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 HNcaCO_3D.nan

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NAN KB¹, Alex Eletsy², John Glushka²

¹Network for Advanced NMR (NAN); ²University of Georgia



NAN-KB UGA

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Protocol status: Working

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 a 3D HN(CA)CO pulse sequence with sensitivity enhancement, gradient coherence selection and water flip-back with non-uniform (NUS) sampling scheme. This produces a 3D phase-sensitive dataset that correlates backbone ^1HN and ^{15}N resonances of residue (i) with ^{13}CO of residues (i) and (i-1). The sequential (i-1) ^{13}CO peaks is typically weaker than intra-residue (i) ^{13}CO peak.

Usually optional for backbone resonance assignment, but may be useful cases of poor quality HNCACB, or degenerate CA and CB shifts. Has slightly better sensitivity than HNCACB, however, ^{13}CO shifts cannot be used to differentiate residue types. Can be acquired with NUS sampling unless sensitivity limited.

Required isotope labeling: U- ^{15}N , ^{13}C . Samples with additional ^2H labeling should use separate HNCA(CO) version with ^2H decoupling.

Optimal MW is ≤ 25 kDa. Larger systems may benefit from 3D TROSY-HN(CO)CA version. Compare 2D H-N planes of HNCO and TROSY-HNCO to check which one yields better S/N.

This pulse sequence can be used for:

- spin system identification
- resolving signal degeneracy in 2D ^{15}N HSQC.
- backbone resonance assignment: sequential linking of spins systems based on ^{13}CO peak matching (in conjunction with 3D HNCO. Complements linking via HNCA and HNCACB.
- resonance assignment of ^{13}CO spins
- chemical shift-based secondary structure prediction (e.g. TALOS), together with other resonances

Field strength preference: though signal dispersion is usually not an issue for HN(CA)CO, higher field strength is often preferred for higher sensitivity, assuming the same probe type.

It uses the standard Bruker Topspin pulseprogram 'hncacogp3d'

Attachments



[biotop.pdf](#)

2.5MB



[NUS_poisson_gap_file...](#)

12KB

Guidelines

The number of directly acquired points (**3 TD**) should be set so the acquisition time $t_{3,\max}$ (**3 AQ**) is between ~50 ms (for larger proteins ~25 kDa) and ~120 ms (for smaller proteins). Longer times may cause excessive probe and sample heating during ^{15}N decoupling, and resolve undesirable $^3J_{\text{HN,HA}}$ splittings.

Since the F2(15N) is a constant-time dimension, number of acquired points **2 TD** should be set to the largest possible value for optimal S/N. The maximum **2 TD** value is $2 \cdot \text{int}(d30/\text{in}30)$, where d30 is the decremented delay, and in30 is the decrement value. Both d30 and in30 are computed internally according to pulse program code and their values are shown in ased view. Note that $\text{in}30 = \text{in}10 = 1/(4 \cdot \text{SW}(\text{N}))$. In TopSpin 4.x the **ased** command would produce a warning if **2 TD** is set too large, and reset the internal td2 parameter to the maximum possible value.

Since 3D HN(CA)CO only has 2 peaks per residue, NUS sampling amount can be as low as 5-10% provided there is sufficient S/N.

Individual F1(Cab)-F3(HN) or F2(N)-F3(HN) 2D planes can be acquired by setting, respectively, 2 TD or 1 TD to 1.

To check whether TROSY-HN(CA)CO or regular HN(CA)CO yields better S/N for your sample at a particular field strength, record and compare the respective 2D F2(N)-F3(HN) planes of TROSY-HNCO and regular HNCO using identical spectral parameters.

Before start

This is a simplified protocol with minimum figures. For more detailed Bruker Topspin GUI content refer to protocols: HSQC_15N.nan, HSQC_CT_13C_ali.nan, HNCO_3D.nan or HNCA_3D.nan

This protocol requires a sample is inserted, tuned/matched on ^1H , ^{15}N , and ^{13}C 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.

It is recommended to calibrate ^1H carrier offset, ^1H H₂O 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. Prior acquisition of 2D ^{15}N HSQC, and 3D HNCO is also recommended.



Create HNcaCO experiment file

- 1 Join an existing dataset and experiment (e.g. 1D proton, 2D 15N HSQC, 2D 13C HSQC, etc) 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 HNcaCO_3D_NUS_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:
Return to the 'Acquire' menu and click 'Tune' (or type **atma** on command line).

Load pulse calibrations: use getprosol (step 2.1) or bioTop (steps 2.2)

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Note

Loading the HNcaCO_3D_NUS_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) Load optimized parameter from **BioTop**. This module allows to optimize and define additional common parameters for a given dataset that can be applied to multiple experiments.

- 2.1 Loading pulse widths and power levels with **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 ^{15}N and ^{13}C pulse widths and power levels from the 'edprosol' table, and are assumed to be sufficiently accurate.

