IFUs: disentangling the light from neighbor fibers

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The dream IFU spectrograph packs many fibers in the smallest possible space. Overpacking fibers increases the amount of cross talk between fibers.
To decrease, and almost eliminate, crosstalk we *simultaneously* fit Gaussians to the spatial profiles of a group of fibers (defined by a block of fibers at the spectrograph).
Using previous knowledge of the spectrum position and fwhm for every fiber at every wavelength, we are able to fix the fwhm and the position for the Gaussians and solve
only for amplitude, $I(\lambda)$ which is our final spectrum

The SIFS (SOAR Integral Field Spectrograph) team has opted for a closely packed spectrograph, using 50µm fibers and a spacing=fwhm=3 pixels. The Eucalyptus
spectrograph (512 fibers – 0.9¨ separation) is a prototype for SIFS operating at Observatório do Pico dos Dias in Brazil. Eucalyptus uses 50µm and a spacing=fwhm= 5
pixels. To analyze the efficiency of Gaussian fits we are studying the performance of Eucalyptus and the behavior of simulated spectra as a function of fiber spacing,
fwhm and data signal to noise ratios.

Goals:
- Show the limits of aperture extraction and Gaussian fits methods.
- Analyze the dependence of contamination as a function of SN.
- Study the relation between quality of parameters (spectrum width and position) and contamination.
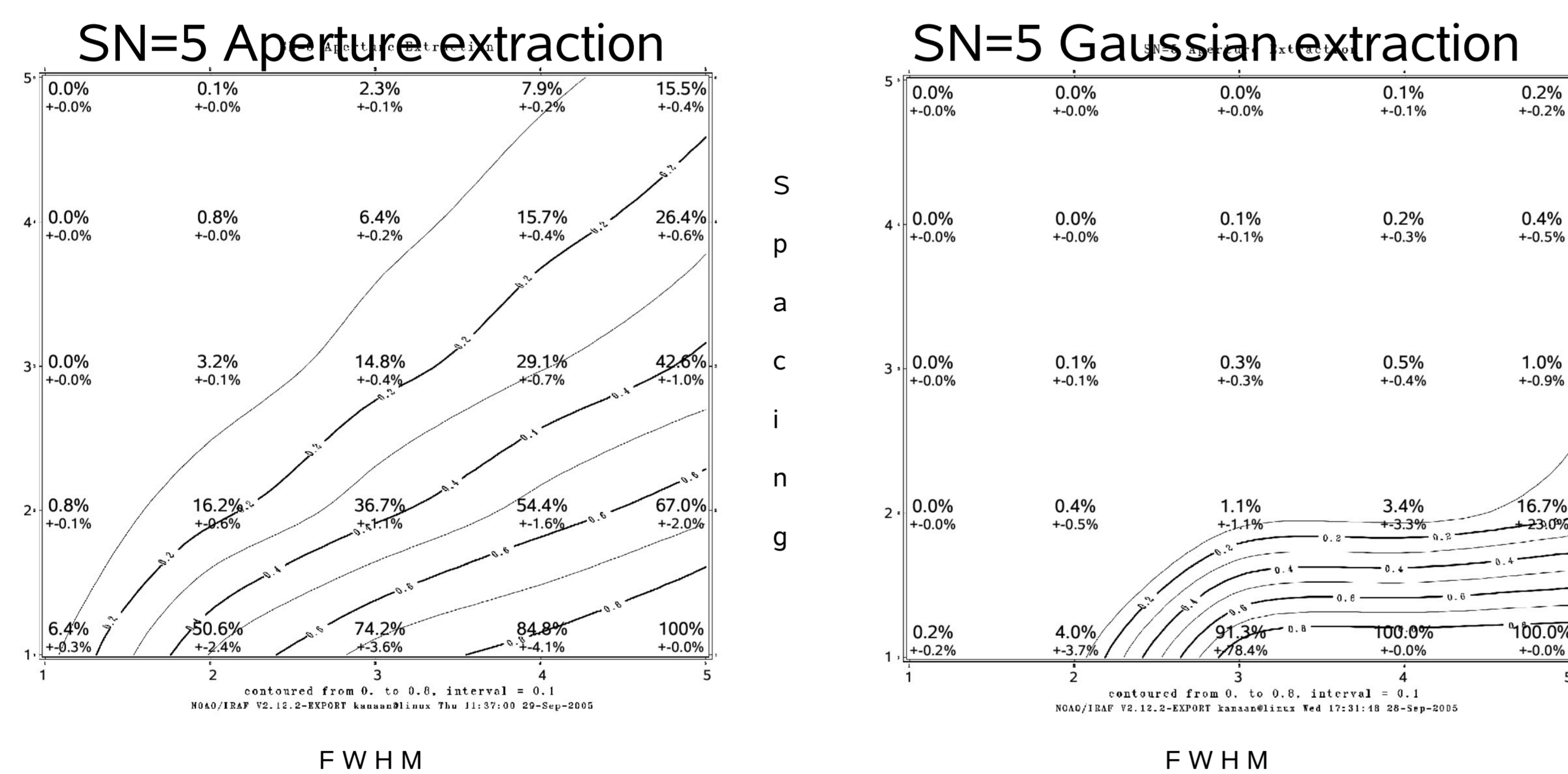
How do we measure contamination?

