

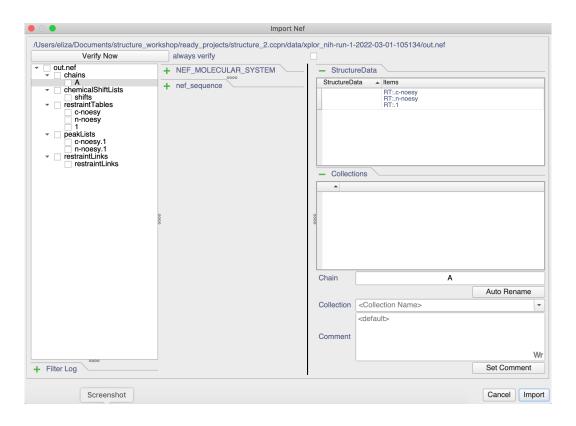
# How To Use NEF to import and export CcpNmr data

```
data_project_1

save_nef_mmr_meta_data

_nef_nmr_meta_datas_f_ramecode
    _nef_nmr_meta_datas_f_ramecode
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    _nef_nmr_meta_datas_f_ramecode
    _nef_nmr_meta_datas_f_ramecode
    _nef_nmr_meta_datas_format_name
    _nef_nmr_meta_datas_program_name
    _nef_nmr_meta_datas_program_name
    _nef_nmr_meta_datas_program_version
    _nef_nmr_meta_datas_cordinate_file_
    _nef_nmr_meta_datas_cordinate_file_
    _nef_nmr_meta_datas_cordinate_file_
    _nef_nmr_meta_datas_cordinate_file_
    _nef_mmr_meta_datas_cordinate_file_
    _nef_molecular_system

_nef_molecular_systems_f_category
    _nef_molecular_systems_f_category
    _nef_molecular_system.sf_category
    _nef_molecular_system.sf_category
    _nef_sequence.index
    _nef_sequence.cindex
    _nef_sequence.cinding
    _nef_sequ
```



## Introduction

This How-To will guide you through the action of using the NMR Exchange Format, NEF, to move data from one CcpNmr project to another. This is only a practical example and not the main purpose of NEF, for documentation and other usages please visit:

https://github.com/NMRExchangeFormat/NEF.

In this How-To you will export the chain, chemical shift list and peak list from one project and import it to another using a NEF file. You can download example data for this How-To from our website at

https://ccpn.ac.uk/support/tutorials/#nef.

### Start CcpNmr Analysis V3

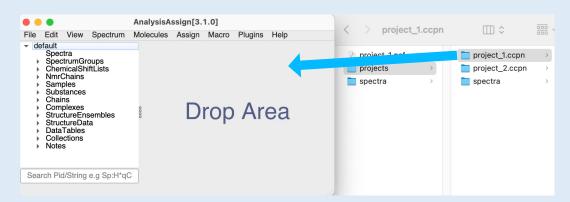
Apple and Linux users by using the terminal command: bin/assign

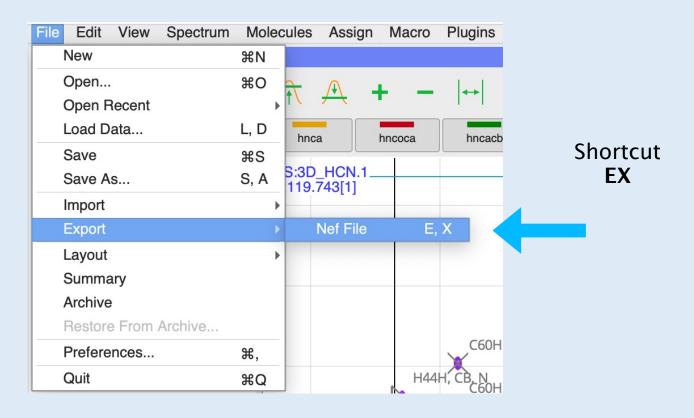
Windows users by double-clicking on the *assign.bat* file

NMRbox users by using the terminal command analysisassign

# **Export to NEF**

#### Open project\_1.ccpn





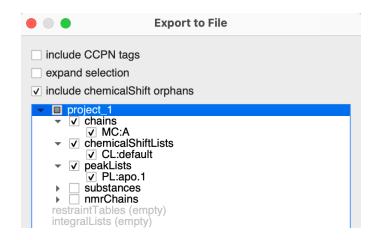
## $\mathbf{1}_{\mathsf{A}}$ Open the project containing the data you want to export

