momentMap` and `detectionMap` respectively), with the latter also displayed in a PGPLOT window (regardless of the state of `flagMaps`).

5 Notes and hints on the use of *Duchamp*

In using *Duchamp*, the user has to make a number of decisions about the way the program runs. This section is designed to give the user some idea about what to choose.

The main choice is whether or not to use the wavelet reconstruction. The main benefits of this are the marked reduction in the noise level, leading to regularly-shaped detections, and good reliability for faint sources. The main drawback with its use is the long execution time: to reconstruct a $170 \times 160 \times 1024$ (HIPASS) cube often requires three iterations and takes about 20-25 minutes to run completely. Note that this is for the three-dimensional reconstruction: using `reconDim=1` makes the reconstruction quicker (the full program then takes about 6 minutes), but it is still the largest part of the time.

The searching part of the procedure is much quicker: searching an un-reconstructed cube leads to execution times of only a couple of minutes. Alternatively, using the ability to read in previously-saved reconstructed arrays makes running the reconstruction more than once a more feasible prospect.

On the positive side, the shape of the detections in a cube that has been reconstructed will be much more regular and smooth – the ragged edges that objects in the raw cube possess are smoothed by the removal of most of the noise. This enables better determination of the shapes and characteristics of objects.

A further point to consider when using the reconstruction is that if the two-dimensional reconstruction is chosen (`reconDim=2`), it can be susceptible to edge effects. If the valid area in the cube (i.e. the part that is not BLANK) has non-rectangular edges, the convolution can produce artefacts in the reconstruction that mimic the edges and can lead (depending on the selection threshold) to some spurious sources. Caution is advised with such data – the user is advised to check carefully the reconstructed cube for the presence of such artefacts. Note, however, that the 1- and 3-dimensional reconstructions are *not* susceptible in the same way, since the spectral direction does not generally exhibit these BLANK edges, and so we recommend the use of either of these.

If one chooses the reconstruction method, a further decision is required on the signal-to-noise cutoff used in determining acceptable wavelet coefficients. A larger value will remove more noise from the cube, at the expense of losing fainter sources, while a smaller value will include more noise, which may produce spurious detections, but will be more sensitive to faint sources. Values of less than about 3σ tend to not reduce the noise a great deal and can lead to many spurious sources (although this will depend on the nature of the cube).

When it comes to searching, the FDR method produces more reliable results than simple sigma-clipping, particularly in the absence of reconstruction. However, it does not work in exactly the way one would expect for a given value of `alpha`. For instance, setting fairly liberal values of `alpha` (say, 0.1) will often lead to a much smaller fraction of false detections (i.e. much less than 10%). This is the effect of the merging algorithms, that combine the sources after the detection stage, and reject detections not meeting the minimum pixel or channel requirements. It is thus better to aim for larger `alpha` values than those derived from a straight conversion of the desired false detection rate.

Finally, as *Duchamp* is still undergoing development, there are some elements that are not fully developed. In particular, it is not as clever as I would like at avoiding interference. The ability to place requirements on the minimum number of channels and pixels partially circumvents this problem, but work is being done to make *Duchamp* smarter at rejecting signals that are clearly (to a human eye at least) interference. See the following section for further improvements that are planned.

6 Future Developments

This is both a list of planned improvements and a wish-list of features that would be nice to include (but are not planned in the immediate future). Let me know if there are items not on this list, or items on the list you would like prioritised.

- Better determination of the noise characteristics of spectral-line cubes, including understanding how the noise is generated and developing a model for it. **Planned.**
- Include more source analysis. Examples could be: shape information; measurements of HI mass; more variety of measurements of velocity width and profile. **Some planned.**
- Provide some indication of the significance of the detection (i.e. some S/N-like value). **Planned.**
- Improved ability to reject interference, possibly on the spectral shape of features. **Planned.**
- Ability to separate (de-blend) distinct sources that have been merged. **Planned.**
- Link to lists of possible counterparts (e.g. via NED/SIMBAD/other VO tools?). **Wish-list.**
- On-line web service interface, so a user can upload a cube and get back a source-list. **Wish-list**.
- Embed *Duchamp* in a GUI, to move away from the text-based interaction. **Wish-list**.

References

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A Obtaining and Installing *Duchamp*

The *Duchamp* web page can be found at the following location:
http://www.atnf.csiro.au/people/Matthew.Whiting/Duchamp
Here you can find a gzipped tar archive of the source code that can be downloaded and extracted, as well as this User's Guide in postscript and hyperlinked PDF formats.

