

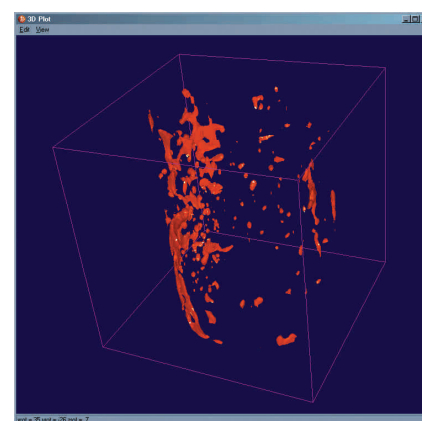
# NMR imaging multi-dimensional data processing software



## Prospa<sup>®</sup> the new way to process your NMR imaging data.

Prospa<sup>®</sup> is specifically designed for scientists and researchers working in the field of NMR imaging.

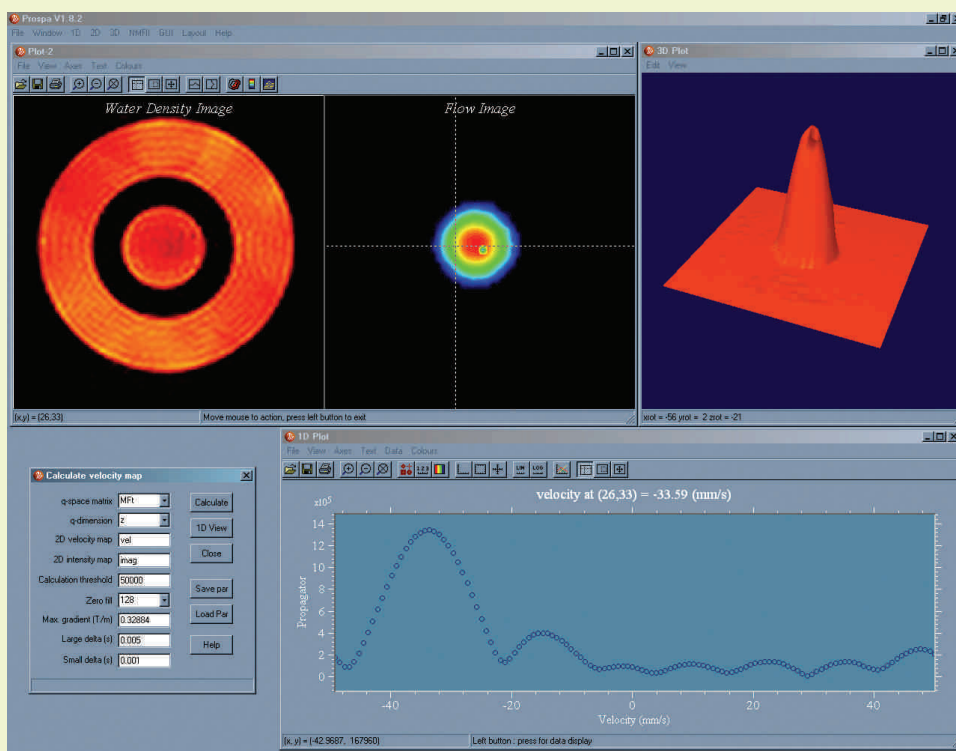
Prospa<sup>®</sup> is a fast, flexible, fully featured and easy-to-use software package designed for the processing and display of multi-dimensional NMR imaging data sets.



This 3D image shows the location of water within a porous media (sea ice).

### Prospa<sup>®</sup>

- Import data directly from commercial spectrometers.
- Export data and images in a variety of formats.
- Generate density, velocity, diffusion or relaxation images directly from raw NMR data.
- Increase computation speed with multi-dimensional matrix manipulation.
- Automate any processing task using a simple macro language.
- Create your own window and controls for setting processing parameters.
- Display 1D, 2D and 3D data sets in a range of formats and styles.
- Easily extend the macro language to provide new data processing functionality.

