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T1_15N_TROSY.nan

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We use this protocol and it's working

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Disclaimer

This protocol is part of the knowledge base content of NAN: The Network for Advanced NMR (<https://usnan.nmrhub.org/>)

Specific filenames, paths, and parameter values apply to spectrometers in the NMR facility of the Complex Carbohydrate Research Center (CCRC) at the University of Georgia.

Abstract

This protocol describes running ^{15}N T_1 TROSY experiment with temperature compensation, sensitivity enhancement, gradient coherence selection, water flip-back, and optional ^{13}C decoupling. This is a pseudo-3D experiment, with the third dimension F1(T1) sampling a list of T_1 relaxation delays provided in a separate text file. ^1H BIP shaped 180° pulses are used to suppress cross-relaxation and cross-correlated relaxation between ^1H and ^{15}N spins during T_1 relaxation delay.

Temperature compensation involves application of pulses prior to recycle delay delivering the same total RF power for each T_1 delay. Total acquisition time thus strongly depends on the maximum T_1 delay.

This experiment is primarily used for studying protein backbone dynamics on the picosecond to nanosecond scale in combination with ^{15}N T_2 TROSY, $\{^1\text{H}\}$ - ^{15}N HNOE-TROSY, etc.

Required isotope labeling: U- ^{15}N , or U- ^{15}N , ^{13}C (with or without ^2H). Also suitable for samples with selective ("sparse") ^{15}N -labeling of certain amino acid types.

Optimal MW is ≥ 30 -35 kDa, depending on magnetic field strength. For smaller systems ^{15}N T_1 HSQC may be more appropriate.

Field strength preference: detailed analysis of protein backbone dynamics often requires measurement of ^{15}N relaxation rates at multiple fields, though TROSY is most efficient around 800-1200 MHz.

It uses the Topspin library pulseprogram 'trt1etf3gpsitc3d'.

Attachments



[biotop.pdf](#)

2.5MB

Guidelines

The number of directly acquired points (**3 TD**) should be set so the acquisition time $t_{3,\max}$ (**3 AQ**) is between ~50-200 ms, depending on ^1H linewidth. It may be preferable to set **3 AQ** on the longer side, since there is no risk of additional RF heating because TROSY does not employ ^{15}N decoupling. For samples with large ^1H linewidths (fast T_2 relaxation) S/N can be improved by apodization during FT processing if needed.

"Effective" $^1J_{\text{NH}}$ coupling value **CNST4** determines the length of the INEPT transfer delays. For larger proteins **CNST4** can be increased (i.e. > 93 Hz) to reduce losses due to relaxation. **CNST4** can be optimized by arraying using **popt** with ^{15}N HSQC or ^{15}N TROSY experiment in 1D mode.

For samples with ^{13}C labeling use **-DLABEL_CN** ZGOPTNS flag to enable ^{13}C decoupling during ^{15}N evolution. **CNST21** and **CNST22** are used to define the ^{13}C channel offset for decoupling.

Since ^{15}N T_1 TROSY is a quantitative experiment, it is recommended to use longer **D1** recycle delays and a sufficient number of dummy scans **DS**. ^1H spectral width **3 SW** should be set a few ppm wider than required by the peak dispersion to allow for more "empty" noise regions for better baseline correction during FT processing.

T_1 relaxation delays should be multiples of 10 ms, and should include ~8 points or more. The shortest delay should be 20 ms or more, to avoid loop counter being less than 1. For optimal fitting precision, the longest delay should be at least as long as the expected T_1 relaxation time (usually in the range of 2-5 s). This may vary from protein to protein, as T_1 increases with MW. Due to temperature compensation, the longest delay also determines the overall experiment time, thus it should not be set excessively long.

Before start

A sample must be inserted in the magnet either locally by the user after training, or by facility staff if running remotely.

This protocol requires a sample is locked, tuned/matched on ^1H , ^{13}C and ^{15}N channels, and shimmed. At a minimum, ^1H 90° pulse width and offset O1 should be calibrated and a 1D proton spectrum with water suppression has been collected according to the protocol **PRESAT_bio.nan**. Prior acquisition of a **2D ^{15}N HSQC** is also recommended, according to protocol **HSQC_15N.nan**.

General aspects of the use of the **bioTop** module are described in more detail in the protocols listed below.

It is recommended to calibrate ^1H carrier offset, ^1H H_2O selective flip-back pulse, as well as ^1H , ^{13}C , and ^{15}N 90° pulse widths using the "Optimization" tab of BioTop. Alternatively, ^1H 90° pulse width and offset can be calibrated using other methods, such as pulsecal or calibo1p1. Additional parameters, like ^{15}N and ^{13}C offsets and spectral width can be either optimized or manually entered in the "Optimization" tab of BioTop. Note that since BioTop optimizations are saved in the dataset folder, all experiments should be created under the same dataset name when using BioTop for acquisition setup.

Refer to protocols

1. Acquisition Setup Workflow, Solution NMR Structural Biology
2. PRESAT_bio.nan
3. HSQC_15N.nan
4. HNCO_3D.nan
5. Biotop-Calibration and Acquisition setup

Create T1_15N_TROSY experiment file

- 1 Start with existing dataset containing 1D proton or 15N-HSQC data for this sample.
- 1.1 Open create dataset window with **edc** command or through menu.
Edit text in Title box.
- 1.2 To select starting parameter set, check 'Read parameterset' box, and click Select.
For standard NAN parameter sets, change the Source directory at upper right corner of the window:
Source = /opt/NAN_SB/par
Click 'Select' to bring up list of parameter sets.
Select T1_15N_TROSY_xxx.par, where xxx=900,800 or 600.
Click OK at bottom of window to create the new EXPNO directory.
- 1.3 If not done, tune Nitrogen and Carbon channels:
-on the Acquire menu, click Tune (or type atma on command line).