Duchamp can be built on Unix systems by typing:

```
> ./configure
> make
> make clean (optional -- to remove the object files)
```

Run in this manner, `configure` should find all the necessary libraries, but if the above-mentioned libraries have been installed in non-standard locations, you can specify additional directories to look in. There are separate options for library files (eg. libcpgplot.a) and header files (eg. cpgplot.h).

For example, if WCSLIB had been installed in `/home/mduchamp/wcslib`, there are two libraries that are likely to be in separate subdirectories: `C/` and `pgsbox/`. Each subdirectory needs to be searched for library and header files, so one could build Duchamp by typing:

```
> ./configure \
LIBDIRS="/home/mduchamp/wcslib/C /home/mduchamp/wcslib/pgsbox" \
INCDIRS="/home/mduchamp/wcslib/C /home/mduchamp/wcslib/pgsbox"
```

And then just run make in the usual fashion:

```
> make
```

This will produce the executable `Duchamp`. There are two possible ways to run it. The first is:

```
> Duchamp -f [FITS file]
```

where `[FITS file]` is the file you wish to search. This method simply uses the default values of all parameters.

The second method allows some determination of the parameter values by the user. Type:

```
> Duchamp -p [parameter file]
```

where `[parameterFile]` is a file with the input parameters, including the name of the cube you want to search. There are two example input files included with the distribution. The smaller one, `InputExample`, shows the typical parameters one might want to set. The large one, `InputComplete`, lists all possible parameters that can be entered, and a brief description of them. To get going quickly, just replace the "your-file-here" in `InputExample` with your image name, and type

```
> Duchamp -p InputExample
```

The following appendices provide details on the individual parameters, and show examples of the output files that *Duchamp* produces.

B Available parameters

The full list of parameters that can be listed in the input file are given here. If not listed, they take the default value given in parentheses. Since the order of the parameters in the input file does not matter, they are grouped here in logical sections.

Input-output related

ImageFile (no default assumed): The filename of the data cube to be analysed.

flagSubsection `[false]`**:** A flag to indicate whether one wants a subsection of the requested image.

Subsection `[ [*,*,*] ]`**:** The requested subsection, which should be specified in the format `[x1:x2,y1:y2,z1:z2]`, where the limits are inclusive. If the full range of a dimension is required, use a `*`, e.g. if you want the full spectral range of a subsection of the image, use `[30:140,30:140,*]`.

flagReconExists `[false]`**:** A flag to indicate whether the reconstructed array has been saved by a previous run of *Duchamp*. If set true, the reconstructed array will be read from the file given by `reconFile`, rather than calculated directly.

reconFile (no default assumed): The FITS file that contains the reconstructed array. If `flagReconExists` is true and this parameter is not defined, the default file searched will be determined by the *à trous* parameters (see §3.3).

OutFile `[duchamp-Results.txt]`**:** The file containing the final list of detections. This also records the list of input parameters.

SpectraFile `[duchamp-Spectra.ps]`**:** The postscript file containing the resulting integrated spectra and images of the detections.

flagLog `[true]`**:** A flag to indicate whether intermediate detections should be logged.

LogFile `[duchamp-Logfile.txt]`**:** The file in which intermediate detections are logged. These are detections that have not been merged. This is primarily for use in debugging and diagnostic purposes – normal use of the program will probably not require this.

flagOutputRecon `[false]`**:** A flag to say whether or not to save the reconstructed cube as a FITS file. The filename will be derived from the ImageFile – the reconstruction of `image.fits` will be saved as `image.RECON?.fits`, where `?` stands for the value of `snrRecon` (see below).

flagOutputResid `[false]`**:** As for `flagOutputRecon`, but for the residual array – the difference between the original cube and the reconstructed cube. The filename will be `image.RESID?.fits`.

flagVOT `[false]`**:** A flag to say whether to create a VOTable file corresponding to the information in `outfile`. This will be an XML file in the Virtual Observatory VOTable format.

votFile `[duchamp-Results.xml]`**:** The VOTable file with the list of final detections. Some input parameters are also recorded.

flagKarma `[false]`**:** A flag to say whether to create a Karma annotation file corresponding to the information in `outfile`. This can be used as an overlay for the Karma programs such as `kvis`.

karmaFile `[duchamp-Results.ann]`**:** The Karma annotation file showing the list of final detections.

flagMaps `[true]`**:** A flag to say whether to save postscript files showing the 0th moment map of the whole cube (parameter `momentMap`) and the detection image (`detectionMap`).

momentMap `[duchamp-MomentMap.ps]`**:** A postscript file containing a map of the 0th moment of the detected sources, as well as pixel and WCS coordinates.

detectionMap `[duchamp-DetectionMap.ps]`**:** A postscript file showing each of the detected objects, coloured in greyscale by the number of channels spanned by each pixel. Also shows pixel and WCS coordinates.