- Open the project **project\_1.ccpn** in the **projects** folder of the data provided.
- Open the NEF export popup:

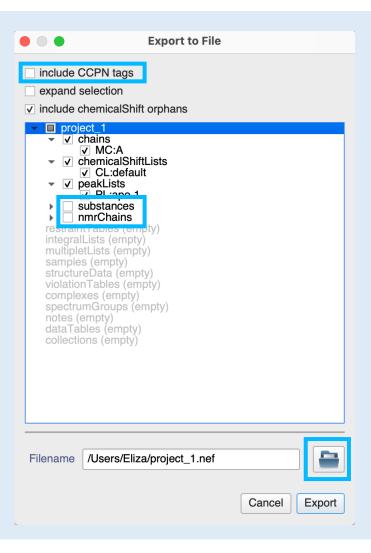
Main Menu → File → Export → Nef File (or shortcut EX)

The NEF exporter dialog will appear.

Expand the chains, chemicalShiftLists and peakLists branches



2



# $\mathbf{1}_{\mathsf{B}}$ Select exporting options

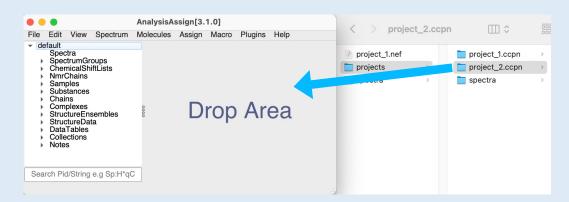
Elements not listed in the project are grayed out and not available for selection. We will export a Chain, ChemicalShiftList and PeakList (peak positions and heights/volumes) without the spectra.

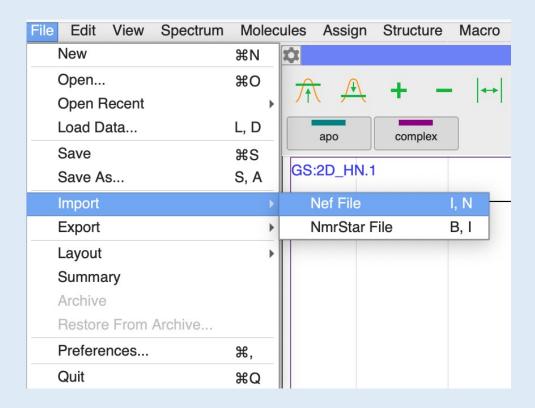
- Deselect Include CCPN tags
- Select
  - · chains: MC:A
  - · chemicalShiftLists: CL:default
  - peakLists: PL:apo.1
- · Deselect substances and nmrChains
- Click on the folder icon to select the path where you want to save the NEF file.
- Click Export

*Note*: If you wish to export actual spectra (data locations), with all their display properties, you should select **Include CCPN tags**.

project\_2.ccpn

#### Open project\_2.ccpn





Shortcut **IN** 

## $1_{\mathsf{C}}$ Import to a target project

- Open the project project\_2.ccpn
- · Open the NEF import popup with

Main Menu → File → Import → Import Nef File (or shortcut IN)

A new File Dialog will appear.

