

IMAGIC-COMMAND

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&SHIFT-IMAGE
&SHIFT-RANDOMLY
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&THREED-FILTER
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&THREED-FOURIER-CROSS-INFO
&THREED-IMPOSE-SYMMETRY
&THREED-MASK
&THREED-MODEL-MOLECULE
&THREED-NORM-VARIANCE
&THREED-PEAK-FIND
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&THREED-RESTACK
&THREED-ROTATE
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&THREED-SHELL
&THREED-SHIFT
&THREED-SMOOTH
&THREED-SPHERICAL-TO-CARTESIAN
&THREED-STEREO
&THREED-SUBFILE
&THREED-SURFACE-VIEWS
&THREED-TEST-IMAGE
&THREED-THINNING-MASK
&THREED-TOMOGRAPHIC-RECONSTRUCT
&THREED-TRANSLATE

&THREED-XZ-TRANSDPOSE
&THREED-Z-INTERPOLATION
&THREED-Z-OPERATIONS
&THREED-Z-SHIFT
&THREED-ZOOM
&THRESHOLD-IMAGE
&TRANSFER-FUNCTION
&TRANSDPOSE-IMAGE
&TRUE-THREED-RECONSTRUCTION
&UP-SIDE-DOWN
&VIEW-IMAGE
&WALSH-TRANSFORMATION
&ZERO-FLOAT-IMAGES
&ZOOM-IMAGE

* ICM-file: util:gen_util.icm
-

The "*" is a legitimate answer to every question that appears on the terminal screen. Its normal operation is to break off the current operation and return to the IMAGIC program. In the IMAGIC supervising program, however, it will bring you back to the host's operating system; it is thus equivalent to END, EXIT or BYE.

? ICM-file: util:gen_util.icm
-

The "?" (question mark) is an important tool in the IMAGIC image processing software system. It is a legitimate answer to every question that appears on the terminal screen. As such it is normally synonymous to "HELP".

However, at the IMAGIC-COMMAND level "?" will merely give a list of the matching commands, whereas "HELP" gives the additional explanation on the matching commands. At this level, "?" is normally equivalent to "MENU" For a list of matching commands type:

? NAME
? *NAME

or, equivalently:

MENU NAME
MENU *NAME

**To continue give RETURN, or give a "*" to stop :

IMAGIC-COMMAND : abbr-help

Type a "?" or "HELP" for help on the abbreviation : ?

IMAGIC-COMMAND names may be abbreviated as long as the abbreviated name is not ambiguous. As an example of the possible ways to abbreviate a IMAGIC-COMMAND name we use a long example "REALS-FROM-IMAGE-FILE". Possible abbreviations:

"REALS-FROM"	"reals"	"r-from"
"r-f-i"	"R--I"	"REA"

All hyphens ("-") preceding a partial word in the abbreviation MUST be given in the abbreviated name.

Not all of these abbreviations will correspond unambiguously with the command.

NOTE 1: Try the abbreviation rules in combination with the MENU command like in: "MEN -help" or in: "? r--i"

**To continue give RETURN, or give a "*" to stop :

NOTE 2: if a matching command name is found in the user command file, the system command file is no longer searched. Therefore, a command in the user command file always OVERRULES system commands which could also match with the abbreviated command given.

Add a constant value to all pixels in an image (or in a sequence of images). This command will lead you to the ARITHM program which has many more options than just the adding of a constant.

Add images to one another. This command will lead you to the TWOIMAG program which has many more options than just the adding of two images.

command) is designed for large images mainly. For manipulating smaller images the INCORE programs are more efficient. Hint type: "? *INCO" in the IMAGIC-COMMAND mode to find out what the options are.

ADD-NOISE

ICM-file: stand:standard.icm

Add a noise to all pixels in an image (or in a sequence of images). This command will lead you to the ARITHM program which has many more options than just the adding of noise.

ALIGN-DIRECT-IMAGES

ICM-file: align:align.icm

This is the workhorse of the alignment procedures. It aligns images relative to a reference using the image information directly rather than using the autocorrelations of the images.

The input images to this command should be relatively well centered and have normally undergone standardization using the ALIGN-PREPARE-MOLECULES or the ALIGN-PREPARE-FILTERED commands, for example (in particular, have a look at the corresponding INCORE commands). The input images may also already have undergone alignments with this or one of the other alignment commands.

The successive interpolations needed for the rotations/shifts in such an iterative alignment approach leads to a degradation of the highest frequency components of the images due to the continuous interpolations. In IMAGIC, however, an equivalent rotation angle and

**To continue give RETURN, or give a "*" to stop :
equivalent shift parameters are calculated allowing the aligned image to be recalculated at all times from the original input file with just one single interpolation (EQUIVALENT-ROTATION).

REMARKS:

With this command the rotational alignment is performed with the image itself rather than with its ACF (Auto-Correlation-Function) in which the fine detail ("phases" are gone) has largely disappeared.

However, contrary to the ACF's, the images themselves are NOT centered around the origin making that the alignment is rather an approximation which should be repeated iteratively. Normally, an estimated visual centering is a

REFERENCE (of direct alignment technique):

**To continue give RETURN, or give a "*" to stop :

Steinkillberg & Schramm, "Eine verbesserte Drehkorrelationsmethode fuer die Strukturbestimmung biologischer Makromolekuehle durch Mittelung elektronenmikroskopischer Bilder", Hoppe-Seylers Z.Physiol.Chem 361 (1980) 1363-1369.

ALIGN-FIRST-REFERENCE

ICM-file: align:align.icm

The input images to this command should be relatively well centered and have normally undergone standardization (using INCORE-PREPARE-FILTERED for example).

After a first (direct) alignment of the images relative to the first (noisy) reference, the program sums those images of the aligned data-set which have the highest cross-correlation coefficient relative to the reference image.

The new image-sum is then contoured with the contour used for the first reference, and the resulting image is used as a new reference for a new (direct) alignment.

NOTE: You have also the option to do "mirror alignments", i.e., alignments with mirrored versions of the reference image.

**To continue give RETURN, or give a "*" to stop :

All calculations are done IN CORE (= bloody fast)

The ALIFIRST program associated with this command replaces the long IMAGIC command file originally associated with this command. The new program is easier to maintain, faster, has more options, and a more flexible user-interface than the earlier command file, and it represents the current trend in IMAGIC to move away from command files towards stand-alone programs.

ALIGN-MAGNIFICATION

ICM-file: align:align.icm

Find best magnification factor between a set of 2D images and a specified 2D reference image.

A reference image is (de)magnified into a range of differently zoomed images and the input images are compared to this set by means of simple correlation values.

This program allows you to determine the center of mass of an image.

This command actually leads you to the ALIMASS program which has many more options to center images:

MASK: Shifting the center of mass of the MASK (outside = zero) imposed on the input image to the logical center of the output image (half+1 in both vertical and horizontal directions). The weight of all non-zero pixels in the input image is set to unity in calculating the center of mass: this means the image is shifted to the center of mass of the mask rather than of the object in the image.

ABSOLUTE: The absolute value of the image densities is used to find the "mass center". This option is intended to be an alternative to the simple mass-centering option

**To continue give RETURN, or give a "*" to stop :
to be used for zero-average phase-contrast type of images.

SELF-CENTER: The input image is iteratively centered relative to a rotationally symmetrized version of itself so as to obtain a good centering of relatively globular particles.

Same command as CENTER-IMAGES.

This command is a nice tool for multi-reference alignments. if the first alignment is done (use ALIGN-FIRST-REFERENCE or ALIGN-DIRECT).

The input images will be aligned to the reference image. In the next step equivalent rotation is done and the new alignment is compared with the (best) old alignment of the input file ("conditional copy"). Only the "best" of the two aligned images is stored in the output file.

NOTE: You have also the choice to do "mirror alignment".

NOTE: All calculations are done IN CORE.

This command is used to perform an incore multi-reference alignment with noisy references.

The input images to this command are normally already (roughly) aligned images, aligned relative to one or more earlier references.

After a first (direct) alignment of the images relative to the new (noisy) reference, those images of the aligned set are added together that have the highest cross-correlation coefficient relative to the reference image.

The new image-sum is then contoured with the contour used for the input reference, and the resulting image is then used as a new reference for a second (direct) alignment to refine the alignment.

In the next step the equivalent rotation is done and the

**To continue give RETURN, or give a "*" to stop :
new alignment is compared with the (best) old alignment of the input file ("conditional copy"). Only the "best" of the two aligned images is stored in the output file.

NOTE: You have also the choice to do "mirror alignment".

NOTE: All calculations are done IN CORE

Every output image of this command will contain the image aligned relative to the current reference if the new alignment was better the old alignment in the input file. Else the old one is stored in the output file.

The original images must be reachable for an "equivalent rotation" with only one interpolation. These are commonly the band-pass filtered images.

The reference comes from a separate file, and this file is only used once. The reference has ordinarily been contoured interactively and pretreated. If you give no

**To continue give RETURN, or give a "*" to stop :
location number the LAST image in the file will be the one used as reference.

NOTE : If an image has been mirrored during an alignment procedure its reference number is negative.
Please only specify POSITIVE numbers.

An intermediate sum of the best aligned images will be used as a new reference for a second alignment step. The quality of the second (intermediate) reference will depend on how many images are added into it. Please give the number of images to be added.

density contributions. NOT necessary for ice ???? !!!!!

Note: -999. means no threshold

An intermediate sum of the best aligned images will be used

**To continue give RETURN, or give a "*" to stop :
as a new reference for a second alignment step. Please
give the filename for this image file.

Mirror alignment means that after a first alignment of an
image to the current reference the image is mirrored and
the alignment is redone. If this mirror alignment is
better the aligned mirror image is stored, else the
unmirrored is used.

NOTE : If an image has been mirrored during an
alignment procedure its reference number is
negative.

Same command as NOISY-MRALIGN

ALIGN-PARALLEL ICM-file: align:align.icm

Command to align images to the corresponding images in a
reference file (location by location).
That means: the input image in the first specified location
is aligned to the image in first specified reference file
location, image #2 to reference #2 and so on.

This command is very helpful during a 3D reconstruction:
the (input) projection images (used to calculate a 3D
structure) can be aligned to this reconstruction. The 3D
model is reprojected into the same directions as the (input)
projections (command THREED-FORWARD). Then the (input)
projections can be aligned to these reprojections location
by location using ALIGN-PARALLEL.

ALIGN-ROTATIONAL ICM-file: align:align.icm

This program allows to align images ROTATIONALLY only.

The input images should be relatively well centered and
have normally undergone standardisation using for example
the INCORE-PREPARE-FILTERED command.

The input images may already have undergone alignments with
this or one of the other alignment commands.

The output images of this program will contain images

alignment only). The output file must be different from the input file.

The reference image required for the rotational alignment is normally extracted from somewhere and written to its own file. Using the DISPLAY program, a contour is ordinarily drawn around it. The image is then PRETREATED by zeroing everything outside this contour, and by thresholding

**To continue give RETURN, or give a "*" to stop :
everything inside this contour. This final pretreated image is the LAST image in the reference file.

When doing a MULTI-REFERENCE-ALIGNMENT, you may want to keep track of the references by numbering them sequentially, 1, 2, 3, etc. This number is simply written into the header of the output file into position IDAT(107). The program will prompt you for this number.

The ALIDIR program (associated with this command) also allows you to restrict the rotation to a specified range. This may be useful for 2D crystals or for cases where you have some symmetry in your single molecules.

ALIGN-SELF-CENTER

ICM-file: align:align.icm

This program aligns images using a novel yet somewhat tricky approach. A rotationally averaged version of each input image is generated, and each input image is then translationally aligned relative to that rotationally averaged version of itself. The procedure is normally iterated twice. Since all translational alignments are performed with correlation techniques (many FFTs) the procedure takes some time to complete.

Nevertheless this approach may be one of the best techniques available to roughly center a set of molecular images, reference images, or any other type of blobs. Have fun trying out this new approach.

The algorithm is implemented as an option in the ALIMASS program (as of April 1991) which is part of the IMAGIC-5 ALIGN module.

ALIGN-TANDEM

ICM-file: align:align.icm

Command to subsequently align images location by location, i.e. the image in loc#2 is aligned to the image in loc#1, the image in loc#3 is aligned to the ALIGNED image of loc#2 ... the image in loc#(n) is aligned to the ALIGNED image of loc#(n-1) ... etc.

The purpose of ALIGN-TANDEM is to align 2D sections of a 3D object. The aligned sections can then be treated with any THREED-... IMAGIC command, especially command THREED-SEXY can be used to get surface representations of the 3D object.

NOTE: The program performs in-core alignments.

ALIGN-TRANSLATIONAL

ICM-file: align:align.icm

This program allows to align images TRANSLATIONALLY only. (actually, the ALIDIR program associated with this command has more options than just this translational alignment).

The input images should be relatively well centered and have normally undergone standardisation using for example the INCORE-PREPARE-FILTERED command.

The input images may already have undergone alignments with this or one of the other alignment commands.

The output images of this program will contain images aligned relative to the current reference (translational alignment only). The output file must be different from the input file.

The reference image is normally extracted from somewhere and written to its own file. Using the DISPLAY program, a

**To continue give RETURN, or give a "*" to stop :
contour is ordinarily drawn around it. The image is then PRETREATED by zeroing everything outside this contour, and by thresholding everything inside this contour. This final pretreated image is the LAST image in the reference file.

When doing a MULTI-REFERENCE-ALIGNMENT, you want to keep track of the references by numbering them sequentially, 1, 2, 3, etc. This number is simply written into the header of the output file into position IDAT(107). The ALIDIR program will prompt you for this number.

Occasionally some images are shifted out of the image field when compared w.r.t. certain references. Maybe the image is bad. Maybe it just doesn't jive with this particular reference whereas w.r.t. another reference it would be well aligned. The best thing then is just to do nothing. The ALIDIR program accepts a maximum radial shift beyond which you don't shift the image. Either you can specify this in pixels directly, or as a fraction of the file size.

**To continue give RETURN, or give a "*" to stop :

ANGULAR-RECONSTITUTION

ICM-file: angrec:angrec.icm

Command to do ANGULAR-RECONSTITUTION.

It can be used for various tasks like finding the Euler orientations of projections relative to each other or relative to a set of projection images which have already had Euler angles assigned to them (anchor set). ANGULAR exploits the KNOWN pointgroup symmetry of the oligomeric molecule during the "brute-force" search for the best Euler orientation of the new projection.

Reference:

Marin van Heel,

"Angular Reconstitution: a-posteriori determination of projection directions for 3D reconstruction",
Ultramicroscopy 21 (1987) 111-124.

Marin van Heel et al.

**To continue give RETURN, or give a "*" to stop :

"Single-particle electron microscopy: towards atomic resolution",
Quart. Rev. Biophys. (200) 307-369.

APPEND-IMAGE-FILE

ICM-file: stand:standard.icm

Append a set of images from one file to the end of another file with the same characteristics, i.e., the images of the input and output file must be of the same type and size.

A true copy is performed, i.e., there is no encoding or decoding of data.

NOTE: This may cause troubles if the line-length is not a multiple of TWO and your data are of type 'PACK'.

ARITHM-WITH-CURVE

ICM-file: spectra:spectra.icm

Various arithmetic operations on 1D data. A single input curve or a sequences of such curves present in the input file are manipulated to produce an output file (may be the same as the input file) containing the manipulated curve(s)

Options include:

ADD a constant to the curve

SUBTRACT a constant from curve values

MULTIPLY curve values by a constant

DIVIDE curve values by a constant

LOGARITHM the values along the curve

**To continue give RETURN, or give a "*" to stop :
various MASKING options,

FILTER options etc...

For an up-to-date account of all available options,
start the program interactively and ask for more help.

ARITHMETIC-WITH-IMAGE

ICM-file: stand:standard.icm

Performs various arithmetic and masking operations on image
data as well as on Fourier Transforms.

Options are:

ADD : Add a constant value to input image

CIRCLE : Output image (transform) is input image
multiplied by a circular mask

CORRECT : Option used to reverse the contrast of the FT
of an electron micrograph to correct for
reversals of the transfer function.

DIVIDE : Divide input image by a constant

GAUSSIAN : Output image (transform) is input image

**To continue give RETURN, or give a "*" to stop :
multiplied by a Gaussian mask

LOGARITHM: Output image is the natural log of input image

LORENTZIAN: Output image (transform) is input image
multiplied by a Lorentzian mask

NOISE : Output image (transform) is input image
with noise added to it

MIRROR : Image is mirrored, i.e., image lines are
flipped over

MULTIPLY : Multiply input image by a constant

RING : Only a ring of the input image (transform) is

SQUARES : Output image is the square of the input image

**To continue give RETURN, or give a "*" to stop :

SUBTRACT : Subtract a constant from input image

THREED : The mask that is applied is three-dimensional
The section number (that is the location number)
is also included in the mask: the mask is
thus ball-shaped, ellipsoidal or the Gaussian
equivalent of such a shape. NOTE that with this
option there is a difference between giving the
radius as a fraction or as pixels. As fraction
the mask will be an ellipsoid that adapts to the
to the file dimensions in X, Y and Z directions.
This option can be combined with the earlier
masking options (GAUSS, CIRCLE, LORENTZ...).

THRESHOLD: Output image only contains the input image
densities above a certain threshold

AUTO-CORRELATION

ICM-file: fft:fft.icm

Autocorrelation of (large) images in IMAGIC files.