Illuminating one single fiber and then measuring the intensity in this
fiber and in its immediate neighbors. We then measure the relative
brightness of the non-illuminated neighbor relative to the illuminated
fiber. We call this ratio the contamination. We measure the
contamination using Gaussian fits and using aperture extractions.

We have performed Monte-Carlo simulations to measure the
contamination of synthetic IFU spectra created by **Coala**, the IFU
data simulator.

To measure contamination in **Eucalyptus** we masked fibers, using
the masks shown on the side.

Using **Coala** we could vary the spacing between fibers as well as the
FWHM of the fiber spectrum. The results of these simulations are
shown below. We varied spacing from 1 to 5 pixels and FWHM from
1 to 5 pixels.

Spectra taken with the **Eucalyptus** spectrograph have a spacing
between the centers of adjacent fibers of 5 pixels and fwhm of 5
pixels.

Method:

The trick in our procedure is to isolate fibers when determining the
position and width of their spectra. This is done using masks which
allow the passage of light for one fiber blocking the next four (in our
case). This mask is moved five times to allow gathering information
for every fiber. We fit (non linearly) individual Gaussians to each fiber
and determine its position and width from the masking procedure
described above, this is done for all wavelengths covered by the
spectrum.

When observing science objects then the spectra of neighbor fibers
are superposed and we fit Gaussians simultaneously to all fibers in a
block (32 in our spectrograph). However, this fit is linear, as we are
fitting only for amplitude, as we know position and width. This makes
the solution fast and unique.

The above pictures show a "flat-field"
image taken with the Eucalyptus
spectrograph. The fiber spacing is
roughly 5 pixels, the same as the
FWHM. The big dip is the edge of one
block of 32 fibers.

The above pictures show a "flat-field"
image taken through the mask. One
out of every five fibers sees the light.
The isolation created allows a safe
non linear fit to the spatial direction of
each spectrum at all wavelengths.

SN=5 Aperture extraction

SN=5 Gaussian extraction

Contamination as a function of fiber spacing (in pixels) and spectrum FWHM (in pixels). The large numbers on top of contour lines
show the average contamination measured in our Monte-Carlo simulations. The smaller numbers show the standard deviation of
the contamination.

The contour lines are lines of "iso-contamination"

For spacing=fwhm contamination is approximately constant for aperture extraction and close to 15%.

Using Gaussian fits contamination increases as we lower SN. Down to SN=5 contamination is less than 1% for spacing=fwhm, and
less than 5% for spacing=fwhm/2.

One major source of errors in this whole procedure comes from changes in the values for fwhm
and position of fibers between the time we calibrate the instrument using masks and the time of
actual observations.