- Select the previously saved NEF file
- Click Open to continue

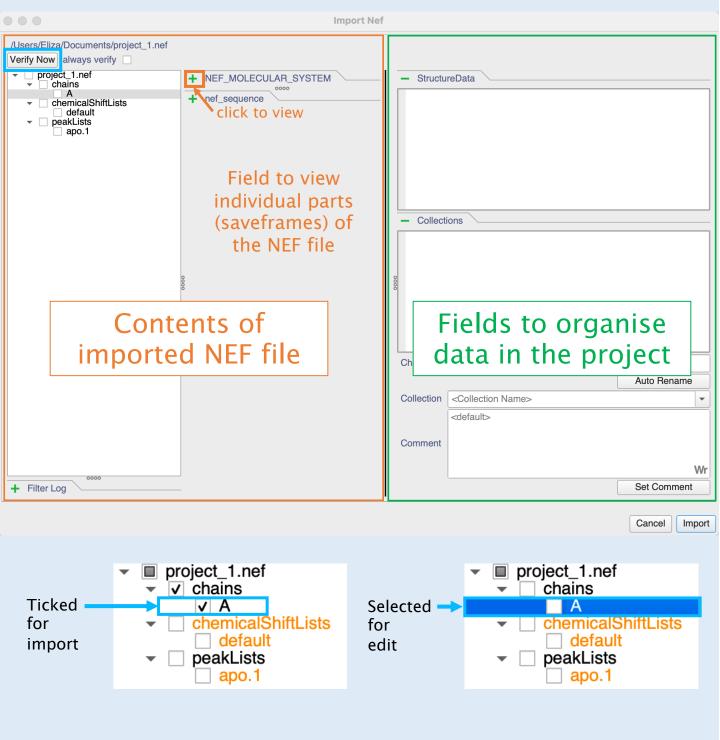
A new popup will ask if you want to **Import** your NEF file or load it as a **New project**.

Click Import

The Import Nef popup will open.

project\_2.ccpn

#### Nef importer



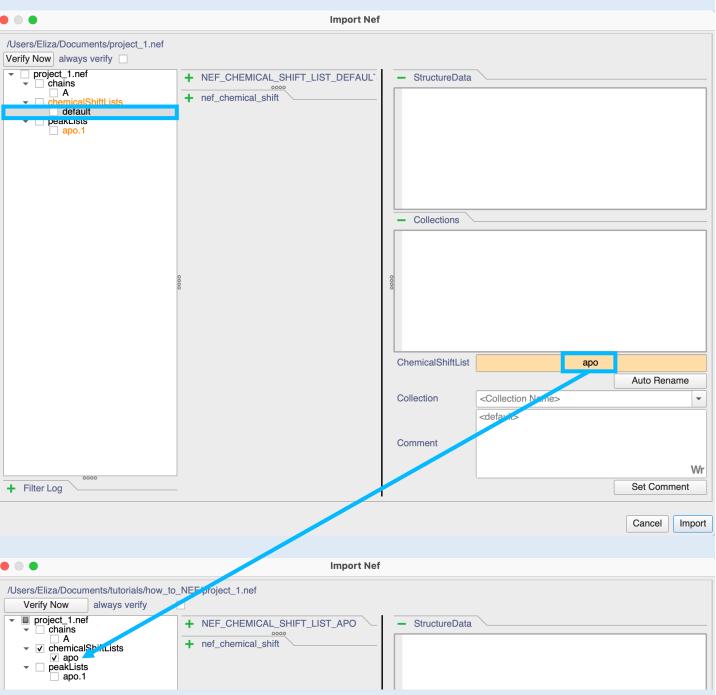
## $\mathbf{1}_{D}$ View incoming data from NEF file

#### Click Verify Now

You will see that some elements are now coloured in orange, this indicates that objects with that name already exist in the project and their name must be changed before being adding to the project.

project\_2.ccpn





#### $\mathbf{1}_{\mathsf{F}}$ Rename incoming items of data

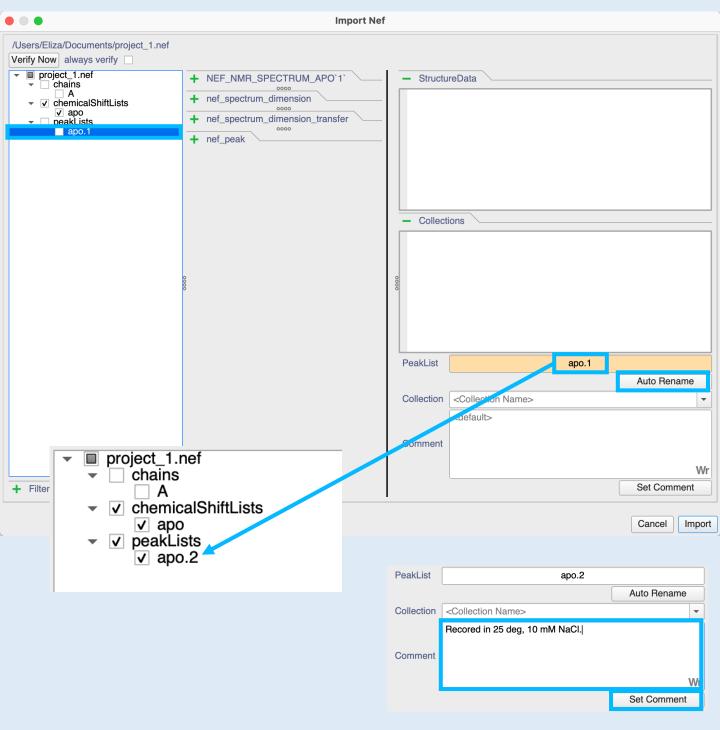
 Click on the default chemicalShiftList on the left-hand side to select it for editing. It will appear in the right-hand side where it can be re-name, e.g. to apo. Press Enter to confirm the change. This will update the name on the left-hand side