The autocorrelation is calculated in two steps: first
a 2D image is Fourier-transformed to find the complex
transformed of the image (phases and amplitudes).
Then, the complex value in each of the pixels in the
the complex FT is squared (which operation makes the
values real) prior to a reverse Fourier transform which
brings us back to real space.

Since the input images are considered to be cyclical for the
FFT operations (the left edged touches the right edge, the
top edge touches the bottom one), one may be bothered by
so-called "wrap-around" artefacts when calculating the ACFs
(also known as "aliasing"). To avoid this effect one needs
to mask the image with, for example, a circular mask,
and/or pad the input image with zeroes (after floating the
image to zero average density...). Use such commands as

**To continue give RETURN, or give a "*" to stop :

"CUT-IMAGE" and/or "MASK-IMAGE" to perform such operations.

One may pad the images with zeroes to twice their original
linear dimensions (PAD in SUBFILE) to absolutely avoid
the effect. However, since many images are already
supplied with a mask which is smaller than the image,
the SMALLPAD option (padding to 3/2 of the linear
file dimensions) is often sufficient and may save
a lot of CPU time.

programs also support ACF functions like SPECIAL-FUNCTIONS (in module DSCF) and INCORE-FFT2D-OPERATIONS (module FFT).

NOTE also that we now know that for most operations the SCF (Self-Correlation-Function; command: SEL_CORRELATION) gives more satisfactory results than the ACF.

AVERAGE-NFOLD-ROTATIONAL ICM-file: incore:incore.icm

Compute n-fold rotational averages of a set of (centered) incore images. The input images are assumed to be centered at the geometric center of the input image(s).

Same command as IMPOSE-SYMMETRY.

For 3D symmetrisation please use: THREED-IMPOSE-SYMMETRY.

AVERAGE-ROTATIONAL ICM-file: stand:standard.icm

For a given input image (small or large), the rotational average is calculated and it is outputted in two fundamentally different ways:

1. As an image of the same size as the input image. This output image can, for example be used to center the original input image using some form of translational alignment with the rotational symmetric version as reference.
2. As a plot (".PLT" style file) which can be brought to high-quality hardcopy by using one of the plotting commands ("PLOT-ALL", for example)

IMAGIC-COMMAND : +help B

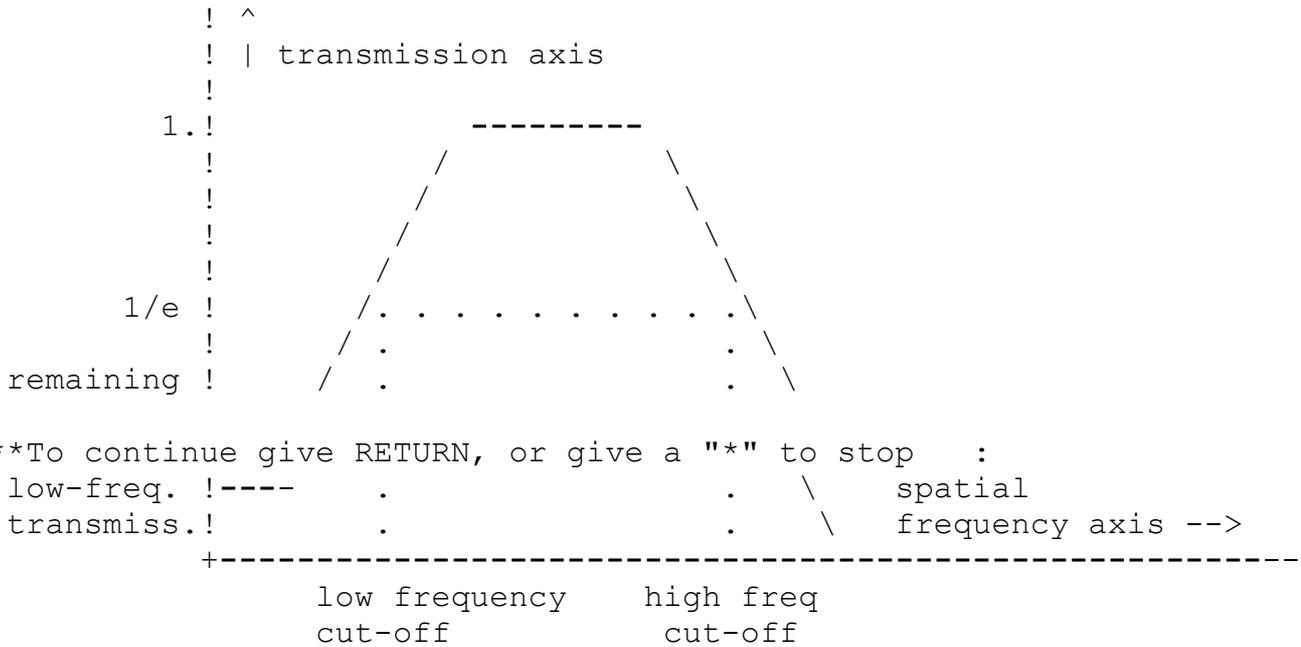
BAH ICM-file: misc:misc.icm

A simple command with a simple result.

BAND-PASS-FILTER ICM-file: fft:fft.icm

This command will bring you to the FILT_ALL program in which the band-pass filtering in only one of the options.

following parameters:



The HIGH frequency cut-off is associated with a LOW-PASS Gaussian filter which will gradually cut off spatial frequencies higher than this value.

The LOW frequency cut-off is associated with a HIGH-PASS Gaussian filter which will gradually cut off spatial frequencies lower than this value.

The remaining transmission allows you to leave a fraction of the low-frequency components (say, 0.001) intact such that one always restore these low-frequency components at a later stage by inverse filtering, without dividing by zero.

Same command as: BAND-PASS-FILTER

**To continue give RETURN, or give a "*" to stop :

BLOCK-CONVOLUTION-2D-FILTER ICM-file: block:block.icm

A two-dimensional block-convolution is filtering operation produces an output image by averaging the input pixels within a rectangular window (a "block") to produce one pixel of the output image. This type of operation can be rather fast since "running averages" algorithms are essentially independent of the size of the window. There are two main ways of using this filter:

1. Low pass filter:

One output pixel is simply the average of all pixels within the block-filter window. The larger the size of the window, the stronger the low-pass filter effect.

2. High pass filter:

The output image is created by subtracting the low-pass image described above from the original input image. This

**To continue give RETURN, or give a "*" to stop :
will thus lead to emphasizing the fine details in the output image.

However, with some effort you can do more complicated filters like band-pass filters by consecutive application of the block filter operation: first do a high-pass filter with a large window followed by a low-pass filter with a small window.

BLOW-UP-IMAGE

ICM-file: stand:standard.icm

Blow up an image to a larger image format by interpolation. The blow up factors may be different for the X and Y directions and the command may thus be used to correct for the weird aspect-ratios that some display systems or hardcopy devices have. All aspect ratios not equal one are weird. This command leads you to the ROTATE program into which all these options are built in.

The difference between BLOW-UP and ZOOM-IMAGE is that the ZOOM command magnifies or demagnifies the image within the same image file format. ZOOM thus allows for more subtle magnification changes than BLOW-UP.

The BLOW-UP command is often used to magnify and beautify end results of image processing. One sometimes applies CONTOURS to the blown-up results to please the eye, or the referees of a paper you are working on.

**To continue give RETURN, or give a "*" to stop :

BYE

ICM-file: util:gen_util.icm

The "BYE" command will bring you back to the host's operating system; it is thus equivalent to "END", "EXIT" or "*". If you are in MODE-ACCUMULATE, that mode of operation will NOT be discontinued. You can thus continue to accumulate commands after leaving IMAGIC with one of these commands.

IMAGIC-COMMAND : +help C

CENTER-IMAGES

ICM-file: align:align.icm

This command centers images.

Different options are available for centering the input image(s):

MASS: Straightforward shifting the center of mass of the input image to the logical center of the output image (half+1 in both vertical and horizontal directions).

MASK: Shifting the center of mass of the MASK (outside = zero) imposed on the input image to the logical center of the output image (half+1 in both vertical and horizontal directions). The weight of all non-zero pixels in the input image is set to unity in calculating the center of mass: this means the image is shifted to the center of mass of the mask rather than of the object in the image.

**To continue give RETURN, or give a "*" to stop :

ABSOLUTE: The absolute value of the image densities is used to find the "mass center". This option is intended to be an alternative to the simple mass-centering option to be used for zero-average phase-contrast type of images.

SELFCENTER: The input image is iteratively centered relative to a rotationally symmetrized version of itself so as to obtain a good centering of relatively globular particles.

CLASS-NAMES-MSA

ICM-file: msa:msa.icm

This command uses a ".CLS" input file (produced by MSA-CLASSIFY) to generate a file in which the NAMES of the input images, (spectra, sequence-histograms, etc.) are printed out by class in the same order as they appear in the CLS file. NOTE that this option is only useful for those IMAGIC files in which the names of the individuals have been explicitly written into the header at some time in the past!

Special versions of this command/program may exist for specific applications (such as protein-SEQUENCE analysis) which produce more extended (and more application-specific) output.

CLEAR-PROTECTION

ICM-file: util:unx_util.icm

Clear the protection of a protected image file.
It is merely a direct call to the UNIX utilities.

COARSER-SAMPLING

ICM-file: stand:standard.icm

Generate a new image file with fewer pixels, i.e., fewer pixels per line and fewer lines. The output pixels will be generated by averaging 2x2, or 3x3, or 4x4 etc. input pixels.

WARNING: the logical origin of the image (IYLP/2+1) may be shifted by half a pixel in this operation/ Unshifted (but interpolated) coarser images are obtained by low-pass filtering the image and changing the file size using the BLOW-UP command.

COMPUTE-RECIPROCAL-VECTORS

ICM-file: crystal:crystal.icm

For poor people who don't own a pocket calculator or for one reason or the other refuse to use it.

This programs helps you convert the positions of peaks in power spectra into reciprocal lattice vectors which you can feed to the FOURIER-PEAK-FILTERING command.

CONTOUR-IMAGE

ICM-file: stand:standard.icm

Contour an image: the output image will be the same as the input image but will have isolines of densities superimposed.

The resulting images are often very pleasing to the eye, and - even more important - pleasing to the eye of the scientific journal editor. However, images without isolines are often easier to interpret visually. Iso-lines tend to attract the eye of the observer and thus tend to distract from the real image information.

Positive image areas will contain BLACK (=negative) contours and negative image areas will have WHITE (=positive) contours, at least, that is one of the options you will have. The default values for the contours are aimed at images with (which is standard in IMAGIC) zero average density and standard deviation of 10. The user may, of course, override the contour level defaults.

**To continue give RETURN, or give a "*" to stop :

contour stored in a "plt" file to mask an image
please use command: IMPOSE-PLT-CONTOUR.

CONVERT-IMAGE-FORMAT

ICM-file: stand:standard.icm

This command is used to convert images from one IMAGIC format to another. For example an image of 'PACK' or 'RECO' type may be converted to 'REAL' format. Moreover, the COMPLEX data type may be converted to REAL amplitudes, phases, real or imaginary parts.

Import and export of image files to and from the IMAGIC formats is performed by the command IMPORT-EXPORT.

NOTE:

Raw images inputted from digitizing devices typically have only 8 bits/pixel (one byte/pixel), i.e., are of the IMAGIC type 'PACK'. It is very difficult to do anything useful with such images since any image processing will typically cause over- and under-flow situations. The 'PACK' format is, of course, very good for long-term storage since it is so compact. For processing, however, convert these images

**To continue give RETURN, or give a "*" to stop :
to 'REAL' as soon as possible. If YOU don't do it, some
IMAGIC programs will do it implicitly.

COPY-IMAGES

ICM-file: stand:standard.icm

Copy an image file using COPYIM. The COPYIM command is fast since it does a raw copy of the image data without decoding the data. You nevertheless normally have the option to do a full copy using the host operating system which may be even faster than the IMAGIC copy. The IMAGIC copy, however, lets you copy parts of an input file (just specific locations) to the output or even to the end of the same (the input!) file.

CORRECT-DISTORTION

ICM-file: misc:misc.icm

Correction of distortions. The current options include the correction of PINCUSSION or BARREL distortions.

CORRELATE-MOUNT-IMAGES

ICM-file: stand:standard.icm

Mount a set of input images (patches) into a larger output image.

The command was implemented in conjunction with the patchwork densitometer project. Given a suite of image patches, scanned with an overlap between neighboring patches, this command will first find the shift between the patches by correlating the overlapping regions and then mount the patches to a large image where the shifts have been compensated for. In the overlapping regions, intensities from neighboring patches are blended together by means of linear interpolation.

NOTE: If you want to mount patches (images) without any correlation or blending together of neighbouring images you can use the much faster command MOUNT-IMAGES.

CORRELATION-AVERAGING

ICM-file: crystal:crystal.icm

This command performs a complete cycle of correlation averaging.

The basic idea of correlation averaging is to cross-correlate the crystal image(s) with a reference crystal patch so as to create a cross-correlation-function (CCF) in which one can then search for peaks which correspond repeats of the motif present in the reference image.

Two input images files are required that should contain images of the same size:

A: an image of a 2D-crystal pretreated such that, for example, the average density is zero. The image info should preferably not extend up to the edge of the image to avoid wrap-around artefacts.

NOTE: The image file A: may also contain a SEQUENCE of

**To continue give RETURN, or give a "*" to stop :
crystal patches which will all be cross-correlated with the reference image B. The patches may be generated by dividing a large crystal up into many patches. An advantage of working with patches is that pretreatment of the patches is more subtle and the procedure is much faster than the processing of a single very large input image. This option provides a very natural way of processing crystal images produced through the new "spot-scanning" technique.

B: a reference image which contains a small crystal patch centered around the origin. This reference may be the result of an earlier Fourier space peak-filtering procedure, the result of an earlier round of the correlation averaging procedure, or just some crystal patch extracted from some

In this command the two input images A and B will both be Fourier transformed (file sizes must be compatible with our mixed radix FFT2D algorithm!) and the transforms will then be (conjugate) multiplied with each other.

**To continue give RETURN, or give a "*" to stop :

The resulting FT may be multiplied by a band-pass filter so as to suppress the influence of the very low and/or the very high frequency image components. The result of this operation will then be inverse Fourier transformed to yield the Cross Correlation Function (CCF) between the images A and B. Alternatively, the MCF can be used as a correlation function for this purpose.

The CCF/MCF is subsequently searched for peaks and a sorted list of peaks is produced.

The corresponding image areas are extracted from the image A and subsequently given a small additional shift to account for the non-integer peak coordinates determined by a least squares fit of a paraboloid over the peak coordinates.

The last step in the procedure is the summing of all the small image patches into a total sum. To be able to

**To continue give RETURN, or give a "*" to stop :
perform an MSA on the individual extracted crystal patches, the extracted images are NOT deleted in the procedure.

BEWARE: the small images may take up much more disk space than the original 2D crystal image!

CPU-USE-DISPLAY ICM-file: util:unx_util.icm

Shows informations about the current UNIX processes,
including the CPU usage. (UNIX system call)

CREATE-DSCF-MASK ICM-file: dscf:dscf.icm

This command creates a mask which is later needed for the MSA classification procedure performed on the DSCF images.

Same command as DSCF-CREATE-MSA-MASK.

CREATE-HEADER-FILE ICM-file: stand:standard.icm

Command to create an IMAGIC header file.

Purpose:

Various external (pure) data formats are immediately compatible with the IMAGIC image data format (".img" file) which contains all pixel values in the image one after the other without any interruption. The ".img" (8-bit BYTE or 16-bit INTEGERS or 32-bit REALS or 2*32-bit COMPLEX) can then be "generated" by copying or renaming the external file to have the extension ".img" in the host operating system. A corresponding IMAGIC header file can then be generated using this command.

CROSS-CORRELATION

ICM-file: fft:fft.icm

Cross-correlation between one (reference) image, and one or more other images present on the same file. Aimed at operating on large (ex-core) images.

Most correlation averaging and/or alignment commands that use cross-correlation, call this operation in its in-core version (cf INCORELB.FOR or INCFFTLB.FOR)

The reference image need to be of the same size as the other input image(s).

CTF-CORRECTION

ICM-file: phase:phase.icm

This command can be used for:

- A) Interactive plotting of electron microscopical transfer functions with choice of the microscopical parameters. Final result may be stored in a PLT file.
- B) Impose a transfer function onto one or more input images.
- C) Impose a transfer function onto one 3D input volume.
- D) "Correct" the Phase Contrast Transfer Function of an electron microscopical image.
- E) "Correct" the Phase Contrast Transfer Function of a 3D electron microscopical reconstruction.

Same command as TRANSFER-FUNCTION.

**To continue give RETURN, or give a "*" to stop :

CUT-CURVE

ICM-file: spectra:spectra.icm

CUT a curve to create a curve of different size on disk.

NOTE that the cutting is to be interpreted flexibly since the "cut" curve can be larger than the input curve.

CUT-IMAGES

ICM-file: stand:standard.icm

Same command as SUBFILE-OF-IMAGE.

This command extracts one or more small image(s) from an input image or a set of input images. The program has a large number of options to choose from.