Modifying the cube

flagBlankPix `[true]`**:** A flag to say whether to remove BLANK pixels from the analysis – these are pixels set to some particular value because they fall outside the imaged area.

blankPixValue `[-8.00061]`**:** The value of the BLANK pixels, if this information is not contained in the FITS header (the usual procedure is to obtain this value from the header information – in which case the value set by this parameter is ignored).

flagMW `[false]`**:** A flag to say whether to ignore channels contaminated by Milky Way (or other) emission – the searching algorithms will not look at these channels.

maxMW `[112]`**:** The maximum channel number containing "Milky Way" emission.

minMW `[75]`**:** The minimum channel number containing "Milky Way" emission. Note that the range specified by `maxMW` and `minMW` is inclusive.

flagBaseline `[false]`**:** A flag to say whether to remove the baseline from each spectrum in the cube for the purposes of reconstruction and detection.

Detection related

General detection

flagNegative `[false]`**:** A flag to indicate that the features being searched for are negative. The cube will be inverted prior to searching.

snrCut `[3.]`**:** The cut-off value for thresholding, in terms of number of σ above the mean.

flagGrowth `[false]`**:** A flag indicating whether or not to grow the detected objects to a smaller threshold.

growthCut `[2.]`**:** The smaller threshold using in growing detections. In units of σ above the mean.

À trous reconstruction

flagATrous `[true]`: A flag indicating whether or not to reconstruct the cube using the *à trous* wavelet reconstruction. See §3.3 for details.

reconDim `[3]`: The number of dimensions to use in the reconstruction. 1 means reconstruct each spectrum separately, 2 means each channel map is done separately, and 3 means do the whole cube in one go.

scaleMin `[1]`: The minimum wavelet scale to be used in the reconstruction. A value of 1 means "use all scales".

snrRecon `[4]`: The thresholding cutoff used in the reconstruction – only wavelet coefficients this many σ above the mean (or greater) are included in the reconstruction.

filterCode `[1]`: The code number of the filter to use in the reconstruction. The options are:

- **1:** B_3-spline filter: coefficients = $(\frac{1}{16}, \frac{1}{4}, \frac{3}{8}, \frac{1}{4}, \frac{1}{16})$
- **2:** Triangle filter: coefficients = $(\frac{1}{4}, \frac{1}{2}, \frac{1}{4})$
- **3:** Haar wavelet: coefficients = $(0, \frac{1}{2}, \frac{1}{2})$

FDR method

flagFDR `[false]`: A flag indicating whether or not to use the False Discovery Rate method in thresholding the pixels.

alphaFDR `[0.01]`: The α parameter used in the FDR analysis. The average number of false detections, as a fraction of the total number, will be less than α (see §3.5).

Merging detections

minPix `[2]`: The minimum number of spatial pixels for a single detection to be counted.

minChannels `[3]`: The minimum number of consecutive channels that must be present in a detection.

flagAdjacent `[true]`: A flag indicating whether to use the "adjacent pixel" criterion to decide whether to merge objects. If not, the next two parameters are used to determine whether objects are within the necessary thresholds.

threshSpatial `[3.]`: The maximum allowed minimum spatial separation (in pixels) between two detections for them to be merged into one. Only used if `flagAdjacent = false`.

threshVelocity `[7.]`: The maximum allowed minimum channel separation between two detections for them to be merged into one.

Other parameters

spectralMethod `[peak]`: This indicates which method is used to plot the output spectra: `peak` means plot the spectrum containing the detection's peak pixel; `sum` means sum the spectra of each detected spatial pixel, and correct for the beam size. Any other choice defaults to `peak`.

spectralUnits `[km/s]`**:** The user can specify the units of the spectral axis. Assuming the WCS of the FITS file is valid, the spectral axis is transformed into velocity, and put into these units for all output and for calculations such as the integrated flux of a detection.

drawBorders `[true]`**:** A flag indicating whether borders are to be drawn around the detected objects in the moment maps included in the output (see for example Fig. 1).

verbose `[true]`**:** A flag indicating whether to print the progress of computationally-intensive algorithms (such as the searching and merging) to screen.