The chemicalShiftList has been now ticked automatically. If a name is edited, the software assumes this element is supposed to be imported into the project.

continued...

project\_2.ccpn

#### Nef importer



#### contintued... Rename incoming items of data

- Click on the apo.1 peakList on the left-hand side to select it for editing It will appear on the right-hand side.
- · Click on the Auto Rename button.

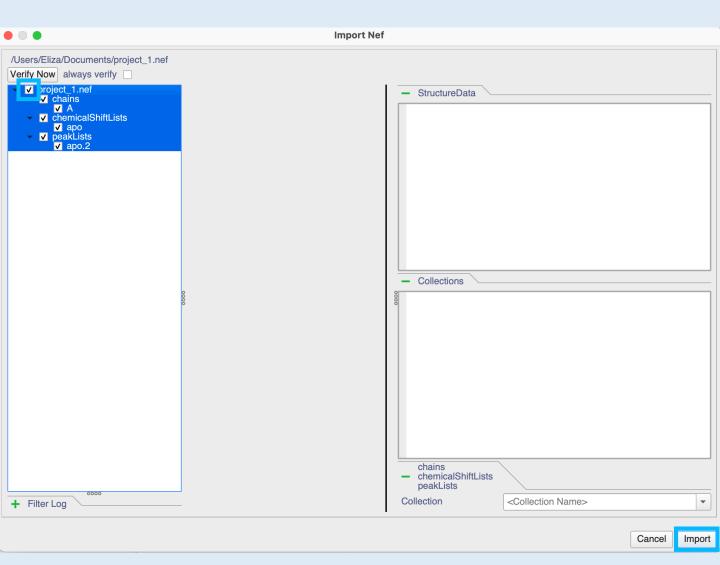
This will change the peak list serial on the left-hand side and will tick the peak list automatically.

You can add a comment to any of the item of data you want to import when it is selected for editing:

Type some text in the Comment box and click Set Comment to confirm.

project\_2.ccpn

#### Nef importer



## $\mathbf{1}_{\mathsf{F}}$ Import and inspect imported data

- Tick the box next to the project\_1.nef to select the contents of an entire
   NEF file to be imported into your project.
- Click Import.

The newly imported items of data will appear in the sidebar.

Note that when you import a PeakList, then any PeakLabels (NmrAtoms) which are missing, will be automatically created and added to the project.

```
Spectra
    SP:apo
       PeakLists
           <New PeakList>
PL:apo 1
         PL:apo.2
       MunipierLists
IntegralLists
   SP:complex
SpectrumGroups
ChemicalShiftLists
    <New ChemicalShiftList>
   CL:apo
   <New NmrChain>
NC:@-
   NC:A
Samples
Substances
Chains
    New Chain>
▶ MC:A
```

# **CcpNmr Analysis Version 3**



#### **Contact Us**

#### Website:

www.ccpn.ac.uk

#### **Suggestions and comments:**

support@ccpn.ac.uk

#### Issues and bug reports:

https://www.ccpn.ac.uk/forums/

## Cite Us

Skinner, S. P. *et al.* CcpNmr AnalysisAssign: a flexible platform for integrated NMR analysis. *J. Biomol. NMR* (2016). doi:10.1007/s10858-016-0060-y

## **Cite NEF**

Gutmanas, A. et al. NMR Exchange Format: A unified and open standard for representation of NMR restraint data. Nature Structural and Molecular Biology 22, 433–434 (2015).