Some typical applications:

- a. Extract many small images from a big input image driven by a peak-table stored in IMAGIC "PLT" format
- b. PAD an input image with zeroes to avoid wrap-around artefact in subsequent Fourier-space manipulations
- c. Divide a large input image checkerboard-wise into a large set of small output images to be used for, for example, texture analysis

**To continue give RETURN, or give a "*" to stop :

- d. Why don't you just start the program and appreciate its beauties with your own eyes ...

CYLINDER-COOS-IMAGE

ICM-file: dscf:dscf.icm

Convert an image to cylindrical coordinates.

This command will lead you to the SPECFUNC program which has many more options than just the calculation of cylinder coordinates.

IMAGIC-COMMAND : +help D

DELETE-IMAGE-FILE

ICM-file: stand:standard.icm

Delete an image file plus corresponding header file. The "PLT-file" will also be deleted if present.

The deleting operation is often done simpler using the host operating system facilities, however, in batch runs this

of IMAGIC

DISPLAY-IMAGE

ICM-file: display:display.icm

Display a beautiful image in beautiful colours on various display systems.

The DISPLAY program associated with this command is one of the most insensivly used IMAGIC programs. It is a highly interactive program in which many local commands can be used to control the parameter settings for displaying images of series of images.

To get an impression of the many options offered the best thing to do is to start the program interactively and explore its possibilities with the interactive help provided locally.

On a modern workstation one uses this program typically to control an X-windows display window on the workstation. Since one can have a virtually unlimited number of such windows (only limited by the memory available on the

**To continue give RETURN, or give a "*" to stop :
workstation), one can start the program over and again in different terminal window and thus have many display systems available for view "before" and "after" situations etc. It really is a very flexible tool with very many possibilities.

NOTE: One very important function of this program is to interactively determine coordinates associated with some aspects of 2D or 3D image files and store such coordinates in the so called "PLT" formatted files. From there, the coos can be picked up by subsequent programs for various purposes.

DIVIDE-BY-CONSTANT

ICM-file: stand:standard.icm

Divide every pixel in an image by a constant. This command will bring you into the ARITHM program which has many more options than just this division.

DIVIDE-IMAGES

ICM-file: stand:standard.icm

DIVIDE images BY one another. This command will lead you to the TWOIMAG program which has many more options than just the DIVIDING of two images.

NOTE: the program TWOIMAG (which is started in this command) is designed for large images mainly. For manipulating smaller images the INCORE programs are more efficient. Hint type: "? *INCO" in the IMAGIC-COMMAND mode to find out what the options are.

DOUBLE-AUTO-CORRELATION ICM-file: dscf:dscf.icm

Command to calculate the Double Auto-Correlation function (DACF) an image.

For a reference, see:

Schatz M. and Van Heel M., "Invariant classification of molecular views in electron micrographs", Ultramicroscopy 32 (1990) 255-264.

This command will lead you to the SPECFUNC program which has many more options than just the calculation of cylinder coordinates.

DOUBLE-SELF-CORRELATION ICM-file: dscf:dscf.icm

Command to calculate the Double Self-Correlation function (DSCF) of an image.

For a reference, see:

Schatz M. and Van Heel M., "Invariant recognition of molecular projections in vitreous ice preparations", Ultramicroscopy 45 (1992) 15-22.

This command will lead you to the SPECFUNC program which has many more options than just the calculation of cylinder coordinates.

DSCF-ALIGN-DIRECT-IMAGES ICM-file: dscf:dscf.icm

This is the command for the a direct alignment within the DSCF procedure if NO equivalent rotation and NO comparison with other alignments should be done.

This command starts with an input file which is assumed to be treated by any classification procedure you want (as MSA-RUN/ MSA-CLASSIFY or the DSCF/MSA procedure for example).

Because every class has a different reference, the class

classification (.CLS) file (for example in the DSCF procedure the classification is not done with the original images and therefore the only information about the classification is in the .CLS file).

The references for each class should have been written one by one in a certain reference file (as done by DSCF-CREATE-

**To continue give RETURN, or give a "*" to stop :
REFERENCES for example) prior to running this program.

All input images will be aligned relative to their class reference and all aligned images are written into one output file without changing the location numbers.

You have the choice to also do "mirror alignments". This means that if an image of the input file correlates better to the mirror reference than to the "normal" reference, this program mirrors this image, too. This is an important procedure within the DSCF alignment procedure because DSCF does not distinguish image and mirror image.

DSCF-ALIGN-FIRST-REFERENCE ICM-file: dscf:dscf.icm

Program for a first "mirror" alignment within the DSCF procedure.

D_ALI1ST (the IMAGIC program associated with this command) starts with an input file which is assumed to be treated by any classification procedure you want (as MSA-RUN/ MSA-CLASSIFY or the DSCF/MSA procedure for example). Since every class will be aligned by a different reference, the class number of each image MUST have been written into a given classification (.CLS) file (for example in the DSCF procedure the classification is not done with the original images and therefore the only information about the classification is in the .CLS file).

Every input image will be aligned relative to its class reference. In a second loop the image is mirrored and again the alignment is calculated. If the mirror alignment is the better one the aligned image remains mirrored, else

**To continue give RETURN, or give a "*" to stop :
the non-mirrored aligned image is stored. (This is an important procedure within the DSCF alignment procedure because DSCF does not distinguish image and mirror image.

In every class an intermediate sum of the best aligned images ("conditional sums") is calculated, contoured and used as class refernces for a second (better) alignment.

All aligned images are written into one output file without changing the location numbers.

DSCF-ALIGN-NEW-REFERENCE

ICM-file: dscf:dscf.icm

This command is used to perform a multi-reference alignment within the DSCF procedure.

This command starts with an input file which is assumed to have been treated by a classification procedure (as MSA-RUN/MSA-CLASSIFY or the DSCF/MSA procedure for example) with the results written in a classification (.CLS) file and normally a first alignment.

The references for each class should have been written one by one in a single reference file (as done by DSCF-CREATE-REFERENCES for example).

All input images will be aligned relative to their class reference. The new alignment and the (best) old one are compared for every image and only the best one is stored in the output file. If necessary, equivalent rotations are performed. The location numbers of the images are not

**To continue give RETURN, or give a "*" to stop :
changed.

You have the choice to do also "mirror alignment". This means that if an image of the input file is better correlated to the mirror reference than to the "normal" reference, this program mirrors this image, too. This is an important procedure within the DSCF alignment procedure because DSCF does not distinguish image and mirror image.

DSCF-ALIGN-REFERENCES

ICM-file: dscf:dscf.icm

This command aligns new class references in the input to those in a (given) old reference file.

Same command as ALIGN-PARALLEL.

DSCF-CREATE-MSA-MASK

ICM-file: dscf:dscf.icm

This command creates a mask which is later needed for the MSA classification procedure performed on the DSCF images.

Same command as CREATE-DSCF-MASK.

DSCF-CREATE-REFERENCES

ICM-file: dscf:dscf.icm

This command creates references for each class desired by the normally following IMAGIC alignment programs. The first image of each class as written in the classification (.CLS) file is taken for reference of this class. Since the order of the images in the .CLS is by their variance contribution to the class (they are sorted!), the first image in the .CLS file is the image that is closest to the center of mass of the class.

The references are contoured by a mask and are mass centered. Then everything outside the contour is zeroed. Those final images are the alignment references. All references are written into one file.

DSCF-SUM-CLASSES ICM-file: dscf:dscf.icm

This command uses a given classification (.CLS) file to build the class averages using the original or aligned input images. If desired the command creates standard-deviation images that show which areas of the corresponding class sums show the largest deviation from the average value.

DSCF-WRITE-CLASS-NUMBER ICM-file: dscf:dscf.icm

This command is used to write the class number out of a given classification (.CLS) file into images headers. This is necessary for example in the DSCF procedure because in this case the classification is not done with the original images. May be you use this command more than once. Therefore the header values for the class numbers are first set to zero.

IMAGIC-COMMAND : +help E

EIGEN-FILTERING-MSA ICM-file: msa:msa.icm

Given a set of images (or other data) for which the coordinates relative to a given set of eigenimages (eigenvectors) have been calculated, this command allows you to "rebuild" the set of input images as a linear combination of the main eigenimages. This way, output images are created which contain ONLY those properties of the input data described by the main eigenvectors.

Prerequisite is that the factorial coordinates for the set

previously using the MSA-RUN (data belonging to the original data set) or the EXPLANATORY_MSA (explanatory data) commands relative to the current set of eigenvectors.

NOTE: this command can also be used for decompressing a data set of which only the factorial coordinates are available ("compressed" information).

**To continue give RETURN, or give a "*" to stop :

EM2EM ICM-file: stand:standard.icm

Command to convert images to and from various data formats that are used within the "3-D Electron Microcopy Community".

If you want to convert between different IMAGIC formats (REAL, INTG, PACK etc.) please use command CONVERT-IMAGE.

END ICM-file: util:gen_util.icm

The "END" command will bring you back to the host's operating system; it is thus equivalent to "BYE", "EXIT" or "*". If you are in MODE-ACCUMULATE, that mode of operation will NOT be discontinued! You can thus continue to accumulate commands after leaving IMAGIC with one of these commands!

EQUIVALENT-ROTATION ICM-file: align:align.icm

This command allows you to recreate a set of aligned images from an original set of images with just one interpolation step.

It may also be used to impose a set of rotation and shift parameters to another set of images that need not be the original ones used for the alignment.

In an alignment procedure images may have been interpolated (rotations and real-shifts) a number of times in a row thus gradually reducing the high frequency components of the images. During alignments, however, "equivalent" shift and rotation parameters are carried along with the aid of which the output file may be recreated in just one interpolation step.

NOTE: various of the newer INCORE commands perform the equivalent rotation always, without asking any

questions.

NOTE: See also INCORE-EQUIVALENT-ROTATION

EULER-ANGULAR-RECONSTITUTION ICM-file: angrec:angrec.icm

Command to do ANGULAR-RECONSTITUTION.

It can be used for various tasks like finding the Euler orientations of projections relative to each other or relative to a set of projection images which have already had Euler angles assigned to them (anchor set). EULER exploits the KNOWN pointgroup symmetry of the oligomeric molecule during the "brute-force" search for the best Euler orientation of the new projection.

Reference:

Marin van Heel,
"Angular Reconstitution: a-posteriori determination of projection directions for 3D reconstruction",
Ultramicroscopy 21 (1987) 111-124.

Marin van Heel et al.

**To continue give RETURN, or give a "*" to stop :
"Single-particle electron microscopy: towards atomic resolution",
Quart. Rev. Biophys. (200) 307-369.

EXCLUSIVE-COPY ICM-file: incore:incore.icm

This program is used for EXTRACTING images from an input file, and writing them out to an output file, in any order that you wish. Thus it can be used to select a small number of images from a large input file, or for REORDERING the images in an input file. One can also copy all images from one file to another EXCLUDING certain specified images. This command does in one step what previously required using combinations of the COPY-IMAGE and APPEND-IMAGE commands many times over.

EXIT ICM-file: util:gen_util.icm

The "EXIT" command will bring you back to the host's operating system; it is thus equivalent to "END", "BYE" or "*". If you are in MODE-ACCUMULATE, that mode of operation will NOT be discontinued! You can thus continue to

commands!

EXPLANATORY-CLASSIFY-MSA

ICM-file: msa:msa.icm

Given a (new) data-set for which the factorial coordinates have been determined either by EXPLANATORY-MSA, or (if the new data was a-posteriori extracted from the original data set) by MSA-RUN, we can use this command to find distance relations of the new data relative to the individuals and classes of the earlier data set.

This command thus allows to study new data relative to the earlier "learning set", and it thus is an important pattern recognition tool.

EXPLANATORY-MSA

ICM-file: msa:msa.icm

Find factorial coordinates of a new data-set (normally images) relative to a previously determined set of eigenvectors ("eigenimages"). These coordinates can subsequently be used to place the new data in relation to earlier data and classes thereof (EXPLANATORY-CLASSIFY). This command thus allows you to study new data relative to an earlier "learning set".

EXTRACT-ALIGNED-IMAGES

ICM-file: align:align.icm

The input image file is assumed to contain aligned images treated by multi-reference alignment(s). The command then extracts all those images correlating best to the specified reference(s).

In a multi-reference alignment scheme, the alignment of each original image is relative to that reference image which - after alignment - correlated best with the original. The number of that "best" reference image is stored in the header of the original image.

This command thus allows for the a-posteriori separation of the various subsets of images correlating best to the various reference images applied to the set of originals.

IMAGIC-COMMAND : +help F

FFT2D

ICM-file: fft:fft.icm

General program for performing large 2D FFTs.

This command is just an alternative name for the command:
FOURIER-TRANSFORM-2D

For additional help and more extended documentation look
there (HELP FOURIER-TRANSFORM).

FILTER-CURVE ICM-file: spectra:spectra.icm

This program contains many options for processing spectra
and other linear data.

Some of the options:

- Power spectrum calculation
- Amplitude spectrum calculation
- Gaussian low-pass filter
- Gaussian high-pass filter
- Gaussian band-pass filter (GREAT!)
- Inverse filter (undoing high-pass)

**To continue give RETURN, or give a "*" to stop :

etc...

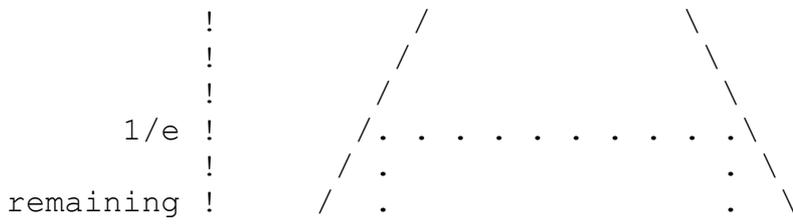
For an up-to-date account of all available options,
start the program interactively and ask for more help.

FILTER-IMAGES ICM-file: fft:fft.icm

This command will bring you to the `FILT_ALL` program in which
the band-pass filtering in only one of the options.

The band pass filter is a double Gaussian filter with the
following parameters:

```
! ^
! | transmission axis
!
1.! , ----- ,
.
```



**To continue give RETURN, or give a "*" to stop :

low-freq. !----- . \ spatial
transmiss.! . \ frequency axis -->

+-----+
low frequency high freq
cut-off cut-off

The HIGH frequency cut-off is associated with a LOW-PASS Gaussian filter which will gradually cut off spatial frequencies higher than this value.

The LOW frequency cut-off is associated with a HIGH-PASS Gaussian filter which will gradually cut off spatial frequencies lower than this value.

The remaining transmission allows you to leave a fraction of the low-frequency components (say, 0.001) intact such that one always restore these low-frequency components at a later stage by inverse filtering, without dividing by zero.

Same command as: BAND-PASS-FILTER

**To continue give RETURN, or give a "*" to stop :

FIND-OBJECTS ICM-file: morfo:morfomet.icm

Command to find objects in an IMAGIC image file.

The ways of defining an "object" is defining a threshold applicable to a set of densities (an "image").

The command combines many pre-threshold operations (filters, variance-image, ...) with many different post-threshold operations with which one can play to produce optimum results.

Same command as MORFOMETRIC-CALCULATIONS.

FOURIER-CROSS-INFORMATION ICM-file: fft:fft.icm

This command is used to compare two images in Fourier space with each other using the Fourier-Cross-Inforamtion (FCI). For comparison some other functions like the Fourier Ring Correlation (FRC) are also available.

"Fourier Cross Information between two images
or 3D volumes"

NOTE: these techniques give the similarity in terms of cross-resolution between two images; if the statistical significant resolution is searched within one set of noisy images, go for the command: INFORMATION-IN-SEQUENCE or I-IMAGE.

FOURIER-PEAK-FILTERING

ICM-file: crystal:crystal.icm

Filter out the peaks in the Fourier Transform of a two-dimensional crystal.

Already a very old technique (the first version of this particular program stems from the year 1977) which masks the FT of a (noisy) 2D crystal image by a regular array of circular holes with variable hole size. The size of the hole determines over what size of real space area, one average the crystal, i.e., how many unit cells are effectively averaged to produce the filtered output image.

It is also possible to read in the peak coordinates and corresponding mask radii from a PLT-file (produced by DISPLAY, option COOS, for example)

NOTE: This program does only the masking. You thus must provide it with an input FT, and you will have to reverse transform (IMAGIC-command FFT2D) the masked

**To continue give RETURN, or give a "*" to stop :
transform to obtain an image you can look at.

NOTE: This kind of processing is not very subtle since it is based on the implicit assumption that the input crystal is a perfect crystal with a repeating motif placed on an ideal undistorted lattice. Correlation averaging (see corresponding IMAGIC command) is much more subtle and can replace/supersede this Fourier space manipulation procedure almost always.

FOURIER-PEAKS-SEARCH

ICM-file: crystal:crystal.icm

This command produces a table of peaks from a Fourier Transform. Normally the input file will contain the transform of a periodic object like a two-dimensional protein crystal. The output of this operation will be a table X and Y coos of the peaks and the height of each peak. The list will be sorted (largest first).

For performing the calculations, the FT (input file) may

a power-spectrum or amplitude spectrum upon which the peak search operation is then performed.

NOTE: since Friedel pairs (Hermitian symmetry!) have the same height Friedel pairs will be immediate neighbours on the list!