C Example parameter files

This is what a typical parameter file would look like.

```
imageFile        /DATA/SITAR_1/whi550/cubes/H201_abcde_luther_chop.fits
logFile          logfile.txt
outFile          results.txt
spectraFile      spectra.ps
flagSubsection   0
flagOutputRecon  0
flagOutputResid  0
flagBlankPix     1
flagMW           1
minMW            75
maxMW            112
minPix           3
flagGrowth       1
growthCut        1.5
flagATrous       0
scaleMin         1
snrRecon         4
flagFDR          1
alphaFDR         0.1
numPixPSF        20
snrCut           3
threshSpatial    3
threshVelocity   7
```

Note that it is not necessary to include all these parameters in the file, only those that need to be changed from the defaults (as listed in Appendix B), which in this case would be very few. A minimal parameter file might look like:

```
imageFile        /DATA/SITAR_1/whi550/cubes/H201_abcde_luther_chop.fits
flagLog          0
snrRecon         3
snrCut           2.5
minChannels      4
```

This will reconstruct the cube with a lower SNR value than the default, select objects at a lower threshold, with a looser minimum channel requirement, and not keep a log of the intermediate detections.

The following page demonstrates how the parameters are presented to the user, both on the screen at execution time, and in the output and log files. On each line, there is a description on the parameter, the relevant parameter name that is used in the input file (if there is one that the user can enter), and the value of the parameter being used.

Typical presentation of parameters in output and log files:

```
---- Parameters ----
Image to be analysed..........................[imageFile]  =  input.fits
Intermediate Logfile............................[logFile]  =  duchamp-Logfile.txt
Final Results file..............................[outFile]  =  duchamp-Results.txt
Spectrum file...............................[spectraFile]  =  duchamp-Spectra.ps
0th Moment Map................................[momentMap]  =  duchamp-MomentMap.ps
Detection Map..............................[detectionMap]  =  duchamp-DetectionMap.ps
Saving reconstructed cube?..............[flagoutputrecon]  =  false
Saving residuals from reconstruction?..[flagoutputresid]  =  false
------
Searching for Negative features?...........[flagNegative]  =  false
Fixing Blank Pixels?.......................[flagBlankPix]  =  true
Blank Pixel Value........................................  =  -8.00061
Removing Milky Way channels?.....................[flagMW]  =  true
Milky Way Channels........................[minMW - maxMW]  =  75-112
Beam Size (pixels).......................................  =  10.1788
Removing baselines before search?..........[flagBaseline]  =  false
Minimum # Pixels in a detection...................[minPix]  =  2
Minimum # Channels in a detection...........[minChannels]  =  3
Growing objects after detection?.............[flagGrowth]  =  false
Using A Trous reconstruction?................[flagATrous]  =  true
Number of dimensions in reconstruction.........[reconDim]  =  3
Minimum scale in reconstruction................[scaleMin]  =  1
SNR Threshold within reconstruction............[snrRecon]  =  4
Filter being used for reconstruction.........[filterCode]  =  1 (B3 spline function)
Using FDR analysis?.............................[flagFDR]  =  false
SNR Threshold......................................[snrCut]  =  3
Using Adjacent-pixel criterion?............[flagAdjacent]  =  true
Max. velocity separation for merging.....[threshVelocity]  =  7
Method of spectral plotting..............[spectralMethod]  =  peak
```

D Example results file

This the typical content of an output file, after running *Duchamp* with the parameters illustrated on the previous page.

```
Results of the \duchamp\ source finder: Tue May 23 14:51:38 2006
---- Parameters ----
     (... omitted for clarity -- see previous page for examples...)
--------------------
Total number of detections = 25
--------------------
```