Shifts of the spectrograph detector lead to errors in position and defocusing of the spectrograph
camera lead to errors in fwhm. We have performed simulations to measure the importance of
these erros and conclude that errors in fwhm and position can not be larger than 0.1 pixel.

The 0.1 pixel imposes the need for a very stable spectrograph. This is not too hard for a bench
mounted spectrograph. Also, one single flat field spectrum (with no masks) may be taken right
before the object observations to measure possible shifts in the fiber positions.

Our simulations show how the contamination changes as we introduce errors in fwhm and
position:

Error in fiber position:	0.0	0.1	0.2	Error in fiber fwhm:	0.0	0.1	0.2
Contamination:	0.1%	4.0%	8.6%	Contamination:	0.1%	3.0%	5.8%

Gaussian fits provide results with contaminations much lower than aperture extractions.

According to our simulations Gaussian fits could be used down to spacings as low as ½ the
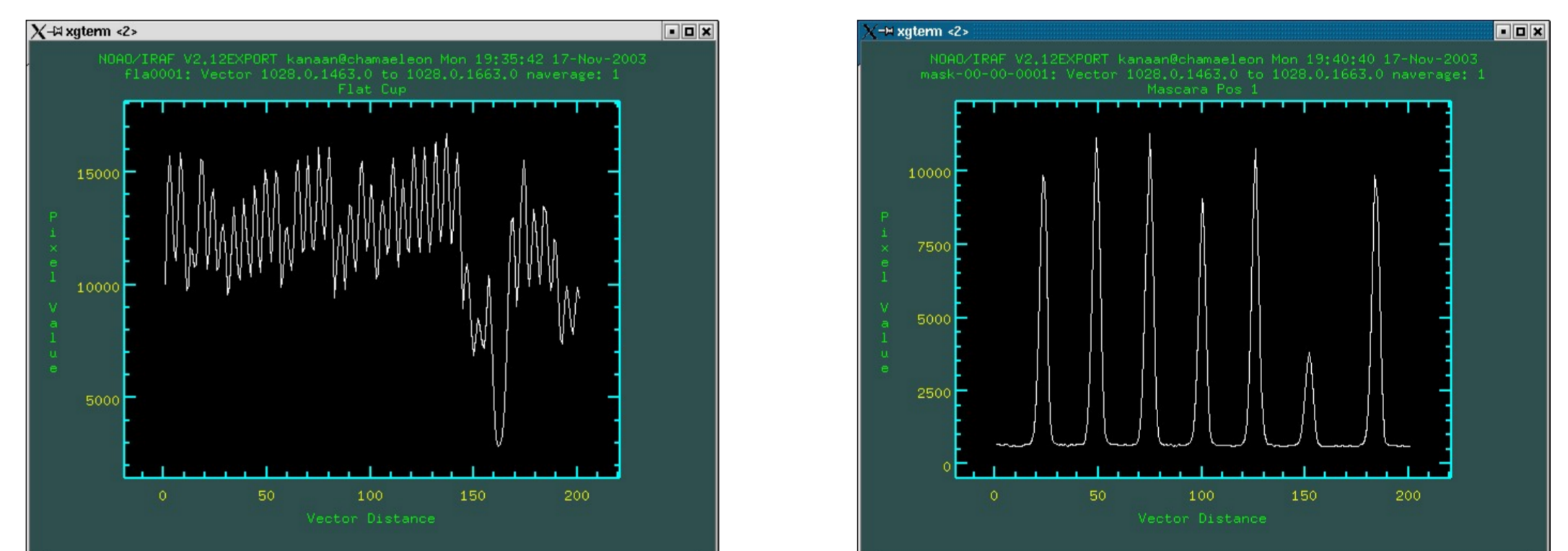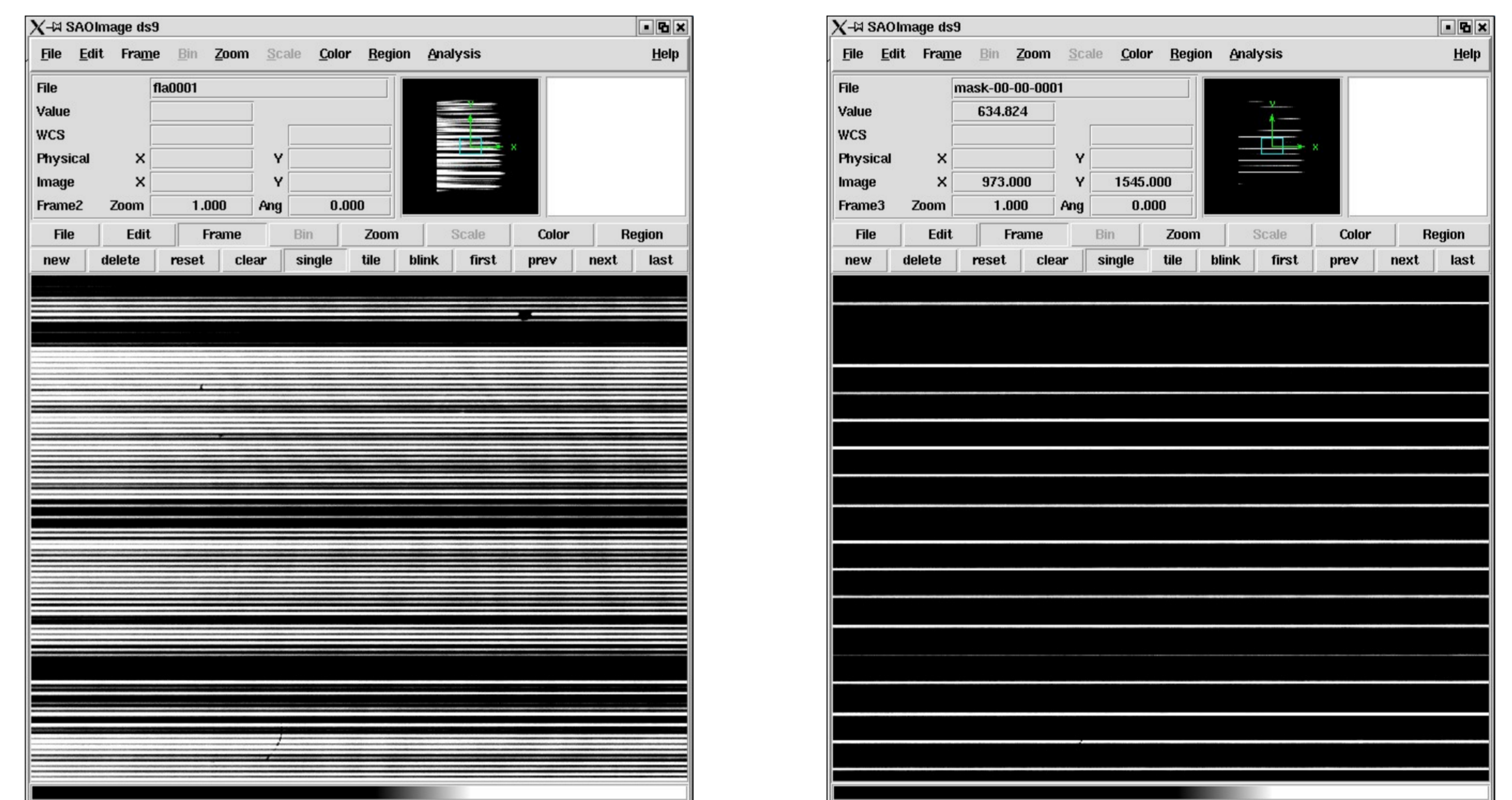fwhm of the fiber spectra.

The use of masks is essential for good Gaussian fits as well as for aperture extraction.
Aperture tracing of spectra separated by one pixel is only possible with the use of masks.

Gaussian fits are very sensitive to the precision in the fiber parameters, position and width
(fwhm), so, for a successful usage of Gaussian fits good calibrations and a stable
spectrograph are a must.