FOURIER-RING-CORRELATION ICM-file: fft:fft.icm

This command is used to compare two images in Fourier space with each other using the Fourier-Ring-Correlation technique or with the enhanced phase residual technique called the Fourier Ring Phase Residual. For a review of these techniques see:

Marin van Heel, "Similarity measures between images", Ultramicroscopy 21 (1987) 95-100.

There are other options available in this command like the more sophisticated Fourier Cross Information (FCI).

NOTE: these techniques give the similarity in terms of cross-resolution between two images; if the statistical significant resolution is searched within one set of noisy images, go for the command: INFORMATION-IN-SEQUENCE

**To continue give RETURN, or give a "*" to stop :

FOURIER-SHELL-CORRELATION ICM-file: threed:threed.icm

Compare two true 3D images, e.g., two reconstructions or the reconstruction with the original image.

Note that a THREED-FFT will be performed on the input 3D volumes prior to doing the Fourier ring correlation. The input images thus are supposed to be REAL 3D input images.

The 3D Fourier-Schell correlation is the 3D extension of the FRC (Fourier Ring Correlation) technique originally designed to compare two similar images with each other.

A reference for the Fourier Ring Correlation:

Marin van Heel, "Similarity measures between images", Ultramicroscopy 21 (1987) 95-100.

For the Fourier Shell Correlation:

**To continue give RETURN, or give a "*" to stop :

general geometry three dimensional reconstruction",
Optik 73 (1986) 146-156.

FOURIER-TRANSFORM-2D

ICM-file: fft:fft.icm

General program for performing large 2D FFTs.
The program can handle large (huge) 2D data and is
essentially limited by the available disk space rather
than by the available memory.

HOWEVER, if you are really doing very large transforms
with this program you need to reserve as much physical
memory as you can get since the algorithm is more efficient
(in number of IOs required) if a large memory buffer is
available. The "working-set" for the process thus needs
to be large.

The FFT2D program is built around one of the best
known matrix transposing algorithm, the "TRANSPO"
mixed-radix perfect shuffle algorithms:

Marin van Heel, "Fast transposing of large multi-dimensional
image data sets", Ultramicroscopy 38 (1991) 75-84.

**To continue give RETURN, or give a "*" to stop :

The Singleton mixed-radix Fourier transform algorithm is used
in the FFT2D program for performing the FFTs:

R.C. Singleton, "An algorithm for computing the mixed radix
fast Fourier transform, IEEE Trans. Audio and electroacoustics
AU-17 (1969) 93-103.

The advantage of having a mixed radix FFT is the flexibility
in choosing the size of the images to be processed to fit the
problem at hand rather than to adapt the data to the limitations
imposed by a radix 2 FFT.

NOTE: for small images (in-core) you may be better off
using the IMAGIC command: INCORE-FFT-OPERATIONS.

IMAGIC-COMMAND : +help G

GENERATE-2D-CRYSTAL

ICM-file: crystal:crystal.icm

Using a "seed" unit cell image, a 2D crystal is generated
with unit vectors determined by the user. The seed image
can be a small image of Einstein, Goebbel, or even ...
of yourself. One can then add noise to the crystal so
as to have a nice noisy crystal for test purposes. The

GREY-LEVEL-HISTOGRAM

ICM-file: stand:standard.icm

Print histogram of density values in images. The program will produce a "PLT" style IMAGIC formatted ASCII file which can be picked up by graphics producing programs like PLOT-ALL.

IMAGIC-COMMAND : +help H

HEADERS-INFORMATION

ICM-file: stand:standard.icm

Change, print, plot, or extract information from IMAGIC image header files.

For example, you may be interested in the statistical distribution of the variances within a set of images. You can then, after running the SURVEY program which store those statistics in one of the header locations, do a HISTOGRAM on that specific location in the HEADERS program.

You could also want to WIPE out all ealier information from the header so as to create a virgin image file. This can sometimes be useful to avoid interference with implicit assumptions in specific image processing procedures.

HELP

ICM-file: util:gen_util.icm

"HELP" is an important tool in the IMAGIC image processing software system. It is a legitimate answer to every question that appears on the terminal screen. As such it is normally synonymous to "?". However, at the IMAGIC-COMMAND level "?" will merely give a list of the matching commands, whereas "HELP" gives the additional explanation on the matching commands.

As an answer to the IMAGIC-COMMAND prompt, "HELP" may give you additional information about individual IMAGIC commands or sets thereof. If you for example type "HELP *ALIGN" you will generate a large amount of help texts on the screen of all IMAGIC commands which contain the string "ALIGN" in some form.

Note however, that a naked "HELP" as answer will only tell you how to produce a more extended response.

**To continue give RETURN, or give a "*" to stop :
If you want to obtain the resulting help on a file
the trick is to write a little command file in which the
IMAGIC program is started and is prompted for the necessary
help. While starting the command file, direct the output
of the command file to a file or the printer

HUGE-ALIGN-NEW-REFERENCE ICM-file: align:align.icm

This command makes things very easy for lazy people. It
performs a set of multi-reference alignments, one after the
other (including mirror alignments if desired). All one
has to have done previously is get the appropriate
references in one image file. The alignment loop can be
stopped by creating a file STOP.ALI in the default
directory (as one can also stop an MSA run by
generating a STOP.MSA file in the working directory).

All alignments in this program are DIRECT alignments
as opposed to ACF (auto-correlation function) alignments
which give much poorer results.

NOTE: All calculations are done IN CORE

IMAGIC-COMMAND : +help I

I-IMAGE ICM-file: fft:fft.icm

Calculates the I-image for a sequence of input images
to estimate the internal information content of a set
of (aligned and classified) images (resolution).

References:

Marin van Heel, and Michael Schatz
XXX

Michael Schatz, and Marin van Heel
The information content of Einstein hidden in white noise

The command is the same as INFORMATION-IN-SEQUENCE which
actually not only calculates the I-image but various other
information measures, like Q-factor, S-image, power
spectrum etc.

**To continue give RETURN, or give a "*" to stop :

Type out image file sizes, modification dates etc.
Just a direct call to the system utilities.

IMPORT-EXPORT-IMAGIC-FORMAT ICM-file: stand:standard.icm

Command to convert images to and from various data formats
that are used within the "Electron Microcopy Community".

If you want to convert between different IMAGIC formats
(REAL, INTG, PACK etc.) use command CONVERT-IMAGE.

IMPORT-PDB-TO-PLT ICM-file: threed:threed.icm

Convert a PDB file to an IMAGIC "plt" file which can
subsequently be used to create a 3D volume with command
THREED-MODEL.

IMPOSE-PLT-CONTOUR ICM-file: stand:standard.icm

The program is mainly aimed at manipulating image data
within a "plt" style contour, drawn interactively in the
DISPLAY icommand. It can mask out the environment and
statistically normalize the image data within this
area-of-interest.

If you want to normalise, zero float image etc. using
special masks like circle, rectangle, ... or no mask
please use command PRETREAT-IMAGE.

NOTE: If you want to create isolines of densities please
use command CONTOUR-IMAGE.

IMPOSE-SYMMETRY ICM-file: incore:incore.icm

Compute n-fold rotational averages of a set of (centered)
incore images. The input images are assumed to be centered
at the geometric center of the input image(s).

Same command as AVERAGE-NFOLD.

For 3D symmetrisation please use: THREED-IMPOSE-SYMMETRY

is done at all.

INCORE-FFT2D-OPERATIONS

ICM-file: fft:fft.icm

Various FFT related operations but done IN-CORE, thus fast but limited to relatively small images.

Options currently include:

FFT2D-FORWARD

FFT2D-REVERSE

ACF

Power Spectrum, etc.

For an up-to-date account of its virtues, simply start this program interactively and ask for further help.

INCORE-MENU

ICM-file: incore:incore.icm

Extensive menu of various image operations performed IN CORE. Originally a little test program to test out IN-CORE subroutines from the INCORELB library, this program grew out of hand and started living a life of its own.

There are too many options to list here and many of the options are also available in more specialized programs. Nevertheless, just for the heck of it, you should - at least once in your life - start this program and see what happens.

INCORE-PREPARE-FILTERED

ICM-file: incore:incore.icm

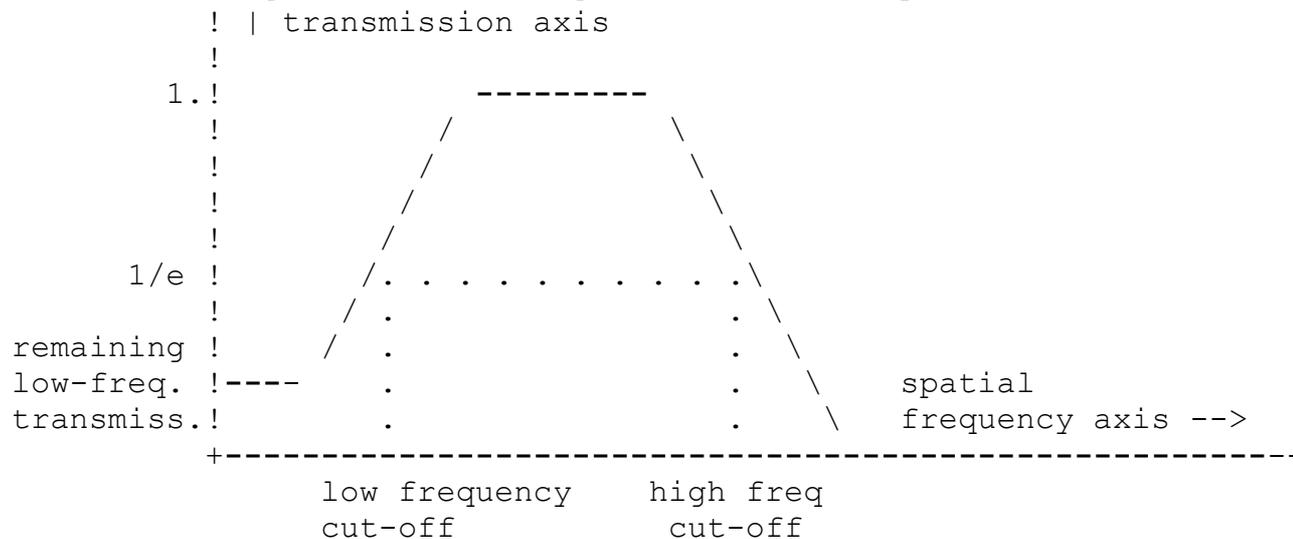
This command is used to standardise the statistics of a sequence of images of single molecules. The input images are thought to be a sequence of images one IMAGIC file that are normally be the result of a particle selection session. Selection of particles is typically done interactively in the DISPLAY program, and the images are then extracted from the original file with the help of the SUBFILE command.

The end result of this operation will be a sequence of band-enhance FILTERED images in the output file with a circular mask superimposed. The filter will reduce the influence of unimportant or disturbing spatial frequencies.

strongly suppressed. The band pass-filter is a double Gaussian filter in Fourier space with the following parameters:

! ^

**To continue give RETURN, or give a "*" to stop :



The HIGH frequency cut-off is associated with a LOW-PASS Gaussian filter which will gradually cut off spatial frequencies higher than this value.

**To continue give RETURN, or give a "*" to stop :

The LOW frequency cut-off is associated with a HIGH-PASS Gaussian filter which will gradually cut off spatial frequencies lower than this value.

The remaining transmission allows you to leave a fraction of the low-frequency components (say, 0.001) intact such that one always restore these low-frequency components at a later stage by inverse filtering, without dividing by zero.

The circular mask serves to reduce the influence of the surroundings of the molecules. The densities in the output images outside the mask will be zero. Inside the mask the densities will be normalized to a given standard deviation and zero mean density. Often the densities must be reversed, so that the protein is represented by positive density values and the stain by negative density values. Thus at the end one can multiply by -1 to give this reversal, or by +1 to leave things alone.

INCORE-SHIFT

ICM-file: incore:incore.icm

This program performs a cyclical shift of an image, but INCORE enabling one to overwrite the input file and thereby save a lot of disk space.

This program performs the TWOIMAG options of SUM and CONDITIONAL SUM, but IN CORE and so much faster because there is no need for intermediate I/O.

The SUMMER program associated with this command also performs many new statistics options not present in the older programs. It has developed to become an important source of statistical information which supplements the results of the MSA-CLASSIFY program and the like.

INFORMATION-IN-SEQUENCE

ICM-file: fft:fft.icm

Calculates various information measures while summing a sequence of Fourier transforms (such as patches extracted from a 2-D crystal in a correlation averaging procedure).

Whereas the Fourier-Ring-Correlation is one of the best techniques to compare the similarity BETWEEN two images (typically two class-averages of similar classes), the similarity measures in the "INFORM" program associated with this command are aimed at finding the internal (noise-limited) resolution of a set of similar images.

Typically original unit-cell images from a 2D crystal, or a class of aligned images from an MSA-CLASSIFY run, the similarity of these images may not at all be obvious due to extreme noise levels in the original images.

Options include:

**To continue give RETURN, or give a "*" to stop :

"Q-image"

"S-image"

"I-image"

The "Q-image" dates back to:

M. van Heel and J. Hollenberg, "On the stretching of distorted images of two-dimensional crystals", in: W. Baumeister and Vogell W. (ed.), Electron microscopy at molecular dimensions, Springer, Berlin (1980) 256-260.

M. Kessel, M. Radermacher and J. Frank, " The structure of the stalk surface layer of a brine pond microorganism: correlation averaging applied to a double layered lattice

**To continue give RETURN, or give a "*" to stop :

"S-image" was published in:

J. Sass, E. Beckmann, G. Bueldt, D.L. Dorset, M. van Heel, J. Rosenbusch, F. Zemlin, E. Zeitler and A. Massalski, "Densely packed Beta-structure at the protein-lipid interface of Porin is revealed by high-resolution cryo-electron microscopy", J. Mol. Biol. 209 (1989) 171-175.

"I-image": unpublished

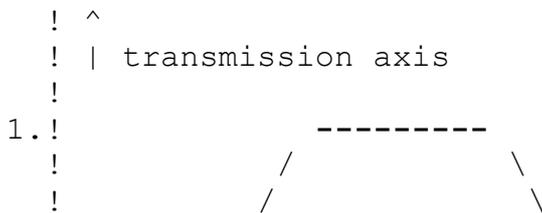
INVERSE-BAND-PASS-FILTER

ICM-file: fft:fft.icm

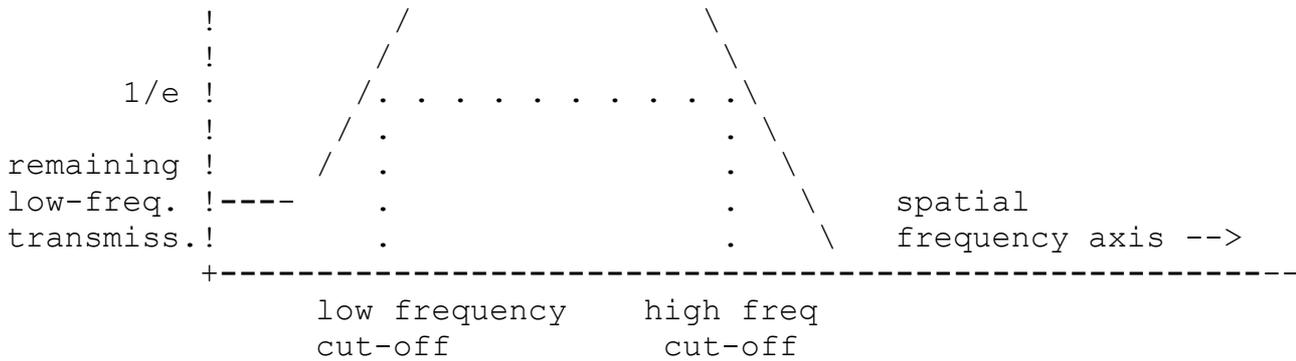
This command will bring you to the FILT_ALL program in which the band-pass filtering in only one of the options.

This command performs a PARTIAL INVERSE of the command BAND-PASS-FILTER. The latter command is used to attenuate both the very low and the very high frequencies in an image. This command allows you to retrieve the very LOW frequencies ONLY - the very high frequencies remain suppressed!

For your information, the band pass filter is a double Gaussian filter with the following parameters:



**To continue give RETURN, or give a "*" to stop :



What can be reversed here is the influence of the LOW frequency cut-off assuming that one has left some of the low-frequency data in the image by choosing the remaining low-frequency transmission larger than "0".

A value of "0" will cause a division by zero at the origin..

IMAGIC-COMMAND : +help J
NO MATCHING COMMAND

IMAGIC-COMMAND : +help K

KILL-FRUSTRATIONS

ICM-file: util:unx_util.icm

A simple command for angry people to get rid off their frustration.

IMAGIC-COMMAND : +help L

LIST-COMMAND-ENTRY

ICM-file: util:gen_util.icm

Produces a listing of an IMAGIC-COMMAND on the user terminal. The listing does NOT include the user interaction.

LOW-PASS-FILTER

ICM-file: fft:fft.icm

This command will bring you to the `FILT_ALL` program in which the band-pass filtering in only one of the options.

Low-pass filtering of one or more images from an IMAGIC input file.

NOTE that this command works on large images as well as small images, but that more efficient "INCORE" programs exist for small images.