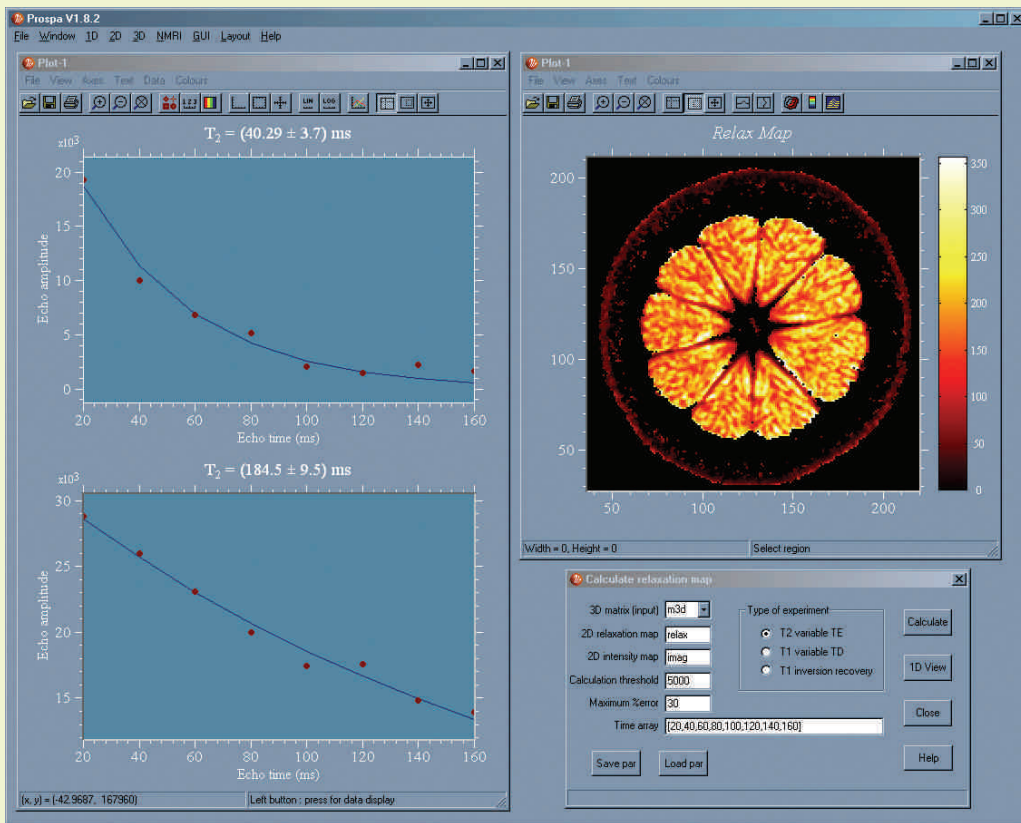


Pipe flow imaging using PGSE: The image on the top left shows the proton density (orange) inside two concentric glass tubes (black). The water in the outer region is stationary while that in the inner tube is flowing out of the picture.

The middle image represents the flow velocities inside the tubes, as does the 3D surface plot on the right

which shows the parabolic velocity profile expected of pipe flow. At the same time the lower 1D graph shows an example of the propagator used to calculate the velocity at each point in the image.

The window on the lower left has been defined by the end user to control this experiment.



$T_2$  relaxation imaging. The image on the right is a relaxation map of a cross-section through a mandarin, calculated from a series of relaxation weighted images. This processing mode is able to display, in

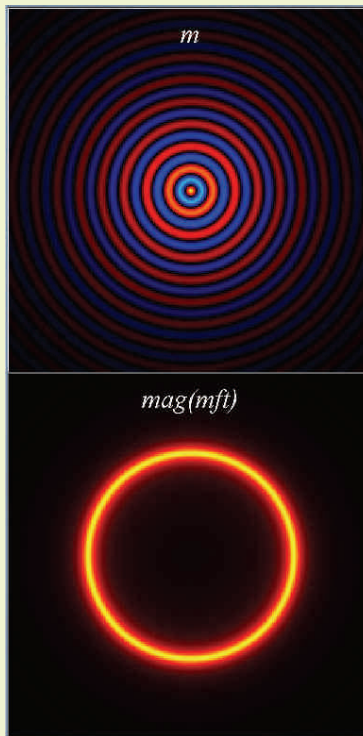
real time, the raw data used to calculate the relaxation time at each point in the image. The graphs on the left illustrate this for points in the skin (top) and body of the fruit (bottom).

```

Edit-1 the_one_ring.mac
File Edit View Procedures.
procedure(the_one_ring)
# Generate data set
n = 1024
x = clonearray([0:1:n-1], n, n)
y = clonearray([0:1:n-1]', n, n)
r = sqrt((x-n/2)^2 + (y-n/2)^2)
m = 100*exp((i*40-2)*r/100)
# Display data set and FT
multiplot("2d", 1, 2)
curplot("2d", 1, 1)
image(m)
mft = ft2d(m, n, n)
curplot("2d", 1, 2)
image(mag(mft))
endproc()
mat m = clonearray(vec v, int w, int h)

```

The Prospa<sup>®</sup> commands can be combined together to form scripts or macros. These allow complex processing to be applied to 2D and 3D data sets, or in this case to generate new data. Note there are no loops in this macro as Prospa<sup>®</sup> can operate directly on matrices.



#### Prospa<sup>®</sup> features include:

- A command line interface
- User defined controls and macros
- Native complex data handling
- Fourier transforms (1D, 2D, 3D)
- A Hilbert transform
- Data scaling and shifting
- Magnitude and power calculations
- Single data point manipulations
- Time domain filters (exponential, Hanning, sine-bell, etc)
- Data integration
- Data set simulation
- Auto and real-time phasing
- $T_1, T_2$ , density, diffusion and velocity imaging
- Over 250 other built-in commands

#### New features coming soon:

- 1D and 2D inverse Laplace transforms
- 3D imaging enhancements

#### Prospa<sup>®</sup> requirements:

- Windows 2000 or XP
- 40 MB of hard disk space to install (plus disk space for data files)
- 128 MB RAM
- 233 MHz processor or faster

Prospa<sup>®</sup> is available and can be purchased by contacting magritek now

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