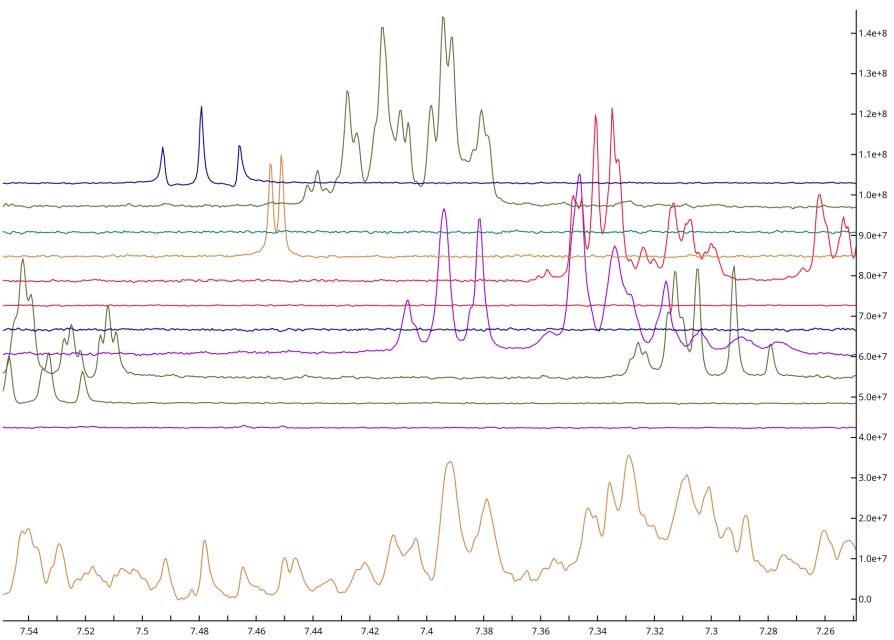
CCPN

CcpNmr AnalysisScreen Version 3

Generate Mixtures



1

Getting started, basic operations

Sidebar

All data contained in a project, such as spectra and peak lists are located in the sidebar. **Double-clicking** on an item will open its properties popup.

Display

A display can contain multiple overlaid spectra which share the same axes. To show/hide a single spectrum, click on its toolbar button. If you close a display, you can open a spectrum by **dragging and dropping** it into the drop area from the sidebar or by **right-clicking** on a sidebar item and selecting **Open as module**. You can also add additional spectra to a spectrum display module later on, or drag several spectra into the drop area together to open them simultaneously.

Mouse

- Pan -> **Left-drag** in display
- Zoom in/out -> **Scroll wheel** in display
- Context menu -> **Right-click**
- Select a peak -> **Left-click** on a peak symbol “X”
- Move a peak -> select first, then **middle-click and drag**

Shortcuts

The program uses several shortcuts, for example **MK** for creating a mark at the current mouse position. You will need to press the first letter on your keyboard e.g. **M**, followed by the second letter, e.g. **K** (case insensitive). Press **Esc** to cancel the first letter.

For more commands and operations

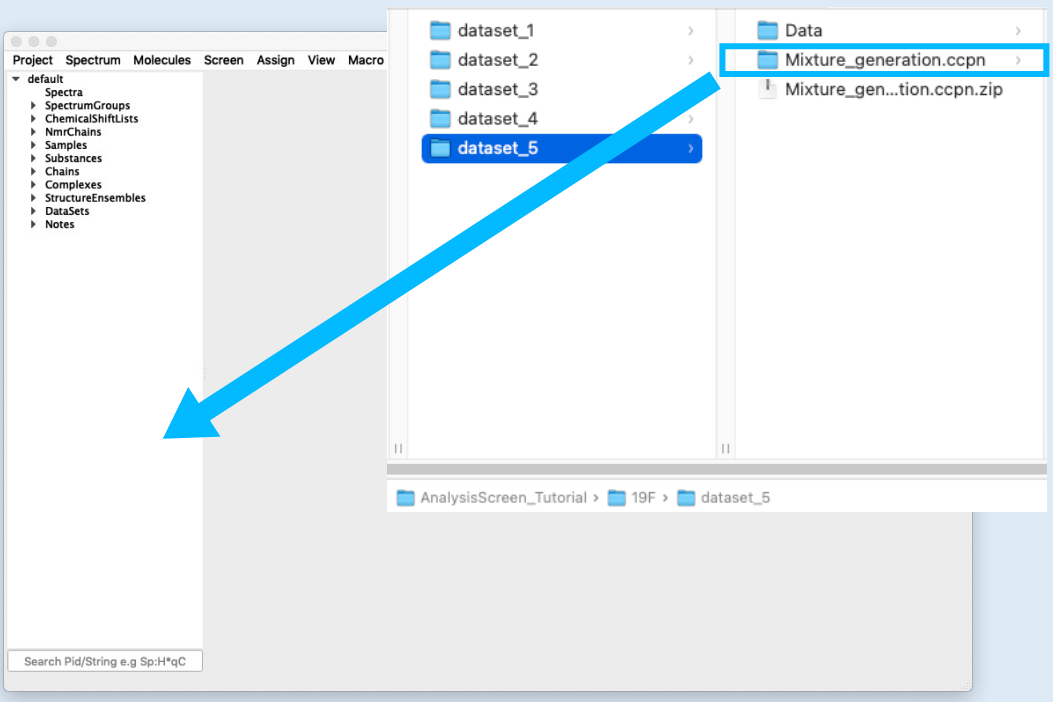
Main Menu ⟶ Help ⟶ Tutorials ⟶ Beginners Tutorial