The command invokes a low pass Gaussian filter with the following parameters:

```
! ^
! | transmission axis
!
1.!-----
```

**To continue give RETURN, or give a "*" to stop :

```
!
!
!
1/e ! . . . . .
!
!
!
```

high frequency
cut-off

The HIGH frequency cut-off is associated with a LOW-PASS Gaussian filter which will gradually cut off spatial frequencies higher than this value.

MANIPULATE-EULER-ANGLES ICM-file: angrec:angrec.icm

Command that allows to move EULER angles stored in an EULER angle (plt) input file (rotate, mirror, copy ...).

These options were originally options in command EULER and have been moved to this separate command.

Same command as: MOVE-EULER-ANGLES

MANIPULATE-PLT ICM-file: stand:standard.icm

Command to manipulate contours or coordinates stored in a PLT file: mirror, shift & rotate, symmetrize, coarse, etc.

Same command as MOVE-PLT.

MAP-EULER-ANGLES ICM-file: threed:threed.icm

Write the distribution of Euler angles into an image file. The Euler angles can be read from an IMAGIC image or "plt" file.

MASK-IMAGE ICM-file: stand:standard.icm

Masking an image or transform with a circular mask, or a Gaussian mask, or a Lorentzian mask or ...

Actually, this command is a parallel entry to the ARITHM command and thus has exactly the same options as that command

MASS-CENTER-OF-IMAGE ICM-file: stand:standard.icm

This program allows you to determine the center of mass of an image.

This command actually leads you to the ALIMASS program which has many more options to center images:

MASK: Shifting the center of mass of the MASK (outside = zero) imposed on the input image to the logical center of the output image (half+1 in both vertical and horizontal directions). The weight of all non-zero pixels in the input image is set to unity in calculating the center of mass: this means the image is shifted to the center of mass of the mask rather than of the object in the image.

ABSOLUTE: The absolute value of the image densities is used to find the "mass center". This option is intended to be an alternative to the simple mass-centering option

**To continue give RETURN, or give a "*" to stop :

to be used for zero-average phase-contrast type of images.

SELFCENTER:

The input image is iteratively centered relative to a rotationally symmetrized version of itself so as to obtain a good centering of relatively globular particles.

Same command as CENTER-IMAGES or ALIGN-MASS-CENTER.

MENU

ICM-file: util:gen_util.icm

The "MENU" command will produce a list of the matching IMAGIC COMMANDS. At the IMAGIC_COMMAND level, "MENU" is normally equivalent to "?". For a list of matching commands type something like:

MENU NAME
or: MENU *NAME

MIRROR-CONTOUR-PLT

ICM-file: stand:standard.icm

Mirror an ".PLT" style coordinates file about its central axis. This can be used to apply a mirrored contour to a corresponding mirrored image, for example.

The command actually leads you to the MOVEPLT program which has many more options for manipulating "PLT" coordinate

...

MIRROR-IMAGE

ICM-file: stand:standard.icm

Create a mirror version of an image. The input image lines are simply flipped over to create the mirror image. In other words, the output image will be the input image, mirrored horizontally.

There also exist commands to mirror an image in top-bottom sence. The correct IMAGIC command for that option is UP-SIDE-DOWN.

MODE-ABORT

ICM-file: util:gen_util.icm

MODE-ABORT aborts a MODE-ACCUMULATE session and deletes the command file that is being build.

MODE-ACCUMULATE

ICM-file: util:gen_util.icm

MODE-ACCUMULATE is an important IMAGIC switch. After having switched over to MODE-ACCUMULATE operation, The commands are no longer executed directly but are rather accumulated on a file for later execution on the batch processor (MODE-SEND-TO-BATCH) or on the terminal (MODE-RUN).

MODE-END-ACCUMULATE

ICM-file: util:gen_util.icm

After having built a job in MODE-ACCUMULATE, the MODE-STOP command will create a command file which may be edited or manipulated otherwise by the user.

Same command as MODE-STOP.

MODE-HELP

ICM-file: util:gen_util.icm

MODE-ACCUMULATE: after this (very important) command, IMAGIC commands will no longer be executed immediately, but will be gathered in a command file. The job that is thus created can be sent to the batch processor by the command:

using the command:

MODE-RUN

MODE-STOP stops IMAGIC so that the batch input file can be edited with any editor before being started.

MODE-END also stops IMAGIC so that the batch input file can be edited with any editor before being started.

MODE-ABORT aborts the accumulation.

**To continue give RETURN, or give a "*" to stop :

MODE-RUN ICM-file: util:gen_util.icm

After having built a job in MODE-ACCUMULATE, the MODE-RUN command will cause the job to be executed on the user's terminal. To keep a log of the operations use MODE-SEND-TO-BATCH or use MODE-STOP.

MODE-SEND-TO-BATCH ICM-file: util:gen_util.icm

After having built a job in MODE-ACCUMULATE, the MODE-SEND-TO-BATCH command will pipe the job to the batch processor with a number of standard settings. If you wish different settings and switches, use MODE-STOP and send the job to the batch processor manually.

MODE-STOP ICM-file: util:gen_util.icm

After having built a job in MODE-ACCUMULATE, the MODE-STOP command will create a command file which may be edited or manipulated otherwise by the user.

Same command as MODE-END.

MORFOMETRIC-CALCULATIONS ICM-file: morfo:morfomet.icm

Command to find objects in an IMAGIC image file.

The ways of defining an "object" is defining a threshold applicable to a set of densities (an "image").

The command combines many pre-threshold operations (filters,

operations with which one can play to produce optimum results.

Same command as FIND-OBJECTS.

MOUNT-IMAGES

ICM-file: stand:standard.icm

Mount a set of input images into a set of larger output images which will typically be "galleries".

You may choose how many input images are mounted into a single output image frame, the width of the background areas around and between the mounted images, etc.

Some applications of this program:

1. Mount a number of small input images into a set of large output images, for example, a set of 96 input images (locations in input file) is mounted in 4x4 groups of a set of 4 output image locations'
2. Mount a set of 1-D slowly changing input curves (IMAGIC/1D) into a single 2D output image for display purposes.

**To continue give RETURN, or give a "*" to stop :

NOTE: The input images are only mounted together. If the images have a certain overlap and should be correlated during mounting use command:
CORRELATE-MOUNT-IMAGES

MOVE-EULER-ANGLES

ICM-file: angrec:angrec.icm

Command that allows to move EULER angles stored in an EULER angle (plt) input file (rotate, mirror, copy ...).

These options were originally options in command EULER and have been moved to this separate command.

Same command as: MANIPULATE-EULER-ANGLES

MOVE-PLT

ICM-file: stand:standard.icm

Manipulate and move PLT coordinates around: mirror, rotate, symmetrise, etc.

The command actually leads you to the MOVEPLT program which has various options for manipulating "PLT" coordinate

program and ash for the interactive help.

Same command as MOVE-PLT.

MOVIE ICM-file: display:display.icm

MOVIE displays a sequence of images in an endless loop.
The command reads all image locations from a file in-core,
and displays the XWindows pixmaps.

NOTE: This command runs only on XWindow devices.

MSA-CLASSIFY-IMAGES ICM-file: msa:msa.icm

This classification program is a post-processor to the MSA
program! The theoretical basis of this variance-oriented
hierachical ascendent classification program (an enhanced
Ward-type algorithm) was published in:

Marin van Heel, Multivariate Classification of Noisy
Images (Randomly Oriented Biological Macromolecules)
Ultramicroscopy 13 (1984) 165-184;

and more recently, more refined procedures (not all
implemented here) were described in:

Marin van Heel, "Classification of very large electron
microscopical image data sets", Optik 82 (1989) 114-126.

Ideas concerning the "simultaneous" classification in the
two conjugate representation spaces are described in:

**To continue give RETURN, or give a "*" to stop :
Lisa Borland and Marin van Heel, "Classification of
image data in conjugate representation spaces",
J.Opt.Soc.Am. A Vol 7 (1990) 601-610.

MSA-CURVE-MASK ICM-file: spectra:spectra.icm

MSA-EXTRACT-SORTED-CLASSES ICM-file: msa:msa.icm

From a set of MSA'ed and CLASSIFY'ed images, we extract the
individuals belonging to the same class to form a separate
IMAGIC file. The individuals in the separate file will be
sorted by their variance contribution to the class, i.e.,

This command/program allows to perform further detailed analysis (using other IMAGIC commands) on the members of a given class exclusively.

MSA-GENERATE-ORIGINAL-COOS ICM-file: msa:msa.icm

This programs will use the information in the headers of the image file, in combination with an associated classification "CLS"-style file, to generate a set of coordinate files ("PLT"-style) containing the central coordinates of the small images within the large images from which they once have been extracted.

The CLS file which is the main input to this program is generated by MSA-CLASSIFY but the image file need only have a one-to-one relation to the MSA-CLASSIFIED image set. Moreover, only the HEADER file of the image file need be available since all the info needed stems from the header (stored there by SUBFILE-like commands) only, the image data are ignored and need not even be on the disk.

MSA-MAP-DISPLAY ICM-file: msa:msa.icm

One way of looking at MSA results is through two-dimensional maps in which one or more data-sets are depicted on a two-dimensional "scatter-plot" spanned by two eigen-vectors at a time.

This IMAGIC program uses coordinates input of:

```
"cases"      :      images,      spectra, ...
"variates":  pixel-vectors, wave numbers, ...
"classes"   :  of cases and/or variates
```

to produce two output formats:

- 1) a simple map in the form of an IMAGIC image file for quick reference.
- 2) a formatted "PLT" style coordinates file which can be brought to high-quality graphics output using

**To continue give RETURN, or give a "*" to stop :
the highly interactive PLOT-COORDINATES command,
or can be exported to non-IMAGIC graphics programs.

Planned extension:

- 3) an "IMG" style output coordinates file which can be brought to high-quality graphics output using

Reason: for large data sets with more than a few thousand elements, manipulating the formatted PLT style files is rather slow and we humans are rather impatient!

MSA-MASK-PREPARE

ICM-file: msa:msa.icm

The MSA requires a so-called MSAMASK. This mask is an IMAGIC file of TYPE 'REAL' which contains zeroes in those areas of the images (or other data) which are NOT to participate in the eigenvector calculations and further statistical procedures.

For preparing such an MSAMASK, you have various options of which this command is just one. If all elements ("variates", pixels, wavenumbers, ...) of the input measurements ("cases", images, spectra, ... are to be active during the statistical procedures, the easiest way to generate an MSAMASK is to use the TEST-IMAGE command (or TEST-CURVE in IMAGIC/1D) to generate a CONSTANT image.

The MSAMASK program is intended only for 2D IMAGES! I.e., two-dimensional data sets for which an irregular mask (an irregular contour) is appropriate. This contour is normally applied to the total sum of an image data-set

**To continue give RETURN, or give a "*" to stop :
within the DISPLAY program. The MSAMASK program can then perform the actual masking task which could, alternatively, also be performed by applying the PRETREAT program on a constant TEST-IMAGE.

MSA-NAMES-IN-CLASSES

ICM-file: msa:msa.icm

Produce a listing of the names (from the IMAGIC header file) of the images (curves, etc ...) sorted by their class memberships as described by a ("CLS" type) classification file.

Prerequisite for this command is that there is useful information in the name of each individual object (location) of the data set. While generating the IMAGIC multi-location input file, this aspect should not be neglected!

MSA-RUN

ICM-file: msa:msa.icm

of the IMAGIC MSA module!

It calculates eigenimages (eigenvectors) and eigenvalues of a set of input data (aligned images, spectra, ...) using an iterative eigenvector algorithm optimized for (extremely) large data sets.

The program allows a choice of metrics to be used for the for the eigenvector determination:

- a. Euclidian metric (Principal Components Analysis: PCA)
- b. Chi-square metric (Correspondence Analysis: CA)
- c. Modulation metric (Modulation Analysis:MA)

**To continue give RETURN, or give a "*" to stop :

The program produces different types of output data:

- a. eigenvectors in "p-space" (the "cases" or image space)
- b. eigenvectors in "n-space" (the "variates" or pixel space)
- c. corresponding Eigenvalues
- d. factorial coordinates of input data in p-space
- e. factorial coordinates of input data in n-space
- f. convergence and consistency parameters

Although the actual algorithm (MvH) remains unpublished the best description of the various concepts is in:

**To continue give RETURN, or give a "*" to stop :

Lisa Borland and Marin van Heel, "Classification of image data in conjugate representation spaces", J.Opt.Soc.Am. A Vol 7 (1990) 601-610.

MSA-SUM-CLASSES

ICM-file: msa:msa.icm

Sum images from the input aligned images file into classes as determined by the CLASSIFY program. The result is a set of noise-free class-averages which can be appreciated visually.

The statistics produced by this program refers to the ORIGINAL data, prior to MSA eigenvector data reduction. They thus complement largely the statistics produced by the

program produces a list file of the IMPORTANT statistical results.

NOTES:

a: The classsums are divided by the number of members in a class.

**To continue give RETURN, or give a "*" to stop :

b: The internal variance of the classes is determined during the summing within the active pixels mask (MSAMASK). A sorted table of the variances (simple Euclidian metrics!) is produce in the output file.

c: Standard deviation images are calculated which tells which areas of the class averages are most reliable (namely those with a low standard deviation).

d: The headers of the output classsums will also contain the factorial coordinates of the sums. It is thus possible to do "weird" things such as classifying the classes or ...

MULTI-REFERENCE-ALIGNMENT

ICM-file: align:align.icm

This command makes things very easy for lazy people. It performs a set of multi-reference alignments, one after the other (including mirror alignments if desired). All one has to have done previously is get the appropriate references in one image file. The alignment loop can be stopped by creating a file STOP.ALI in the default directory (as one can also stop an MSA run by generating a STOP.MSA file in the working directory).

All alignments in this program are DIRECT alignments as opposed to ACF (auto-correlation function) alignments which give much poorer results.

NOTE: All calculations are done IN CORE.

MULTIPLY-BY-CONSTANT

ICM-file: stand:standard.icm

Multiply all pixel values in a set of images by a constant value. The ARITHM program (started by this command) will do all the work for you.

MULTIPLY-IMAGES

ICM-file: stand:standard.icm

Multiply images by one another. A: Multiply a set of input images with the same (second) input image to create a set of output images, or B: multiply corresponding locations of two sets of input images with each other to produce a set of output images.

NOTE: the program TWOIMAG (which is started in this command) is designed for large images mainly. For manipulating smaller images the INCORE programs are more efficient. Hint type: "? *INCO" in the IMAGIC-COMMAND mode to find out what the options are.

MUTUAL-CORRELATION

ICM-file: fft:fft.icm

MUTUAL-correlation between one image, and one or more other images present on the same file. Aimed at cross correlating large (ex-core) images.

Most correlation averaging and/or alignment commands that use cross-correlation, call this operation in its in-core version (cf. INCORELB or INCFCTLB)

The reference image need to be of the same size as the other input image(s).

Reference:

Marin van Heel, Michael Schatz, and Elena Orlova,
"Correlation Functions Revisited",
Ultramicroscopy 46 (1992) 304-316.

IMAGIC-COMMAND : +help N

NOISY-MRALIGN

ICM-file: align:align.icm

This command is used to perform an incore multi-reference alignment with noisy references.

The input images to this command are normally already (roughly) aligned images, aligned relative to one or more earlier references.

After a first (direct) alignment of the images relative to the new (noisy) reference, those images of the aligned set are added together that have the highest cross-correlation coefficient relative to the reference image.

The new image-sum is then contoured with the contour used for the input reference, and the resulting image is then used as a new reference for a second (direct) alignment to refine the alignment.

In the next step the equivalent rotation is done and the

**To continue give RETURN, or give a "*" to stop :
new alignment is compared with the (best) old alignment of the input file ("conditional copy"). Only the "best" of the two aligned images is stored in the output file.

NOTE: You have also the choice to do "mirror alignment".

NOTE: All calculations are done IN CORE

Every output image of this command will contain the image aligned relative to the current reference if the new alignment was better the old alignment in the input file. Else the old one is stored in the output file.

The original images must be reachable for an "equivalent rotation" with only one interpolation. These are commonly the band-pass filtered images.

The reference comes from a separate file, and this file is only used once. The reference has ordinarily been contoured interactively and pretreated. If you give no

**To continue give RETURN, or give a "*" to stop :
location number the LAST image in the file will be the one used as reference.

NOTE : If an image has been mirrored during an alignment procedure its reference number is negative.
Please only specify POSITIVE numbers.

An intermediate sum of the best aligned images will be used as a new reference for a second alignment step. The quality of the second (intermediate) reference will depend on how many images are added into it. Please give the number of images to be added.

You can give a threshold value to cut out unwanted negative density contributions. NOT necessary for ice ??? ?!!!!

Note: -999. means no threshold

An intermediate sum of the best aligned images will be used

**To continue give RETURN, or give a "*" to stop :
as a new reference for a second alignment step. Please give the filename for this image file.

Mirror alignment means that after a first alignment of an

the alignment is redone. If this mirror alignment is better the aligned mirror image is stored, else the unmirrored is used.

NOTE : If an image has been mirrored during an alignment procedure its reference number is negative.

Same command as ALIGN-NOISY-REFERENCE.

NORM-VARIANCE

ICM-file: stand:standard.icm

Within the specified area, the average density of the image is floated to zero and the variance of the image is normalised to a specified value. Outside it, all densities can be zeroed.

Just one of the many parallel entries to the PRETREAT command. Call the command to see all the various options that are available.