Obj#	Name	X	Y	Z	RA	DEC	VEL [km/s]	w_RA [arcmin]	w_DEC [arcmin]	w_VEL [km/s]	F_int [Jy km/s]	F_peak [Jy/beam]	X1	X2	Y1	Y2	Z1	Z2	Npix [pix]	Flag
1	J0618-2532	30.2	86.0	113.3	06:18:12.54	-25:32:44.79	208.502	45.17	34.61	26.383	24.394	0.350	25	35	82	90	112	114	137	E
2	J0609-2156	59.5	140.6	114.6	06:09:19.66	-21:56:31.20	225.572	44.39	31.47	65.957	16.128	0.213	55	65	137	144	113	118	153	
3	J0545-2143	141.2	143.2	114.8	05:45:51.71	-21:43:36.20	228.470	19.61	16.66	26.383	2.412	0.090	139	143	142	145	114	116	29	
4	J0617-2633	33.3	70.8	115.6	06:17:25.52	-26:33:33.83	238.736	65.02	30.10	26.383	9.776	0.117	26	41	68	75	115	117	104	E
5	J0601-2500	86.2	94.9	117.9	06:01:39.54	-25:00:32.46	269.419	27.99	24.02	26.383	3.920	0.124	83	89	92	97	117	119	44	
6	J0602-2547	84.0	83.1	118.0	06:02:18.29	-25:47:31.69	270.319	20.01	19.99	26.383	2.999	0.118	82	86	81	85	117	119	34	
7	J0547-2448	133.0	97.2	118.7	05:47:52.53	-24:48:38.16	279.113	19.72	12.54	26.383	1.474	0.074	131	135	96	98	118	120	21	
8	J0606-2719	71.1	60.0	121.3	06:06:10.99	-27:19:48.61	314.090	52.36	39.59	39.574	14.268	0.150	65	77	55	64	120	123	154	
9	J0611-2137	52.4	145.3	162.5	06:11:20.92	-21:37:29.57	857.955	32.39	23.49	118.722	43.178	0.410	49	56	142	147	158	167	265	E
10	J0600-2859	89.7	35.3	202.4	06:00:34.08	-28:59:00.43	1383.160	23.93	24.10	171.487	24.439	0.173	87	92	33	38	196	209	271	
11	J0558-2638	95.4	70.3	223.1	05:58:53.03	-26:38:45.91	1656.140	11.93	12.07	92.339	1.045	0.063	94	96	69	71	220	227	18	
12	J0617-2723	34.7	58.3	227.4	06:17:07.07	-27:23:50.65	1712.868	16.75	23.53	290.209	8.529	0.093	33	36	56	61	215	237	118	
13	J0558-2525	95.8	88.6	231.7	05:58:49.27	-25:25:33.60	1770.134	27.87	24.16	237.444	12.863	0.115	92	98	86	91	221	239	175	
14	J0600-2141	88.8	144.4	232.5	06:00:54.02	-21:41:57.06	1780.188	27.96	24.13	224.252	30.743	0.166	86	92	142	147	222	239	344	E
15	J0615-2634	40.0	70.8	232.6	06:15:25.50	-26:34:20.04	1782.214	12.44	15.69	52.765	2.084	0.068	39	41	69	72	231	235	31	
16	J0604-2606	76.0	78.4	233.0	06:04:41.13	-26:06:21.19	1787.226	24.13	23.87	211.061	23.563	0.155	73	78	76	81	225	241	278	
17	J0601-2340	87.9	114.9	235.8	06:01:08.83	-23:40:19.37	1824.122	31.95	28.09	237.444	82.380	0.297	85	92	112	118	227	245	647	
18	J0615-2235	38.2	130.5	254.5	06:15:32.09	-22:35:37.24	2070.934	12.29	11.70	105.531	1.555	0.070	37	39	129	131	249	257	24	
19	J0617-2305	31.4	122.8	258.1	06:17:33.45	-23:05:28.94	2118.752	12.34	11.65	26.383	1.022	0.062	30	32	122	124	257	259	16	
20	J0612-2149	49.6	142.2	270.3	06:12:11.04	-21:49:29.72	2279.926	16.27	15.73	395.740	15.156	0.101	48	51	141	144	257	287	204	
21	J0616-2133	35.3	146.0	300.6	06:16:15.78	-21:33:09.69	2679.148	20.22	7.47	224.252	3.014	0.127	33	37	145	146	294	311	28	E
22	J0555-2956	107.3	20.9	367.6	05:55:08.02	-29:56:09.08	3562.236	19.71	20.30	39.574	5.891	0.169	105	109	19	23	366	369	58	
23	J0557-2246	99.8	128.2	434.0	05:57:43.77	-22:46:42.95	4438.776	11.88	16.12	105.531	1.703	0.167	99	101	127	130	430	438	17	N
24	J0616-2648	38.1	67.2	546.8	06:16:02.10	-26:48:35.49	5926.464	12.35	11.67	26.383	1.276	0.064	37	39	66	68	546	548	18	
25	J0552-2916	117.0	30.5	727.0	05:52:13.64	-29:16:58.02	8303.952	11.59	20.25	303.400	35.523	0.479	116	118	28	32	716	739	111	

Note that the width of the table can make it hard to read. A good trick for those using UNIX/Linux is to make use of the `a2ps` command. The following works well, producing a postscript file `results.ps`:

```
a2ps -1 -r -f8 -o duchamp-Results.ps duchamp-Results.txt
```