Calibrate pulses and adjust parameters

2

Note

Loading the T1_15N_TROSY_xxx.par parameter set enters the default parameters into the experiment directory. While they represent a good starting point, they may not be fully optimal or accurate for your particular sample or spectrometer hardware. The probe- and solvent-specific parameters, specifically the ^1H 90° pulse length, and possibly the ^{13}C and ^{15}N 90° pulse lengths, along with other dependent pulse widths and powers may need to be updated.

There are two ways of automatically updating experimental parameters:

- 1) Use **getprosol** command, which typically only updates proton pulse widths and power levels. It is most useful for running routine experiments using the default parameters.
- 2) Or use **bioTop** module that organizes calibrated and defined parameters for a dataset.

2.1 Using getprosol:

Use the calibrated proton P1 value obtained from the proton experiment (protocol PRESAT_bio.nan) and note the standard power level attenuation in dB for P1 (PLW1); otherwise type calibo1p1 and wait till finished.

Then execute the getprosol command:

**getprosol 1H [calibrated P1 value] [power level for P1]**

e.g. getprosol 1H 9.9 -13.14.

Where for example, the calibrated P1=9.9 at power level -13.14 dB attenuation

This also loads 15N and 13C pulse widths and power levels from the 'edprosol' table, and are assumed to be sufficiently accurate.

Skip to step 2.3.**2.2 Use bioTop**

If you previously performed parameter calibrations using the "Optimizations" tab of the BioTop GUI, or entered parameters manually in the "Optimizations" tab, you can **type btprep** at the command line.

See protocol 'BioTop : calibration and acquisition parameters' and attached Bruker manual 'biotop.pdf' for details.

Inspect Parameters

- 2.3** Examine parameters by typing '**eda**', or select the 'Acqpars' tab and get the 'eda' window by clicking on the '**A**' icon. This view shows the three dimensions, F3 (1H) and F2 (15N) and F1 (T1 points) in columns.

Parameters to check:

3 SW: 1H spectral width (~12-15 ppm, defined in BioTop)

2 SW: 15N amide spectral width (~25-40 ppm, defined in BioTop)

O1P: 1H offset defaults to 4.7ppm (calibrated with bioTop)

O2P: 13C offset (~110 ppm, for decoupling when **ZGOPTNS -DLABEL_CN**)

O3P: 15N amide offset (~115-120 ppm, defined in bioTop)

3 TD: Number of 1H time domain real points (~1024-2048, preferably 2^N , keep **3 AQ** at ~50-120 ms)

2 TD: Number of 15N time domain real points (keep 1 AQ at ~30-60 ms)

1 TD: Number of T1 delay points (should match number of lines in **VDLIST**)

- 2.4** Then examine the parameters in Acqpars 'ased' mode (click 'pulse' icon), or **type 'ased'**;

Most of the default parameters are suitable, however it's useful to compare values in the fields against those proposed by the original parameter file and the pulseprogram.

CNST4 - $^1J_{NH}$ value (≥ 93 Hz, used to calculate INEPT transfer delays)

CNST12 - multiplicity factor (NH: 4; NH/NH2: 8)

D1: recycle delay (~1 s for protonated samples, ~2-3 s for perdeuterated samples)

DS: 32-128 'dummy' scans that are not recorded ; allows system to reach steady state equilibration.

NS: multiple of 4; increase for increased signal to noise (S/N increases as $\sqrt{NS}$)

VDLIST: T1 delay list (use multiples of 10 ms). Click on 'E' to edit. The longest delay should be ~2-3s; it determines the temperature compensation.

ZGOPTNS flags

-DLABEL_CN : enable ^{13}C decoupling during ^{15}N evolution for $^{13}\text{C},^{15}\text{N}$ -labeled samples (default)

channel f1:

P1 - ^1H 90° high power pulse (calibrated with calibo1p1 or BioTop)

SPdB1/SPW1 - power level [dB] for ^1H H_2O flip-back shaped pulse (calibrated with BioTop)

channel f2:

CNST21 - ^{13}CO offset (~173 ppm, calibrated with BioTop) for ^{13}C decoupling

CNST22 - ^{13}CA offset (~53 ppm, calibrated with BioTop) for ^{13}C decoupling

channel f3:

P21 - ^{15}N 90° high power pulse (calibrated with BioTop)

Acquire and Process Data

- 3 Type '**rga**' or click on 'Gain' in Topspin Acquire menu to execute automatic gain adjustment.
Type '**expt**' to calculate the expected run time
Type '**zg**' or click on 'Run' in Topspin Acquire menu to begin acquisition.
- 3.1 You can always check the first FID by typing 'efp' to execute an exponential multiplied Fourier transform. It will ask for a FID #, choose the default #1. You can evaluate the 1D spectrum for amide proton signal to noise and water suppression.
- 3.2 2D planes with NUS or uniformly sampled can be processed with Topspin: **xfb**

Protocol references

J.Cavanaugh, W.Fairbrother, A.Palmer, N.Skelton: Protein NMR Spectroscopy: Principles and Practice. Academic Press 2006 ; Hardback ISBN: 97801216449189, eBook ISBN: 9780080471037