⇒ go to step #2.3 If not using BioTop

2.2 Loading experimental parameters from **BioTop**:

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

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

Inspect and adjust Parameters

2.3 Examine parameters by typing '**eda**', or select the 'Acqpars' tab and get the 'eda' view by clicking on the '**A**' icon if not default. This view shows the three dimensions, F3 (1H) and F2 (15N) and F1 (13C) in columns.

Parameters to check:

- **FnTYPE** - 'traditional planes' or 'non-uniform sampling' (see step 2.5 below)
- **NS** - minimum 2; increase for for higher signal to noise (S/N increases as square root of NS)
- **DS** - 32-128 'dummy' scans that are not recorded (multiple of 16); allows system to reach steady state equilibration.
- **SW[ppm]** - 1H (F3) ~12-15 ppm; 15N (F2) ~25-40 ppm; 13CO (F1) ~12-20 ppm; defined in bioTop
- **O1P** - ^1H H₂O offset in Hz (calibrated with BioTop or calibo1p1)
- **O2P** - ^{13}C offset (~173 ppm, defined in bioTop)
- **O3P** - ^{15}N 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 ^{15}N time domain real points ($2 \cdot \text{int}(\text{d30}/\text{in30})$); **2 AQ** ~24ms, CT dimension)
- **1 TD** - Number of ^{13}C time domain real points (**1 AQ** at ~20 ms or more)

- **DIGMOD** - 'digital' (pulse sequence does not use *acqt0* correction)

2.4 Then examine the parameters in Acqpars 'ased' mode (click 'pulse' icon), or **type 'ased'**; Most of the default parameters are appropriate, however it's useful to compare values in the fields against those proposed by the original parameter file and the pulseprogram.

- **D1** - 1-2 sec
- **P1** - ^1H 90° high power pulse (calibrated with calibo1p1 or BioTop)
- **SPdB1** - power level [dB] for ^1H H_2O flip-back shaped pulse (calibrated with BioTop)
- **P3** - ^{13}C 90° high power pulse (calibrated with BioTop)
- **CNST21**: ^{13}C O shift (~173 ppm, defined in bioTop)
- **CNST22**: ^{13}C A shift (~54 ppm, defined in bioTop)
- **P21** - ^{15}N 90° high power pulse (calibrated with BioTop)

Configure NUS (non-uniform sampling) - optional

2.5 After all other acquisition parameters (especially spectral widths and time-domain points) are set, change the **FnTYPE** parameter to 'non-uniform sampling' (type 'eda' and select 'Experimental' to get correct parameter window).

Then select NUS in the 'eda' parameter winow and set the desired **NusAMOUNT** [%] sampling density.

For adequate reconstruction, number of NUS points should be larger than the number of expected peaks. 3D HN(CA)CO yields 2 peaks per residue, thus a 100-residue protein would require more than 200 NUS points.

After this you have the option of using either the built-in sampling schedule generator in Topspin or a third-party one.

To use the built-in sampling schedule generator in TopSpin set the **NUSLIST** parameter to 'automatic'. The sampling schedule will then be generated at acquisition start, and will be purely random apart from point density weighting according to **NusJSP** and **NusT2** parameters.

A better way to generate the sampling schedule is with **nusPGSv8** AU program. This AU program uses **NusAMOUNT** and **TD** values of the current experiment to generate a random schedule with 'Poisson gap' point spacing, and offers additional options for point density weighting and sampling order. (see protocol '**Poisson Gap NUS Acquisition Setup**', and attached files '**nusPGSv8**' and '**poissonv3**'). To use this method, type '**nusPGSv8**' on the command line. You can typically accept the default values in pop-up



dialog windows, since they are suitable for most applications. A schedule will be generated and will be stored to the parameter **NUSLIST**.

If **nusPGSv8** is not installed, copy the attached file 'nusPGSv8' to your user AU directory, */opt/topspin.X.X.X/exp/stan/nmr/au/src/user*, and copy the binary file 'poissonv3' to */opt/topspinX.X.X/prog/bin*.

Acquire and Process Data

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Type '**expt**' to calculate the expected run time

 [go to step #2.3](#) If necessary to re-adjust parameters

Type '**rga**' or click on 'Gain' in Topspin Acquire menu to execute automatic gain adjustment.

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 3D NUS data usually cannot be processed in Topspin without a separate license (see note in step 2.5). 2D planes with NUS or uniformly sampled can be processed in Topspin, though.

Also, a 2D NUS plane can be extracted from a completed 3D NUS data set with the command '**rser2d**', and then processed within Topspin.

Full 3D NUS processing is usually performed using third-party processing software, such as NMRPipe together with specialized NUS reconstruction programs (SMILE, hms1ST, NESTA, etc.).



Protocol references

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'nusPGSv8' written by Scott Anthony Robson 2013