E Example VOTable output

This is part of the VOTable, in XML format, corresponding to the output file in Appendix D (the indentation has been removed to make it fit on the page).


```
<?xml version="1.0"?>
<VOTABLE version="1.1" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
 xsi:noNamespaceSchemaLocation="http://www.ivoa.net/xml/VOTable/VOTable/v1.1">
<COOSYS ID="J2000" equinox="J2000." epoch="J2000." system="eq_FK5"/>
<RESOURCE name="Duchamp Output">
<TABLE name="Detections">
<DESCRIPTION>Detected sources and parameters from running the Duchamp source finder.</DESCRIPTION>
<PARAM name="FITS file" datatype="char" ucd="meta.file;meta.fits" value="/DATA/SITAR_1/whi550/cubes/H201_abcde_luther_chop.fits"/>
<PARAM name="Threshold" datatype="float" ucd="stat.snr" value="2.5">
<PARAM name="ATrous note" datatype="char" ucd="meta.note" value="The a trous reconstruction method was used, with the following parameters.">
<PARAM name="ATrous Dimension" datatype="int" ucd="meta.code;stat" value="3">
<PARAM name="ATrous Cut" datatype="float" ucd="stat.snr" value="4">
<PARAM name="ATrous Minimum Scale" datatype="int" ucd="stat.param" value="1">
<PARAM name="ATrous Filter" datatype="char" ucd="meta.code;stat" value="B3 spline function">
<FIELD name="ID" ID="col1" ucd="meta.id" datatype="int" width="4"/>
<FIELD name="Name" ID="col2" ucd="meta.id;meta.main" datatype="char" arraysize="14"/>
<FIELD name="RA" ID="col3" ucd="pos.eq.ra;meta.main" ref="J2000" datatype="float" width="10" precision="6" unit="deg"/>
<FIELD name="Dec" ID="col4" ucd="pos.eq.dec;meta.main" ref="J2000" datatype="float" width="10" precision="6" unit="deg"/>
<FIELD name="w_RA" ID="col3" ucd="phys.angSize;pos.eq.ra" ref="J2000" datatype="float" width="7" precision="2" unit="arcmin"/>
<FIELD name="w_Dec" ID="col4" ucd="phys.angSize;pos.eq.dec" ref="J2000" datatype="float" width="7" precision="2" unit="arcmin"/>
<FIELD name="Vel" ID="col4" ucd="phys.veloc;src.dopplerVeloc" datatype="float" width="9" precision="3" unit="km/s"/>
<FIELD name="w_Vel" ID="col4" ucd="phys.veloc;src.dopplerVeloc;spect.line.width" datatype="float" width="8" precision="3" unit="km/s"/>
<FIELD name="Integrated_Flux" ID="col4" ucd="phys.flux;spect.line.intensity" datatype="float" width="10" precision="3" unit="km/s"/>
<DATA>
<TABLEDATA>
<TR>
<TD>   1</TD><TD> J0609-2200</TD><TD> 92.410416</TD><TD>-22.013390</TD><TD>  48.50</TD><TD>  39.42</TD><TD>  213.061</TD><TD>  65.957</TD><TD>    17.572</TD>
</TR>
<TR>
<TD>   2</TD><TD> J0608-2605</TD><TD> 92.042633</TD><TD>-26.085157</TD><TD>  44.47</TD><TD>  39.47</TD><TD>  233.119</TD><TD>  39.574</TD><TD>     4.144</TD>
</TR>
<TR>
<TD>   3</TD><TD> J0606-2724</TD><TD> 91.637840</TD><TD>-27.412022</TD><TD>  52.48</TD><TD>  47.57</TD><TD>  302.213</TD><TD>  39.574</TD><TD>    17.066</TD>
</TR>
(... table truncated for clarity ...)
</TABLEDATA>
</DATA>
</TABLE>
</RESOURCE>
</VOTABLE>
```

F Example Karma Annotation File output

This is the format of the Karma Annotation file, showing the locations of the detected objects. This can be loaded by the plotting tools of the Karma package (for instance, `kvis`) as an overlay on the FITS file.

```
# Duchamp Source Finder results for
#  cube /DATA/SITAR_1/whi550/cubes/H201_abcde_luther_chop.fits
COLOR RED
COORD W
CIRCLE 92.3376 -21.9475 0.403992
TEXT 92.3376 -21.9475 1
CIRCLE 91.9676 -26.0193 0.37034
TEXT 91.9676 -26.0193 2
CIRCLE 91.5621 -27.3459 0.437109
TEXT 91.5621 -27.3459 3
CIRCLE 92.8285 -21.6344 0.269914
TEXT 92.8285 -21.6344 4
CIRCLE 90.1381 -28.9838 0.234179
TEXT 90.1381 -28.9838 5
CIRCLE 89.72 -26.6513 0.132743
TEXT 89.72 -26.6513 6
CIRCLE 94.2743 -27.4003 0.195175
TEXT 94.2743 -27.4003 7
CIRCLE 92.2739 -21.6941 0.134538
TEXT 92.2739 -21.6941 8
CIRCLE 89.7133 -25.4259 0.232252
TEXT 89.7133 -25.4259 9
CIRCLE 90.2206 -21.6993 0.266247
TEXT 90.2206 -21.6993 10
CIRCLE 93.8581 -26.5766 0.163153
TEXT 93.8581 -26.5766 11
CIRCLE 91.176 -26.1064 0.234356
TEXT 91.176 -26.1064 12
CIRCLE 90.2844 -23.6716 0.299509
TEXT 90.2844 -23.6716 13
CIRCLE 93.8774 -22.581 0.130925
TEXT 93.8774 -22.581 14
CIRCLE 94.3882 -23.0934 0.137108
TEXT 94.3882 -23.0934 15
CIRCLE 93.0491 -21.8223 0.202928
TEXT 93.0491 -21.8223 16
CIRCLE 94.0685 -21.5603 0.168456
TEXT 94.0685 -21.5603 17
CIRCLE 86.0568 -27.6095 0.101113
TEXT 86.0568 -27.6095 18
CIRCLE 88.7932 -29.9453 0.202624
TEXT 88.7932 -29.9453 19
```

