

XI. 2-D experiments

2-D parameter sets

Typical operation usually collects the normal 1-D in exp1 and 2-D experiments in exp2 or higher. Virtually all 2-D experiments will require a 90 deg. pulse width calibration for setting up the experiment. Also move the spectral window as necessary to observe only the area of interest and set up any water suppression needed.

For homonuclear 2-D experiments like NOESY, the normal 1-D parameters control the f2 dimension (direct dimension) while the f1 axis (indirect dimension) is controlled by parameters identified with a 1 (i.e. **sw1**, **lb1**, **fn1**). In homonuclear experiments, be sure **sw=sw1**. One other very important parameter in 2-D experiments is the number of increments (**ni**). The **ni** specifies the number of "points" in the indirect dimension. Typical values for ni are 128, 256, or 512. Steady state scans are also important in long experiments so be sure to set **ss**. The suggested value is **ss=32**.

A manual page (**man**) for the experiment will also point out parameters that need to be set. To access these use:

>**man('macro name')** or >**printon man('macro name') printoff**
i.e. >**man('NOESY') man('noesy')**

This information is also generally available in the white manuals or online manuals. The manual pages explain things like what is the minimum **nt** allowed. Many of these experiments have phase cycling that may require a **nt** of at least 16. Most of the experiments also require >**phase=1,2** (unless otherwise specified). Be sure to set this before checking the length of the experiment.

To look at length of time the experiment will run use the >**time** macro. Be sure the experiment fits into the time block available. To change the length of time the experiment will run, options include increasing or decreasing **ni**, **nt** or **d1** (or **satdly** in a presat experiment). Check the **at** (acquisition time) to check that a typical number of points is being taken. The typical number of points (**np**) taken is 2048 or 4096. These correspond to **at** times of less than 0.5 seconds. The **at** time in some 2-D experiments *must* be kept short due to high power decoupling during this time period.

When starting a 2-D experiment, always use >**go** instead of >**ga** so that every increment isn't transformed through the entire time the experiment is running. Be sure to look at the first few transients of the experiment before leaving. For instance, one increment will demonstrate enough transients and/or if the water suppression is working properly. To do this use, >**wft(1)** >**wft(2)** >**wft(3)** and so on. The upper case versions of most 2-D pulse sequences will access a central probe file and will use that file to set up most of the parameters including the gradient pulses. These pulse sequences also have linear prediction set up as default in the parameter set. The lower case versions (except for BioPack sequences) are older and may require more calibration particularly, optimization of the gradient pulses.