If you want to use a contour (plt) file to define the area for normalization, use command: IMPOSE-PLT-CONTOUR.

IMAGIC-COMMAND : +help O
NO MATCHING COMMAND

IMAGIC-COMMAND : +help P

PAD-IMAGES

ICM-file: stand:standard.icm

PAD an input image with zeroes to avoid wrap-around artefacts in subsequent Fourier-space manipulations.

This command will lead you to the SUBFILE-OF-IMAGE command which has many more options than just the padding of images. Use option PAD or SMALLPAD.

PDB-TORSION-ANGLES

ICM-file: threed:threed.icm

This icommand reads PDB files files and calculates torsion angles between various amino-acid backbone atoms. The torsion angles are then written out to a plt file. The plt file can be used by an external plotting program to obtain a Ramachandran plot.

PEAK-SEARCH-ALL

ICM-file: stand:standard.icm

Search for the, say 1000, predominant peaks in an input image and write those peaks into a peak-list in IMAGIC "PLT" style format.

You can then check the positions of the peaks by plotting by using commands such as PLOT-ALL (STARS option).

PEAK-SEARCH-TOP

ICM-file: stand:standard.icm

Search for highest (TOP) peak in an image file, and write the coordinates of that peak into the appropriate position in the headers record of the image where it can be picked up by subsequent programs.

PIXEL-DUPLICATION

ICM-file: stand:standard.icm

Generate a new, larger, output image in which the pixels are generated by repeating (duplication) pixels in the input image.

For example, a 64x64 image can be converted into a 128x128 image in which pixels 1,1; 1,2; 2,1; and 2,2 all contain the density value found in the input image at position 1,1.

NOTE: that the BLOW-UP command in IMAGIC allows you to create smooth larger images by interpolation.

PLOT-ALL

ICM-file: plot:plot.icm

This program is the IMAGIC general purpose plotting program. It accepts input both in "PLT" style formatted files and IMAGIC files ("IMG" + "HED") containing 1D data.

The "PLT" files are formatted files which can freely be exchanged with others graphics programs as well. In particular some PC and MAC software packages for producing graphics out produce superb publication-oriented results.

"IMG" + "HED" plot files allow the generation of a PLOT based on the coordinates stored as 1D images (sequences of curves stored in a single IMAGIC file).

The PLOTALL program, associated with this command works within the IMAGIC context and can be used both for

satisfied with the parameter settings, for producing good quality hardcopy printouts on plotters and other hardcopy

**To continue give RETURN, or give a "*" to stop :
devices.

PORNO ICM-file: util:unx_util.icm

Uuihh, uuihh, uuihh ...

PREPARE-MRAREFS ICM-file: align:align.icm

This command is dedicated to all users who find it hard to think things through systematically. It is also dedicated to those other poor souls who have to explain things to them.

PREPARE-MRAREFS makes things very easy for people. All one has to do is copy the references that one wants for an MRA (multi-reference alignment) into one reference file and then contour them with the COOS option of the DISPLAY program.

Now, what PREPARE-MRAREFS does first is prepare mirrors of these images and their contours. All references and their mirror versions then undergo a multi-reference alignment, against each other reference (if desired including the mirror versions). At each step of the alignment, a new reference is selected from the previously aligned file. The contour of this reference is also rotated and shifted from the

**To continue give RETURN, or give a "*" to stop :
original. Each new reference is prepared for MRA by the usual contouring and thresholding within the contour. There are two options to store those aligned, contoured and thresholded output references: Using option TANDEM the output files are written in the following order: referencel, reference2, ... mirrorl, mirror2, ... , and with option ALTERNATE: referencel, mirrorl, reference2, mirror2, ... At then end of it all, all of your references are ready for MRA.

NOTE: IF you do NOT want to perform MRA against mirrored references, use option TANDEM and then just do the multi-reference alignment against the first n reference images.

PRETREAT-CURVE ICM-file: spectra:spectra.icm

Command to manipulate data in a curve (1D image, like spectra,...) , either to float a curve or normalise its variance. This program performs these operations on the whole data set or within specified windows.

Modes of pretreatment:

MASKONLY : Within the specified area(s), the densities are unchanged. Outside it, all densities are ZEROED.

ZEROFLOAT : Within the specified area(s), the average density of the curve is "floated" to zero. Outside it, all densities are ZEROED.

NORMVAR : Within the specified area(s), the average density of the curve is floated to zero and the variance

**To continue give RETURN, or give a "*" to stop :
of the curve is normalised to a specified value.

PEAKHIGHT : Within the specified area(s), the densities are "floated" to be between 0 and 1.

PRETREAT-IMAGE

ICM-file: stand:standard.icm

The purpose of this program is the manipulation of the densities of an image, either to float an image or normalise its variance. The command performs these operations on the WHOLE FILE, within a CIRCLE, etc. If a circle, then all pixels outside the circle will contain only zeroes. The command can also ZERO FLOAT the input images.

Call the command to see all the various options that are available.

NOTE: This command works does NOT work on an area defined by a contour (stored in a .PLT file). For this option please use the command IMPOSE-PLT-CONTOUR.

Same command as PRETREAT-WHOLE-IMAGE.

PRETREAT-WHOLE-IMAGE

ICM-file: stand:standard.icm

The purpose of this program is the manipulation of the densities of an image, either to float an image or normalise its variance. The command performs these operations on the WHOLE FILE, within a CIRCLE, etc. If a circle, then all pixels outside the circle will

the input images.

Call the command to see all the various options that are available.

NOTE: This command works does NOT work on an area defined by a contour (stored in a .PLT file). For this option please use the command IMPOSE-PLT-CONTOUR.

Same command as PRETREAT-IMAGE.

PRINT-GREYVALUES

ICM-file: misc:misc.icm

Command to print the density values of an input image on the monitor.

PRINT-IMAGE

ICM-file: stand:standard.icm

Print an image on the terminal.

This command produces HORRIBLE images on conventional CRT terminals, or WALLPAPER on old-fashioned printers.

Nevertheless, if you are developping porgrams (I mean programs) in a silent secluded corner of your basement on your old VT100 terminal, undisturbed by ringing telephones or by the ventilator of your X-windows workstation, you may be happy to look at the results of your efforts, there and then....

PROTECT-IMAGE

ICM-file: util:unx_util.icm

Protect an image file from being deleted or overwritten. This is merely a direct call to the UNIX utilities.

IMAGIC-COMMAND : +help Q

QUIT

ICM-file: util:gen_util.icm

The "QUIT" command will bring you back to the host's operating system; it is thus equivalent to "END", "EXIT" or "*". If you are in MODE-ACCUMULATE, that mode of operation will NOT be discontinued. You can thus continue to

commands.

IMAGIC-COMMAND : +help R

REALS-FROM-IMAGE-FILE ICM-file: stand:standard.icm

Print real data values from an image file as numbers.
Sometimes (debugging?) you may want to convince yourself
you are still dealing with numbers.

REGENERATE-COMMANDS ICM-file: util:gen_util.icm

IMAGIC COMMANDS reside in the so called "ICM" files.
The "ICM" files are text files containing the definition of
the IMAGIC commands and the interactive help associated
with the command. However, before we can actually use a
command the contents of the "ICM" file(s) has/have to be
transferred to the COMMANDS.DAT file which is a random
access file geared at rapid access times such that commands
can be built up rapidly without continuously scanning
through (slow) sequential files.

The REGENERATE command converts one or more ICM-files to
the direct-access file COMMANDS.DAT. For this purpose the
IMAGIC program opens a file called: "DRIVER.DRV" in the
default directory. The driver file contains the names of
the ICM files to be converted to the local COMMANDS.DAT
file. To regenerate the system files one thus has to set
the IM: directory to be the default directory.

**To continue give RETURN, or give a "*" to stop :

NOTE: the interactive help will remain in the ICM files
such that these files must remain in place for the help
facility to remain available.

NOTE-2: To regenerate you have to give a password
(GOAHEAD) which MUST be given in capital letters!

RENAME-IMAGE-FILE ICM-file: stand:standard.icm

Rename an image file (header, image and plt file,
if available).

ROTATE-CONTOUR ICM-file: stand:standard.icm

ROTATE manipulate and move PLT coordinates around

The command actually leads you to the MOVEPLT program which has various options for manipulating "PLT" coordinate files. For an up-to-date list of its virtues start the program and ash for the interactive help.

ROTATE-IMAGE

ICM-file: stand:standard.icm

Rotate an image over a specified angle. Angle input may be from the header array or may be specified explicitly by the user. Many options will enlighten your path once you have started the ROTATE program.

NOTE: It is important to work with zero-average images since areas of the output image that fall outside of the input image are normally filled with zeroes.

ROTATE-RANDOMLY

ICM-file: align:align.icm

Shift and/or rotate a set of input images over parameters generated by a random number generator.

Can be used to generate test data sets to try out alignment algorithms, for example.

IMAGIC-COMMAND : +help S

S-IMAGE

ICM-file: fft:fft.icm

Calculates the S-image for a sequence of input images to estimate the information (resolution).

Reference:

J. Sass, E. Beckmann, G. Bueldt, D.L. Dorset, M. van Heel, J. Rosenbusch, F. Zemlin, E. Zeitler and A. Massalski, "Densely packed Beta-structure at the protein-lipid interface of Porin is revealed by high-resolution cryo-electron microscopy", J. Mol. Biol. 209 (1989) 171-175.

The command is the same as INFORMATION-IN-SEQUENCE which actually not only calculates the S-image but various other information measures, like Q-factor, I-image, power spectrum etc.

SCAN-IMAGE-LINE

ICM-file: stand:standard.icm

Print a plot of a line-scan through an image. The requested image lines will be converted to the IMAGIC "PLT" format which are then used as input for, for example, the PLOT-ALL command.

SELF-CORRELATION

ICM-file: fft:fft.icm

Self-correlation of (large) images in IMAGIC files.

The self-correlation is calculated in two steps: first a 2D image is Fourier transformed to find the complex transformed of the image (phases and amplitude). Then one takes the amplitudes of these complex values prior to a reverse Fourier transform which brings us back to real space.

Since the input images are considered to be cyclical for the FFT operations (the left edged touches the right edge, the top edge touches the bottom one), one may be bothered by so-called "wrap-around" artefacts when calculating the ACFs (also known as "aliasing"). To avoid this effect one needs to mask the image with, for example, a circular mask, and/or pad the input image with zeroes (after floating the image to zero average density). Use such commands as "CUT-IMAGE" and/or "MASK-IMAGE" to perform such operations.

**To continue give RETURN, or give a "*" to stop :

One can pad the images with zeroes to twice their original linear dimensions (PAD in SUBFILE) to absolutely avoid the effect. However, since many images are already supplied with a mask which is smaller than the image, the SMALLPAD option (padding to 3/2 of the linear file dimensions) is often sufficient and may save a lot of CPU time.

NOTE: that different newer commands and associated programs also support SCF functions like SPECIAL-FUNCTIONS (in module DSCF) and INCORE-FFT2D-OPERATIONS (module FFT).

SHIFT-BY-PIXEL

ICM-file: stand:standard.icm

Shift an image (CYCLICALLY) in X- and Y- directions over an INTEGER number of pixels. Since this type of operation is nowadays mostly performed by subroutines called from alignment programs, this command is seldomly used in this form. One thing it is very good for is for creating

correlation-type of alignments. The use of this program guarantees that the original and the shifted image area identical but for the cyclical shift.

For non-integer shifts, use command SHIFT-IMAGE with option SHIFT.

SHIFT-IMAGE ICM-file: stand:standard.icm

Shift image over both integer and non-integer number of pixels by interpolation.

Where as the SHIFT-BY-PIXEL command will shift an image (CYCLICALLY) over an integer number of pixels in the X- and Y- directions, this command allows you to shift (NON-CYCLICALLY) over fractions of pixel distances. This, is done by interpolation.

This command actually only brings you to the ROTATE program which includes more than only this shift option.

SHIFT-RANDOMLY ICM-file: align:align.icm

Shift and/or rotate a set of input images over parameters generated by a random number generator.

Can be used to generate test data sets to try out alignment algorithms, for example.

SHOW-PIXEL-CLASSES-MSA ICM-file: msa:msa.icm

This command is about appreciating results of classifications performed in the conjugate data space. For more info see:

Lisa Borland and Marin van Heel, "Classification of image data in conjugate representation spaces", J.Opt.Soc.Am. A Vol 7 (1990) 601-610.

The program generates pixel-classes maps such that classifications of pixel-vectors (sequel-vectors in sequence analysis, wave-number vectors etc) can be appreciated visually. The program reads in a "CLS" style file to find out which pixel vectors belong to which class.

SHOW-PROCESS ICM-file: util:unx_util.icm

Shows informations to your current process(es).
(UNIX system call)

SHOW-USER ICM-file: util:unx_util.icm

See who's logged in. The command shows a list
with login name, terminal name, and login time
for each current user. (UNIX system call)

SINECORR ICM-file: angrec:angrec.icm

Command that calculates SINOGRAM CORRELATION functions, and
finds the peaks therein. This command is applied to a set
of SINOGRAMS calculated from the projection images.

The peaklists from this command are used to find the
first angular assignments for a set of 3 projections.

From there on, the sinograms themselves are used to solve
the angular reconstitution problem for the fourth and
subsequent projection using the BRUTE-FORCE algorithm also
integrated into the ANGULAR-RECONSTITUTION command.

SINOGRAM ICM-file: angrec:angrec.icm

Calculates a SINOGRAM from a projection image or any other
type of 2D image.

The sinogram of a 2D image is the collection of its
line-projections in all possible projection directions.
The line projections are mounted under each other to form
the so called sinogram.

Sinograms are important for solving angular reconstitution
problems which is why this command is located in the ANGREC
IMAGIC module.

The program also has a second somewhat unexpected
application: any (synthetic) 2D object can be converted to
the projection of a helical 3D object with the help of
this command.

SMILE ICM-file: util:unx_util.icm

their frustration.

`SORT-PLT-COORDINATES`

ICM-file: crystal:crystal.icm

Sorting and merging operations on PLT coordinate files for various purposes. Various operations on PLT files to produce a new PLT file with different properties are concentrated in this program.

Sorted PLT files have, for example, the advantage that the extraction of small patches centered around the peak positions (as stored in the PLT file) may be quicker.

For more info start the program interactively.

`SPECIAL-FUNCTIONS`

ICM-file: dscf:dscf.icm

Various special functions, in particular INVARIANT functions calculated IN-CORE such as:

ACF autocorrelation function, reference (for example)

Frank J., "The role of correlation techniques in computer image processing", in: Hawkes P.W. (Ed.) Computer processing of electron microscope images, Springer, Berlin (1980), 187-221.

SCF self correlation function

DACF double auto correlation function, reference:

Schatz M. and Van Heel M., "Invariant classification of molecular views in electron micrographs", Ultramicroscopy 32 (1990) 255-264.

**To continue give RETURN, or give a "*" to stop :

DSCF double self correlation function, reference: see DACF

(rotational) Power Spectrum etc.

`SPHERICAL-DENSITY-THREED`

ICM-file: threed:threed.icm

Various options in this command:

a) Plot the radial density distribution of a 3D volume

b) For a complex input volume plot the radial power spectrum

- c) Create a spherically symmetric 3D volume with the input 3Ds radial density distribution imposed.

STREAK-IMAGES

ICM-file: stand:standard.icm

This command replaces an image (or rectangular window of an image) by a line average calculated over the window in a horizontal or vertical direction. This program is a special purpose program used to generate reference images without specific preferences (i.e. feature-less) in one direction.

Such images were, for example, once used as reference images to vertically align sections of helical fibers.

STRUCTURAL-HISTOGRAM

ICM-file: threed:threed.icm

This command creates histogram-images based on the structural properties of an amino-acid.

Structural histograms can be based on a multitude of structural properties such as torsion angles, lengths, volumes etc. At present only one strategy has been implemented, based on the amino-acid backbone torsion angles: phi, psi and omega.

Like the sequence histograms, here we create 2D histograms of the torsion angles of neighboring residues. The bins used are regions in (phi,psi,omega) space.

SUBFILE-OF-IMAGE

ICM-file: stand:standard.icm

This program extracts one or more small image(s) from an input image or a set of input images. The program has a large number of options to choose from.

Some typical applications:

- a. Extract many small images from a big input image driven by a peak-table stored in IMAGIC "PLT" format
- b. PAD an input image with zeroes to avoid wrap-around artefact in subsequent Fourier-space manipulations
- c. Divide a large input image checkerboard-wise into a large set of small output images to be used for, for example, texture analysis

appreciate its beauties with your own eyes ...

**To continue give RETURN, or give a "*" to stop :

SUBTRACT-CONSTANT ICM-file: stand:standard.icm

SUBTRACT a constant value from all pixels in an image. This command will lead you to the ARITHM program which has many more options than just subtracting a constant.

Just one of the many parallel entries to the ARITHM program.

SUBTRACT-IMAGES ICM-file: stand:standard.icm

Subtract images from one another. This command will lead you to the TWOIMAG program which has many more options than just subtracting two images. Use option: SUBTRACT.

NOTE: the program TWOIMAG (which is started in this command) is designed for large images mainly. For manipulating smaller images the INCORE programs are more efficient. Hint type: "? *INCO" in the IMAGIC-COMMAND mode to find out what the options are.