G Robust statistics for a Normal distribution

The Normal, or Gaussian, distribution for mean μ and standard deviation σ can be written as

$$f(x) = \frac{1}{\sqrt{2\pi\sigma^2}}\, e^{-(x-\mu)^2/2\sigma^2}.$$

When one has a purely Gaussian signal, it is straightforward to estimate σ by calculating the standard deviation (or rms) of the data. However, if there is a small amount of signal present on top of Gaussian noise, and one wants to estimate the σ for the noise, the presence of the large values from the signal can bias the estimator to higher values.

An alternative way is to use the median (m) and median absolute deviation from the median (s) to estimate μ and σ. The median is the middle of the distribution, defined for a continuous distribution by

$$\int_{-\infty}^{m} f(x)\mathrm{d}x = \int_{m}^{\infty} f(x)\mathrm{d}x.$$

From symmetry, we quickly see that for the continuous Normal distribution, $m = \mu$. We consider the case henceforth of $\mu = 0$, without loss of generality.

To find s, we find the distribution of the absolute deviation from the median, and then find the median of that distribution. This distribution is given by

$$\begin{aligned} g(x) &= \text{distribution of } |x| \\ &= f(x) + f(-x),\ x \geq 0 \\ &= \sqrt{\frac{2}{\pi\sigma^2}}\, e^{-x^2/2\sigma^2},\ x \geq 0. \end{aligned}$$

So, the median absolute deviation from the median, s, is given by

$$\int_{0}^{s} g(x)\mathrm{d}x = \int_{s}^{\infty} g(x)\mathrm{d}x.$$

Now, $\int_0^\infty e^{-x^2/2\sigma^2}\mathrm{d}x = \sqrt{\pi\sigma^2/2}$, and so $\int_s^\infty e^{-x^2/2\sigma^2}\mathrm{d}x = \sqrt{\pi\sigma^2/2} - \int_0^s e^{-\frac{x^2}{2\sigma^2}}\mathrm{d}x$. Hence, to find s we simply solve the following equation (setting $\sigma = 1$ for simplicity – equivalent to stating x and s in units of σ):

$$\int_0^s e^{-x^2/2}\mathrm{d}x - \sqrt{\pi/8} = 0.$$

This is hard to solve analytically (no nice analytic solution exists for the finite integral that I'm aware of), but straightforward to solve numerically, yielding the value of $s = 0.6744888$. Thus, to estimate σ for a Normally distributed data set, one can calculate s, then divide by 0.6744888 (or multiply by 1.4826042) to obtain the correct estimator.

Note that this is different to solutions quoted elsewhere, specifically in Meyer et al. (2004), where the same robust estimator is used but with an incorrect conversion to standard deviation – they assume $\sigma = s\sqrt{\pi/2}$. This, in fact, is the conversion used to convert the *mean* absolute deviation from the mean to the standard deviation. This means that the cube noise in the HIPASS catalogue (their parameter $\mathrm{Rms}_{\mathrm{cube}}$) should be 18% larger than quoted.

H How Gaussian noise changes with wavelet scale.

The key element in the wavelet reconstruction of an array is the thresholding of the individual wavelet coefficient arrays. This is usually done by choosing a level to be some number of standard deviations above the mean value.

However, since the wavelet arrays are produced by convolving the input array by an increasingly large filter, the pixels in the coefficient arrays become increasingly correlated as the scale of the filter increases. This results in the measured standard deviation from a given coefficient array decreasing with increasing scale. To calculate this, we need to take into account how many other pixels each pixel in the convolved array depends on.

