Processing 1D $^{13}C\{^1H\}$ and 1D ^{13}C DEPT from Siena with MestreNova

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Problem:

I received an email with the following comment: "I am having troubling phasing a 1D 13C spectrum recorded on Siena."

Answer:

This issue is caused by a long pre-acquisition delay for the cryoprobe. This problem is sometimes referred to as the "ring down" problem. Bruker modified their processing procedure to address this problem in Topspin. Processing in MestreNova involves extra steps.

There are two options to address this issue.

1. Tell MestreNova to always use the Topspin processing parameters

Open the MestreNova preferences by clicking the gear button on the top right ⚙. Under the Import tab of the NMR Menu check the boxes for Apodization, Zero Filling and Linear Prediction. Click OK.
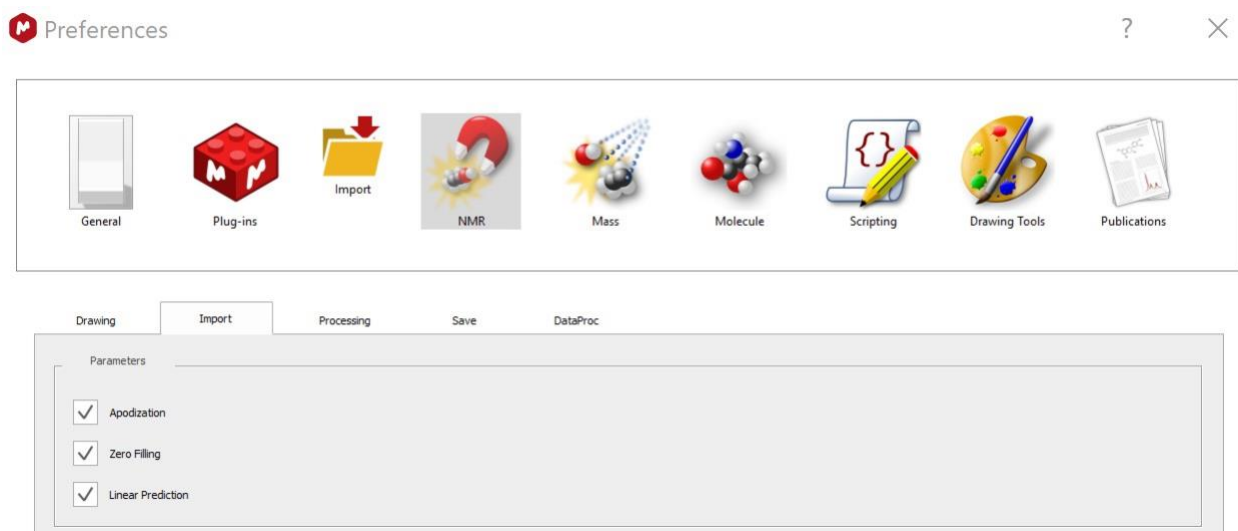
Restart MestreNova. Now when you open data, the Topspin parameters will be automatically imported.

2. Change the MestreNova processing parameters

I find it easiest to use a "Processing Template" to achieve this action. I have saved my template on OneDrive. It should be accessible to people at KU-L at the URL

https://kansas-my.sharepoint.com/:u:/g/personal/justindouglas_home_ku_edu/EdtapUgWFdlBmo41XFOLNNEBV51dOVX-0h3hF9R_g11vA?e=ZzG5f3

Sarah or I can also send this file by email, if you would like.

Download this file and put it someplace "permanent" on your computer.

Open the Processing Template menu under the NMR Processing tab.
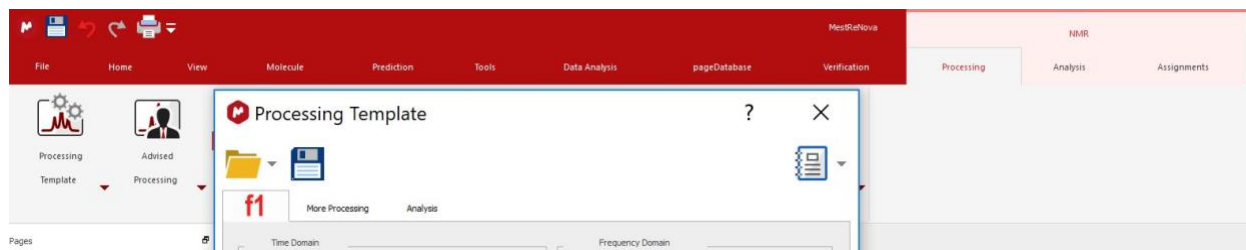
Click the open file button ![button] and navigate to the file you just downloaded. Click Apply and OK.

For future use, MestreNova remembers this file and you can access by clicking the down arrow next to Processing Templates and choosing this template from the list.