SUM-ALIGNED-IMAGES ICM-file: align:align.icm

The input image file is assumed to contain aligned images treated by multi-reference alignment(s). The command then selects all those images correlating best to the specified references and calculates their sum images (total or conditional sum).

SUM-IMAGES ICM-file: stand:standard.icm

Summing set of images to make one output image.

NOTE: Normally when you want to do this you have a large set of small input images and you should rather used the INCORE-SUM command instead. INCORE-SUM is the newer command, and it provides many more options than the oldie SUM-IMAGES.

Simple statistics of (sets of) images. Determines min, max, mean, and sigma and writes these value into headers.

The program is important in the context of imposing good greyvalues while displaying a set of images in an IMAGIC file. Start the program for more info.

NOTE that you can also pickup the results from this statistical analysis in the HEADERS program if you so wish.

IMAGIC-COMMAND : +help T

TEST-CURVE-CREATION

ICM-file: spectra:spectra.icm

Create test functions for various purposes. For eample to play around with Fourier transforms to get a feeling for the behaviour of different functions after transformation.

Options:

Sine function(s)

Cosine function(s)

Noise

Delta function(s)

Sinc function(s)

Rectangle function(s)

**To continue give RETURN, or give a "*" to stop :

triangle function(s)

etc...

For an up-to-date account of all available options, start the program interactively and ask for more help.

TEST-IMAGE-CREATION

ICM-file: stand:standard.icm

Create a test image for various purposes. The many options of this program allow you to create test images with:

BLOBS : Image(s) will contain three Gaussian blobs.
CHECKERS : Creates one or more 'checkerboard' test-images.
CIRCLES : Image(s) will contain filled discs.
CONSTANT : Image(s) will contain a constant density value
which value is determined by the user.
DISC : Image(s) will contain a disc of unit density
centered at the midpoint of the image.
GAUSSNOIS: Images(s) will contain white noise with a
Gaussian distribution, average density and
sigma value are determined by the user.

**To continue give RETURN, or give a "*" to stop :

GRID : Image(s) will contain a mesh pattern in that
16th pixel and line will have value 200.0 and
all other pixels will be zero.
MANDEL : Image(s) generated a la Mandelbrot set, i.e.,
those complex numbers c such that the iterative
series $z \leftarrow z^2 + c$ does not diverge, viz.,
 z remains of size less than 2.
M2NDEL : Image(s) generated a la Mandelbrot set, but
with DOUBLE PRECISION arithmetic.
MCCACT : Mandelbrot inspired cubic cactus, i.e., those
complex numbers c such that the iterative
series $z \leftarrow z^3 + (c-1)z - c$ does not
diverge, viz., z remains of size less than 2.
This beast is due to Bruce Ikenaga of Case
Western Reserve University.

**To continue give RETURN, or give a "*" to stop :

NOISE : Images(s) will contain white noise, randomly
distributed between the values -10.0 and +10.0
NUMLIN : Image(s) will contain numbers corresponding to
the line coordinate, that is, the X-coordinate
of the pixel.
NUMPIX : Image(s) will contain numbers corresponding to
the pixel position within the line, that is,
pixel-density = Y-coordinate of pixel
POINTS : Image(s) will contain points of specified
densities at specified positions.
RECTANGLE: Image will be a rectangle of specified values
both within and without.
SIEMENS : Image(s) will contain a SIEMENS star test

**To continue give RETURN, or give a "*" to stop :

 SPIRAL : Image(s) will contain points along a squared spiral, equally spaced in terms of pathlength.

 WEDGE : Image(s) will contain numbers; these correspond to sum of the line coordinate and the pixel coordinate of the corresponding pixel.

TEST-MIRROR-SYMMETRY ICM-file: incore:incore.icm

Check mirror symmetry of a set of incore molecular images, by finding the best mirror axis. The center of mass of these images must be at the geometric center of the (square) image. If not, an INCORE-ALIGN-MASS command, for example, should be performed first.

TEST-PLT-CREATION ICM-file: stand:standard.icm

Create test .PLT (coordinates) files for various purposes.

These files are standardised formatted files used for various purposes in IMAGIC. In particular 1D curves such as histograms, but also closed contours to be applied as a mask to a 2D image are stored in PLT format. IMAGIC commands exists that allow the manipulation (shift, rotations, ..) of closed contours.

Want to know more? Start the program.

TEST-ROTATIONAL-SYMMETRY ICM-file: incore:incore.icm

Check rotational symmetry of a set of incore molecular images. The center of mass of these images must be at the geometric center of the (square) image. If not, an INCORE-ALIGN-MASS command, for example, should be performed first.

THREED-ALIGN-VOLUMES ICM-file: threed:threed.icm

Command to align two 3D data set to each other, in position, rotation and scaling. This command is based on an iterative procedure that involves aligning forward projections from the two data sets to each other. It is assumed that the data sets

This command generates a 3D mask delineating a 3D object in an IMAGIC 3D map.

The basic idea is essentially the same as that of the automatic particle detection algorithm published in:

Marin van Heel, "Detection of objects in quantum noise limited images", Ultramicroscopy 8 (1982) 331-342.

When "inside" the object in the 3D volume, we have a higher local variance level than outside the object. Whereas in the cited paper the local variance was measured directly in this program, the local linear variation (with respect to zero) is measured. The various consecutive steps in the processing:

- (1) High-pass filter the input volume such that only the relevant high frequency information in the data remain
- (2) Take the ABS (or the squares) of the modulations surviving step (1)
- (3) Low-pass filter the resulting ABS map.
- (4) Binarize the low-pass filtered ABS map.
- (5) Possibly low-pass filter the binary map to make a smooth-edged mask

For refinement purposes, a number of options are available that will let you, for example:

- a) DO-IT-ALL
- b) Change the THRESHOLD to be applied onto the low-pass filtered ABS/VARIANCE map.
- c) Or ...

Command to go through a 3D density distribution - like a 3D reconstruction - to SMOOTH the 3D densities. A noise 3D reconstruction may be polished so as to produce a smoother surface or to remove single voxels above a given threshold prior to a "sexy3D" surface rendering.

Available options :

LOW-PASS-FILTER:

volume by averaging over all voxels in the input volume that are close enough to the output voxel.

WARNING: This "real space" option uses a lot of CPU and the results may not be as good as what you would

**To continue give RETURN, or give a "*" to stop :
get using the Fourier-space low pass filtering operation. Thus it is a better idea to use a command like THREED-FILTER to low-pass a 3D volume.

BLOBBY-FILTER:

The output 3D volume is generated from the input 3D volume by the statistics of the over-a-given-threshold voxels within a given distance of the position of the output voxel.

This option is used, for example, to remove too small details in the image, floating around by themselves unconnected to the main body of the 3D object.
(Remove salt-and-pepper noise)

DILATE:

Extend a mask by including every voxel of the output volume into the mask which is within a certain distance

**To continue give RETURN, or give a "*" to stop :
of the original mask as defined by a threshold value in the input volume.

THINNING:

Reduce a mask by excluding every voxel of the output volume from the mask which is within a certain distance of the edge of the original mask as defined by a threshold value in the input volume.

BINARY:

The output 3D volume is generated from the input 3D by binarisation: an output voxel will be zero if the corresponding input voxel is below the threshold, and the output voxel will be set to 1. if the corresponding input voxel has an above-threshold density.

SOFT-BINARY:

The output 3D volume is generated from the input 3D

**To continue give RETURN, or give a "*" to stop :
volume by looking how far away in the input 3D volume, one finds a voxels with an above-threshold density. The output 3D volume will have values ranging from 0. to 1. depending on how far the voxel is from the above-threshold part of the input 3D.

the results may not be as good as what you would get using the Fourier-space low pass filtering operation. Thus a reasonable alternative processing path would be to first DILATE/EXPAND a mask here, and then using a command like THREED-FILTER to low-pass filter the resulting dilated mask. If you hard zeroes in the 3D mask, you may need to apply some form of threshold to the resuting low-pass filtered mask.

THREED-BLOBBY-FILTER

ICM-file: threed:threed.icm

Command to go through a 3D density distribution - like a 3D reconstruction - to SMOOTH the 3D densities. A noise 3D reconstruction may be polished so as to produce a smoother surface or to remove single voxels above a given threshold prior to a "sexy3D" surface rendering.

Available options :

LOW-PASS-FILTER:

The output 3D volume is generated from the input 3D volume by averaging over all voxels in the input volume that are close enough to the output voxel.

WARNING: This "real space" option uses a lot of CPU and the results may not be as good as what you would get using the Fourier-space low pass filtering

**To continue give RETURN, or give a "*" to stop :
operation. Thus it is a better idea to use
a command like THREED-FILTER to low-pass
a 3D volume.

BLOBBY-FILTER:

The output 3D volume is generated from the input 3D volume by the statistics of the over-a-given-threshold voxels within a given distance of the position of the output voxel.

This option is used, for example, to remove too small details in the image, floating around by themselves unconnected to the main body of the 3D object.
(Remove salt-and-pepper noise)

DILATE:

Extend a mask by including every voxel of the output volume into the mask which is within a certain distance of the original mask as defined by a threshold value in

**To continue give RETURN, or give a "*" to stop :

THINNING:

Reduce a mask by excluding every voxel of the output volume from the mask which is within a certain distance of the edge of the original mask as defined by a threshold value in the input volume.

BINARY:

The output 3D volume is generated from the input 3D by binarisation: an output voxel will be zero if the corresponding input voxel is below the threshold, and the output voxel will be set to 1. if the corresponding input voxel has an above-threshold density.

SOFT-BINARY:

The output 3D volume is generated from the input 3D volume by looking how far in the input 3D volume,

**To continue give RETURN, or give a "*" to stop :
one finds a voxels with an above-threshold density.
The output 3D volume will have values ranging from 0. to 1.
depending on how far the voxel is from the above-threshold
part of the input 3D.

WARNING: This "real space" option uses a lot of CPU and the results may not be as good as what you would get using the Fourier-space low pass filtering operation. Thus a reasonable alternative processing path would be to first DILATE/EXPAND a mask here, and then using a command like THREED-FILTER to low-pass filter the resulting dilated mask. If you hard zeroes in the 3D mask, you may need to apply some form of threshold to the resuting low-pass filtered mask.

THREED-BLOCK-CONVOLUTION-FILTER ICM-file: block:block.icm

A three-dimensional block-convolution is filtering operation produces an output 3D-image by averaging the input voxels within a "block" to produce one voxel of the output 3D-image. This type of operation can be rather fast since "running averages" algorithms are essentially independent of the size of the block. There are two main ways of using this filter:

1. Low pass filter:

One output voxel is simply the average of all voxels within the filter block. The larger the size of the block, the stronger the low-pass filter effect.

2. High pass filter:

THREED-FFT should be performed on the input 3D volumes prior to doing the Fourier ring correlation.

The 3D Fourier-Schell correlation is the 3D extension of the FRC (Fourier Ring Correlation) technique originally designed to compare two similar images with each other.

A reference for the Fourier Ring Correlation:

Marin van Heel, "Similarity measures between images", Ultramicroscopy 21 (1987) 95-100.

For the Fourier Shell Correlation:

George Harauz and Marin van Heel, "Exact filters for general geometry three dimensional reconstruction",

**To continue give RETURN, or give a "*" to stop :
Optik 73 (1986) 146-156.

THREED-CONTOUR-MASK

ICM-file: threed:threed.icm

Mask a 3D data set with a contour such that every section has its own interactively determined contour mask. The contour is generated with the COOS option of the DISPLAY program.

Applications:

- 1) Mask out an object in a 3D data set such that it can be displayed with a stereo representation of the surface
- 2) Mask out a set of images individually without having to copy each image location out of the input file prior to the contouring in the THREED-CONTOUR command. This is, for example important for masking out projections prior to a 3D reconstruction or "reconstitution"

THREED-CONVERT-COORDINATES

ICM-file: threed:threed.icm

Command to transform a 3D volume from/to a cartesian coordinate system to/from a spherical coordinate system.

Same command as THREED-CARTESIAN-TO-SPHERICAL and
THREED-SPHERICAL-TO-CARTESIAN

THREED-DILATE-MASK

ICM-file: threed:threed.icm

reconstruction - to SMOOTH the 3D densities. A noise 3D reconstruction may be polished so as to produce a smoother surface or to remove single voxels above a given threshold prior to a "sexy3D" surface rendering.

Available options :

LOW-PASS-FILTER:

The output 3D volume is generated from the input 3D volume by averaging over all voxels in the input volume that are close enough to the output voxel.

WARNING: This "real space" option uses a lot of CPU and the results may not be as good as what you would get using the Fourier-space low pass filtering

**To continue give RETURN, or give a "*" to stop :
operation. Thus it is a better idea to use
a command like THREED-FILTER to low-pass
a 3D volume.

BLOBBY-FILTER:

The output 3D volume is generated from the input 3D volume by the statistics of the over-a-given-threshold voxels within a given distance of the position of the output voxel.

This option is used, for example, to remove too small details in the image, floating around by themselves unconnected to the main body of the 3D object.
(Remove salt-and-pepper noise)

DILATE:

Extend a mask by including every voxel of the output volume into the mask which is within a certain distance of the original mask as defined by a threshold value in

**To continue give RETURN, or give a "*" to stop :
the input volume.

THINNING:

Reduce a mask by excluding every voxel of the output volume from the mask which is within a certain distance of the edge of the original mask as defined by a threshold value in the input volume.

BINARY:

The output 3D volume is generated from the input 3D by binarisation: an output voxel will be zero if the corresponding input voxel is below the threshold, and the output voxel will be set to 1. if the corresponding input voxel has an above-threshold density.

The output 3D volume is generated from the input 3D volume by looking how far away in the input 3D volume,

**To continue give RETURN, or give a "*" to stop :
one finds a voxels with an above-threshold density.
The output 3D volume will have values ranging from 0. to 1.
depending on how far the voxel is from the above-threshold
part of the input 3D.

WARNING: This "real space" option uses a lot of CPU and
the results may not be as good as what you would
get using the Fourier-space low pass filtering
operation. Thus a reasonable alternative
processing path would be to first DILATE/EXPAND a
mask here, and then using a command like
THREED-FILTER to low-pass filter the resulting
dilated mask. If you hard zeroes in the 3D mask,
you may need to apply some form of threshold to
the resuting low-pass filtered mask.

THREED-FFT ICM-file: threed:threed.icm

Perform a true 3D Fast Fourier Transform - Forward or
Reverse. The method is based on the fast transposing
algorithm dedscribed in:

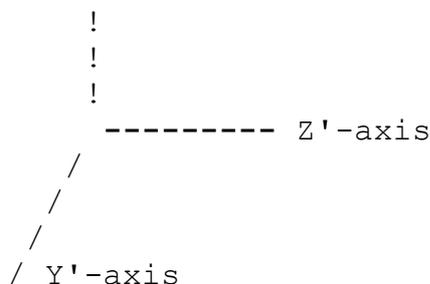
Marin van Heel, "Fast transposing of large multi-
dimensional image data sets", Ultramicroscopy 38
(1991) 75-84.

The input 3D data set has the following coordinate system:

```
      ! Z-axis  
      !  
      !  
      !  
      ----- Y-axis  
      /  
     /
```

**To continue give RETURN, or give a "*" to stop :
/
/ X-axis

The X-Y planes or "sections" are the normal images in
IMAGIC. The different sections of the 3-D data volume are
the different locations in an image file (different
Z-values). After the THREED-FFT operation we obtain the
coordinate system:



**To continue give RETURN, or give a "*" to stop :

Which still is a right-handed coordinate system.
 After a REVERSE FFT operation one goes back to the original
 XYZ coordinate system

THREED-FILTER ICM-file: threed:threed.icm

This command performs Fourier filtration of a true 3D
 image. The 3D image is first Fast Fourier Transformed.
 The transform is treated by a specified mask
 (CIRCULAR, GAUSSIAN, LORENTZIAN, or HIGHPASS). An inverse
 transformation brings you back to real space. The input
 and output files MUST be different.

THREED-FLIP ICM-file: threed:threed.icm

Restack the input 3D data set. This means that the lowest
 section will change positions with the highest section etc.
 Using option FLIP, you may loose the position of the origin
 in the Z direction for an even number of sections. To avoid
 this please use option RESTACK. Then the central plane
 (IZLP/2+1) and plane #1 remain in place. The program thus
 creates an enantiomeric (alternative handedness) version of
 the input 3D file.

The program started by this command contains various other
 options concerning the stacking organisation of 3D data sets.

Same command as THREED-Z-OPERATIONS, THREED-RESTACK,
 THREED-ZSHIFT

THREED-FORWARD-PROJECTION ICM-file: threed:threed.icm

General projections of a 3D volume are computed using a
 large variety of different options. The projection
 directions can be chosen freely (all Euler angles allowed).

Options include:

1. different interpolation schemes for calculating projection pixels.
2. different ways of generating sets of Euler angles
3. different ...

THREED-FOURIER-CROSS-INFO ICM-file: threed:threed.icm

This command is used to compare two 3D volumes in Fourier space with each other using the Fourier-Cross-Information (FCI). The command leads to the program TWO3DIM which has some other options available.

Reference: Marin van Heel, and Michael Schatz,
"Fourier Cross Information between two images
or 3D volumes"

THREED-IMPOSE-SYMMETRY ICM-file: threed:threed.icm

Impose pointgroup symmetry onto 3D density distributions. Currently all cyclical point-groups and dyhedral pointgroups up to D6 (622) are supported.