To demonstrate, suppose we have a 1-D array with N pixel values given by F_i, $i = 1, ..., N$, and we convolve it with the B_3-spline filter, defined by the set of coefficients $\{1/16, 1/4, 3/8, 1/4, 1/16\}$. The flux of the ith pixel in the convolved array will be

$$F'_i = \frac{1}{16}F_{i-2} + \frac{1}{4}F_{i-1} + \frac{3}{8}F_i + \frac{1}{4}F_{i+1} + \frac{1}{16}F_{i+2}$$

and the flux of the corresponding pixel in the wavelet array will be

$$W'_i = F_i - F'_i = \frac{-1}{16}F_{i-2} - \frac{1}{4}F_{i-1} + \frac{5}{8}F_i - \frac{1}{4}F_{i+1} - \frac{1}{16}F_{i+2}$$

Now, assuming each pixel has the same standard deviation $\sigma_i = \sigma$, we can work out the standard deviation for the wavelet array:

$$\sigma'_i = \sigma\sqrt{\left(\frac{1}{16}\right)^2 + \left(\frac{1}{4}\right)^2 + \left(\frac{5}{8}\right)^2 + \left(\frac{1}{4}\right)^2 + \left(\frac{1}{16}\right)^2} = 0.72349\ \sigma$$

Thus, the first scale wavelet coefficient array will have a standard deviation of 72.3% of the input array. This procedure can be followed to calculate the necessary values for all scales, dimensions and filters used by *Duchamp*.

Calculating these values is clearly a critical step in performing the reconstruction. Starck & Murtagh (2002) did so by simulating data sets with Gaussian noise, taking the wavelet transform, and measuring the value of σ for each scale. We take a different approach, by calculating the scaling factors directly from the filter coefficients by taking the wavelet transform of an array made up of a 1 in the central pixel and 0s everywhere else. The scaling value is then derived by taking the square root of the sum (in quadrature) of all the wavelet coefficient values at each scale. We give the scaling factors for the three filters available to *Duchamp* on the following page. These values are hard-coded into *Duchamp*, so no on-the-fly calculation of them is necessary.

Memory limitations prevent us from calculating factors for large scales, particularly for the three-dimensional case (hence the – symbols in the tables). To calculate factors for higher scales than those available, we note the following relationships apply for large scales to a sufficient level of precision:

- 1-D: factor(scale i) = factor(scale $i-1$)/$\sqrt{2}$.
- 2-D: factor(scale i) = factor(scale $i-1$)/2.
- 1-D: factor(scale i) = factor(scale $i-1$)/$\sqrt{8}$.

- **B_3-Spline Function:** $\{1/16, 1/4, 3/8, 1/4, 1/16\}$

Scale	1 dimension	2 dimension	3 dimension
1	0.723489806	0.890796310	0.956543592
2	0.285450405	0.200663851	0.120336499
3	0.177947535	0.0855075048	0.0349500154
4	0.122223156	0.0412474444	0.0118164242
5	0.0858113122	0.0204249666	0.00413233507
6	0.0605703043	0.0101897592	0.00145703714
7	0.0428107206	0.00509204670	0.000514791120
8	0.0302684024	0.00254566946	–
9	0.0214024008	0.00127279050	–
10	0.0151336781	0.000636389722	–
11	0.0107011079	0.000318194170	–
12	0.00756682272	–	–
13	0.00535055108	–	–

- **Triangle Function:** $\{1/4, 1/2, 1/4\}$

Scale	1 dimension	2 dimension	3 dimension
1	0.612372436	0.800390530	0.895954449
2	0.330718914	0.272878894	0.192033014
3	0.211947812	0.119779282	0.0576484078
4	0.145740298	0.0577664785	0.0194912393
5	0.102310944	0.0286163283	0.00681278387
6	0.0722128185	0.0142747506	0.00240175885
7	0.0510388224	0.00713319703	0.000848538128
8	0.0360857673	0.00356607618	0.000299949455
9	0.0255157615	0.00178297280	–
10	0.0180422389	0.000891478237	–
11	0.0127577667	0.000445738098	–
12	0.00902109930	0.000222868922	–
13	0.00637887978	–	–

- **Haar Wavelet:** $\{0, 1/2, 1/2\}$

Scale	1 dimension	2 dimension	3 dimension
1	0.707167810	0.433012702	0.935414347
2	0.500000000	0.216506351	0.330718914
3	0.353553391	0.108253175	0.116926793
4	0.250000000	0.0541265877	0.0413398642
5	0.176776695	0.0270632939	0.0146158492
6	0.125000000	0.0135316469	0.00516748303