Given a 3D density distribution, centered around the 3D volumes center (IXLP/2+1, IYLP/2+1, IZLP/2+1), an output volume is created which has an exact pointgroup symmetry imposed onto it. The symmetry is exact of up an interpolation error (it is impossible to impose exact six-fold symmetry on a D volume sampled on a square lattice).

THREED-MASK ICM-file: threed:threed.icm

Mask a 3D image using one of the options in program ARITHM, e.g., CIRCULAR, GAUSSIAN, LORENTZIAN, or HIGHPASS. The input and output 3D images may be the same, and may represent either real data or Fourier transforms.

The ARITHM program started by this command contains various other options. The option for masking 3D volumes is THREED.

THREED-MODEL-MOLECULE ICM-file: threed:threed.icm

This command starts the MODEL3D program which is aimed at

purposes. The models generated are based on primitives which are typically spheres with some given density.

3D Models may be generated with all possible different pointgroup-symmetries imposed, like for example:

222, 622, 532 (icosahedral), etc.
(for more info start the program)

The command can also be used to create a 3D volume using a "plt" coordinates files which was created using a PDB data file (command: IMPORT-PDP-TO-PLT)

Another typical application of the THREED-MODEL program is to generate a model of a 400-atom metal cluster, project it in different directions (with THREED-FORWARD-PROJECTION) and

**To continue give RETURN, or give a "*" to stop :
then impose the effect of the electron microscopic transfer function on the projections (TRANSFER-FUNCTION) so as to simulate real electron microscopical images of such clusters.

Note that one can also consider to create other types of 3D density distributions with, for example, the command THREED-GENERAL-PHANTOM, and to subsequently symmetrize that volume by using the command THREED-IMPOSE-SYMMETRY.

A "2D" options in this program allows you to generate three-dimensional 2D crystals of only one unit-cell high with different plane-groups imposed. For more info on this option start the program and ask for further interactive HELP.

THREED-NORM-VARIANCE

ICM-file: threed:threed.icm

Command to normalise (global) mean and variance of a 3D volume stored in the image locations of the input file. The command is important if different 3D volumes should be compared with each other.

NOTE: The commands PRETREAT-WHOLE-IMAGE and PRETREAT-IMAGE calculate the normalisation factor for every image location independently. THREED-NORM-VARIANCE, in contrast, treats the file as a 3D volume and uses all locations to normalise the (whole) 3D volume.

THREED-PEAK-FIND

ICM-file: threed:threed.icm

Command to find multiple peaks in a 3D volume. The results

THREED-PROJECTION

ICM-file: threed:threed.icm

Compute either direct or surface projections of a 3D object, at different angles about a tilt axis (the image Z-axis).

For historical reasons, the more general projection options are found under the THREED-FORWARD-PROJECTION command.

The THREED-PROJECTION command brings you to the STEREO program which only includes tomographic ("single tilt-axis") projection options.

The STEREO program is mainly a simple (and the very FIRST, see: M. van Heel, "Stereographic representation of three-dimensional density distributions", Ultramicroscopy 11 (1983) 307-314) program to generate stereo and conventional projections of a 3D object. Newer and more general programs exist with partially overlapping options like: SEXY3D and FORWARD. The associated IMAGIC command

**To continue give RETURN, or give a "*" to stop :
names: THREED-SURFACE-VIEWS, and THREED-FORWARD-PROJECTION

THREED-RADIAL-DENSITY-OPTIONS

ICM-file: threed:threed.icm

If the input 3D image file contains a 3D Fourier Transform (such as calculated by the IMAGIC command THREED-FFT then this command will calculate the power spectrum in each radial shell in Fourier space (RPS).

If the input IMAGIC file contains the original 3D volume then the program will calculate the radial density distribution.

The result will be printed on the screen and a .plt coordinate file will be created with can be displayed with the IMAGIC command PLOT-ALL.

THREED-RESTACK

ICM-file: threed:threed.icm

Restack the input 3D data set. This means that the lowest section will change positions with the highest section etc. Using option FLIP, you may loose the position of the origin in the Z direction for an even number of sections. To avoid this please use option RESTACK. Then the central plane

creates an enantiomeric (alternative handedness) version of the input 3D file.

The program started by this command contains various other options concerning the stacking organisation of 3D data sets.

Same command as THREEED-Z-OPERATIONS, THREEED-ZSHIFT, THREEED-FLIP

THREEED-ROTATE ICM-file: threed:threed.icm

Command to rotate a 3D volume in an arbitrary 3D direction.

3D buffering is used in order to reduce I/O and core memory used.

THREEED-SEXY-STEREO ICM-file: threed:threed.icm

Program to calculate 3D surface views from a 3D density distribution using depth cueing as well as light sources and different shading schemes. It is much more elaborate than the simpler THREEED-STEREO command.

Same command as THREEED-SURFACE-VIEWS.

THREEED-SHADED-STEREO ICM-file: threed:threed.icm

A 2D stereo surface view of a 3D object, from program STEREO, is shaded to enhance its esthetic qualities and features.

The program is a postprocessor for purely z-queued images produced by (for example the THREEED-STEREO command and it renders surfaces facing the observer bright, whereas surfaces facing 90 degrees away from the observer dark.

Please note that there are newer commands like: THREEED-SURFACE-VIEWS.

THREEED-SHELL ICM-file: threed:threed.icm

Command to create a binarised shell structure from a 3D density distribution. The "shelling" algorithm is as follows: A spherical mask is convolved with the density distribution. Whenever all points in the masked region have intensity values exceeding a threshold, the corresponding

This command can be used in order to reduce the amount of material required when making an actual physical model, thereby reducing the cost of making such models.

3D buffering is used in order to reduce I/O and core memory used.

THREED-SHIFT

ICM-file: threed:threed.icm

Command to translate (shift) a 3D volume in an arbitrary 3D direction. Fractional translations are handled via interpolation.

3D buffering is used in order to reduce I/O and core memory used.

Same command as THREED-TRANSLATE.

THREED-SMOOTH

ICM-file: threed:threed.icm

Command to go through a 3D density distribution - like a 3D reconstruction - to SMOOTH the 3D densities. A noisy 3D reconstruction may be polished so as to produce a smoother surface or to remove single voxels above a given threshold prior to a "sexy3D" surface rendering.

Available options :

LOW-PASS-FILTER:

The output 3D volume is generated from the input 3D volume by averaging over all voxels in the input volume that are close enough to the output voxel.

WARNING: This "real space" option uses a lot of CPU and the results may not be as good as what you would get using the Fourier-space low pass filtering

**To continue give RETURN, or give a "*" to stop operation. Thus it is a better idea to use a command like THREED-FILTER to low-pass a 3D volume.

BLOBBY-FILTER:

The output 3D volume is generated from the input 3D volume by the statistics of the over-a-given-threshold voxels within a given distance of the position of the output voxel.

This option is used, for example, to remove too small details in the image, floating around by themselves unconnected to the main body of the 3D object.

(Remove salt-and-pepper noise)

DILATE:

Extend a mask by including every voxel of the output volume into the mask which is within a certain distance of the original mask as defined by a threshold value in

**To continue give RETURN, or give a "*" to stop :
the input volume.

THINNING:

Reduce a mask by excluding every voxel of the output volume from the mask which is within a certain distance of the edge of the original mask as defined by a threshold value in the input volume.

BINARY:

The output 3D volume is generated from the input 3D by binarisation: an output voxel will be zero if the corresponding input voxel is below the threshold, and the output voxel will be set to 1. if the corresponding input voxel has an above-threshold density.

SOFT-BINARY:

The output 3D volume is generated from the input 3D volume by looking how far away in the input 3D volume,

**To continue give RETURN, or give a "*" to stop :
one finds a voxels with an above-threshold density.
The output 3D volume will have values ranging from 0. to 1. depending on how far the voxel is from the above-threshold part of the input 3D.

WARNING: This "real space" option uses a lot of CPU and the results may not be as good as what you would get using the Fourier-space low pass filtering operation. Thus a reasonable alternative processing path would be to first DILATE/EXPAND a mask here, and then using a command like THREED-FILTER to low-pass filter the resulting dilated mask. If you hard zeroeis in the 3D mask, you may need to apply some form of threshold to the resuting low-pass filtered mask.

THREED-SPHERICAL-TO-CARTESIAN ICM-file: threed:threed.icm

Command to transform a 3D volume from/to a cartesian coordinate system to/from a spherical coordinate system.

THREED-CARTESIAN-TO-SPHERICAL

THREED-STEREO

ICM-file: threed:threed.icm

Compute either direct or surface projections of a 3D object, at different angles about a tilt axis (the image Z-axis).

For historical reasons, the more general projection options are found under the THREED-FORWARD-PROJECTION command.

The THREED-PROJECTION command brings you to the STEREO program which only includes tomographic ("single tilt-axis") projection options.

The STEREO program is mainly a simple (and the very FIRST, see:

M. van Heel, "Stereographic representation of three-dimensional density distributions",
Ultramicroscopy 11 (1983) 307-314)

program to generate stereo and conventional projections of

**To continue give RETURN, or give a "*" to stop :
a 3D object. Newer and more general programs exist with partially overlapping options like: SEXY3D and FORWARD. The associated IMAGIC command names are: THREED-SURFACE-VIEWS and THREED-FORWARD-PROJECTION.

THREED-SUBFILE

ICM-file: threed:threed.icm

Command to extract a sub-volume from a 3D volume.
Complex images are supported.

THREED-SURFACE-VIEWS

ICM-file: threed:threed.icm

Program to calculate 3D surface views from a 3D density distribution using depth cueing as well as light sources and different shading schemes. It is much more elaborate than the simpler THREED-STEREO command.

Same command as THREED-SEXY-STEREO.

THREED-TEST-IMAGE

ICM-file: threed:threed.icm

The image will be a cube with dimensions specified by you, the user.

Many different options will be available. However, for testing 3D reconstruction algorithms, etc., you may want to consider the THREED-GENERAL-PHANTOM command since that may be the only 3D test object with a well balanced spatial-frequency composition.

THREED-THINNING-MASK

ICM-file: threed:threed.icm

Command to go through a 3D density distribution - like a 3D reconstruction - to SMOOTH the 3D densities. A noisy 3D reconstruction may be polished so as to produce a smoother surface or to remove single voxels above a given threshold prior to a "sexy3D" surface rendering.

Available options :

LOW-PASS-FILTER:

The output 3D volume is generated from the input 3D volume by averaging over all voxels in the input volume that are close enough to the output voxel.

WARNING: This "real space" option uses a lot of CPU and the results may not be as good as what you would get using the Fourier-space low pass filtering

**To continue give RETURN, or give a "*" to stop :
operation. Thus it is a better idea to use
a command like THREED-FILTER to low-pass
a 3D volume.

BLOBBY-FILTER:

The output 3D volume is generated from the input 3D volume by the statistics of the over-a-given-threshold voxels within a given distance of the position of the output voxel.

This option is used, for example, to remove too small details in the image, floating around by themselves unconnected to the main body of the 3D object.
(Remove salt-and-pepper noise)

DILATE:

Extend a mask by including every voxel of the output volume into the mask which is within a certain distance of the original mask as defined by a threshold value in

**To continue give RETURN, or give a "*" to stop :
the input volume.

THINNING:

Reduce a mask by excluding every voxel of the output volume from the mask which is within a certain distance of the edge of the original mask as defined by a threshold value in the input volume.

BINARY:

The output 3D volume is generated from the input 3D by binarisation: an output voxel will be zero if the corresponding input voxel is below the threshold, and the output voxel will be set to 1. if the corresponding input voxel has an above-threshold density.

SOFT-BINARY:

The output 3D volume is generated from the input 3D volume by looking how far away in the input 3D volume,

**To continue give RETURN, or give a "*" to stop :
one finds a voxels with an above-threshold density.
The output 3D volume will have values ranging from 0. to 1. depending on how far the voxel is from the above-threshold part of the input 3D.

WARNING: This "real space" option uses a lot of CPU and the results may not be as good as what you would get using the Fourier-space low pass filtering operation. Thus a reasonable alternative processing path would be to first DILATE/EXPAND a mask here, and then using a command like THREED-FILTER to low-pass filter the resulting dilated mask. If you hard zeroes in the 3D mask, you may need to apply some form of threshold to the resuting low-pass filtered mask.

THREED-TOMOGRAPHIC-RECONSTRUCT ICM-file: threed:threed.icm

Three-dimensional reconstruction from projections (various techniques) for a single tilt-axis reconstruction geometry. The options include:

Filtered Back-projection with theoretical filters

Filtered back-projection with "exact" filters

Iterative "SMART" reconstruction.

THREED-TRANSLATE ICM-file: threed:threed.icm

Command to translate (shift) a 3D volume in an arbitrary

THREED-Z-SHIFT

ICM-file: util:gen_util.icm
threed:gen_util.icm!

Cyclical shift of the 3D volume in the direction of the Z-axis. Everything that is pushed out the top of the stack re-enters at the bottom. Please use option ZSHIFT.

The program started by this command contains various other options concerning the stacking organisation of 3D data sets.

Same command as THREED-Z-OPERATIONS, THREED-RESTACK,
THREED-FLIP

THREED-ZOOM

ICM-file: threed:threed.icm

This command magnifies a 3D image. That is, the 3D object is made to occupy a larger part of the 3D volume into which it is embedded. The size of the volume as such thus not change. In other words, an input 64x64x64 volume will produce a 64x64x64 volume during this operation.

Different zoom factors in the X, Y, and Z directions are possible and one can thus use this command to change the X, Y, and Z scalings or aspect ratios.

The BLOWUP3D program started by this command contains various other options. For THREED-ZOOM please use option ZOOM.

In contrast to the BLOWUP option, using the ZOOM options means that one has the possibility to make very precise adaptations. Option BLOWUP is limited to integer numbers.

THRESHOLD-IMAGE

ICM-file: stand:standard.icm

Thresholding an image. The ARITHM program that is started by this commands has many more options than just this simple THRESHOLD.

TRANSFER-FUNCTION

ICM-file: phase:phase.icm

This command can be used for:

functions with choice of the microscopical parameters.
Final result may be stored in a PLT file.

- B) Impose a transfer function onto one or more input images.
- C) Impose a transfer function onto one 3D input volume.
- D) "Correct" the Phase Contrast Transfer Function of an electron microscopical image.
- E) "Correct" the Phase Contrast Transfer Function of a 3D electron microscopical reconstruction.

Same command as CTF-CORRECTION.

TRANSDPOSE-IMAGE

ICM-file: fft:fft.icm

Transposing an image, i.e. exchange the X-Y organization of a real or complex image. The algorithm used is the generalized mixed radix perfect shuffle algorithm:

Marin van Heel, "Fast transposing of large multi-dimensional image data sets", Ultramicroscopy 38 (1991) 75-84.

TRUE-THREED-RECONSTRUCTION

ICM-file: threed:threed.icm

This command starts the TRUE3D program which is a 3D reconstruction program based on "exact filters" which is a filtering strategy of adapting the filter (for filtered back-projection reconstruction) to the "exact" overlap by other "central sections" in the reconstruction.

Each projection to be used for the reconstructions is thus adapted to the exact reconstruction geometry. The technique delivers by far superior results than the more conventional approach with analytical (theoretical) filter normally used in conjunction with the filtered back-projection approach.

References:

George Harauz and Marin van Heel, "Exact filters for general geometry three dimensional reconstruction", Optik 73 (1986) 146-156.

**To continue give RETURN, or give a "*" to stop :

M. Radermacher, "Three dimensional reconstruction of single particles from random and nonrandom tilt series, J. Electr. Microsc. Techn. 9 (1988) 359-394.

The "exact" filtered back-projection also has a Fourier space counterpart with which it is essentially identical. The Fourier space version would only be different in terms of the interpolation scheme. This Fourier version will probably be implemented in IMAGIC in the foreseeable future.

UP-SIDE-DOWN

ICM-file: stand:standard.icm

Command to mirror an input image in up-side-down manner. The first line of the image will become the last line of the output image and vice-versa.

NOTE: the MIRROR-IMAGE command will flip images horizontally whereas UP-SIDE-DOWN flips them vertically.

VIEW-IMAGE

ICM-file: view:view.icm

Separate programme

Missing help file (after LOGNAMES translation :
view:view.hlp

Missing help file (before LOGNAMES translation:
view:view.icm

WALSH-TRANSFORMATION

ICM-file: misc:misc.icm

Command to calculate the walsh transform of an input image file

+help X
NO MATCHING COMMAND

+help Y
NO MATCHING COMMAND

: +help Z

ZERO-FLOAT-IMAGES

ICM-file: stand:standard.icm

Within the specified area, the average density of the image is "floated" to zero. Outside it, all densities are zeroed.

Just one of the many parallel entries to the PRETREAT command. Call the command to see all the various options that are available.

ZOOM an image: the image file size remains constant but the image is magnified (or demagnified) within the borders of the same frame.

NOTE that the BLOW-UP command also magnifies or demagnifies input images by interpolation, but it does it by changing the size of the image file. With the ZOOM option, the image size remains unchanged.

NOTE also that both with ZOOM and with BLOW-UP we have the option to use different scale-factors for the X- and the Y- directions such that we can compensate for aspect-ratio problems of hardcopy devices, for example.