OR

Main Menu ⟶ Help ⟶ Show Shortcuts

1 Mixture Generation

In order to decrease the experimental resources in NMR screening, a common approach is to analyse several compounds against a target at the same time. This is can translate into a very crowded spectrum that leads to difficult, error prone and time-consuming interpretation of spectra.
In this section you will learn how to create cocktails of one dimensional reference spectra with minimal peak overlap. The new mixtures can be manually analysed and exported to Excel, ready to be printed and prepared in the lab.
The tutorial uses synthetic spectra, representing the reference spectra of small molecules.



1A Open Project

Open the **Mixture_generation.ccpn** project in the **ScreenTutorial** directory of the tutorial sample data: TutorialData/19F/dataset_5/
You can do this in one of the following ways:

- Drag the project from your file browser into the the sidebar or drop area

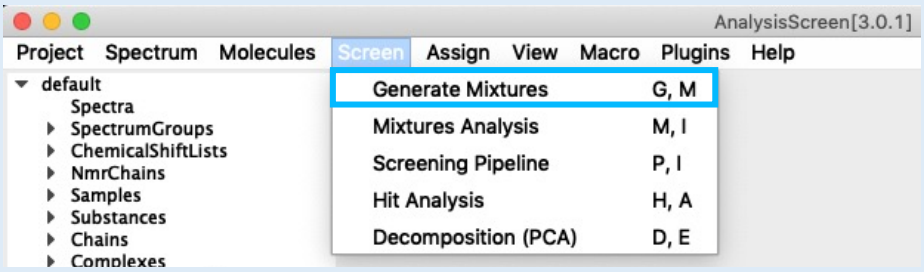
OR

- Go to **Main Menu** ⟶ **Project** ⟶ **Open**… and select the project

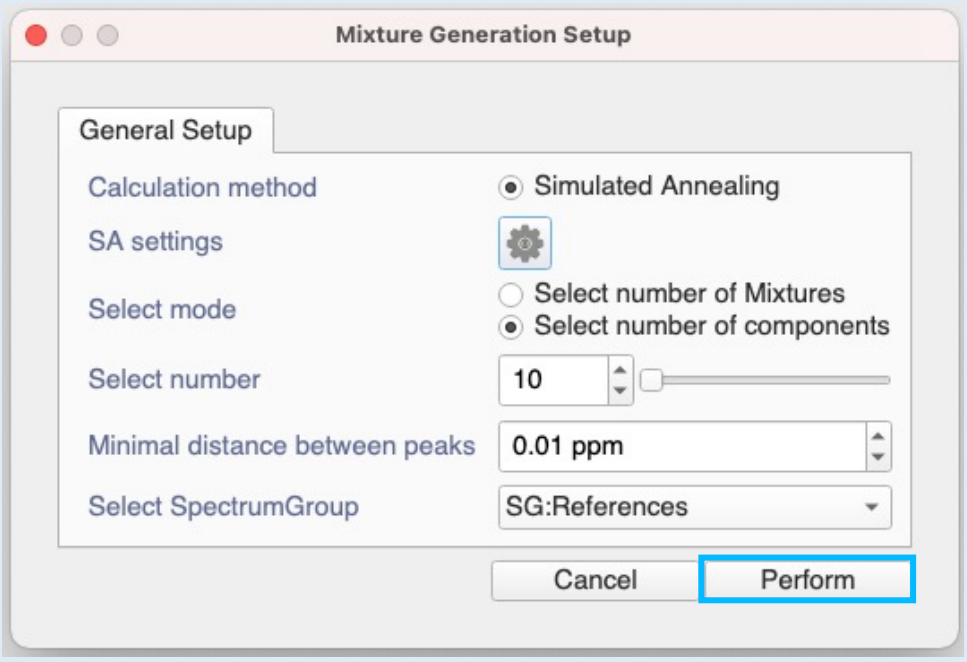
OR

- Use the shortcut **Ctrl**+**O** (or **Cmd**+**O** on a Mac) and select the project

1 Mixture Generation



GM



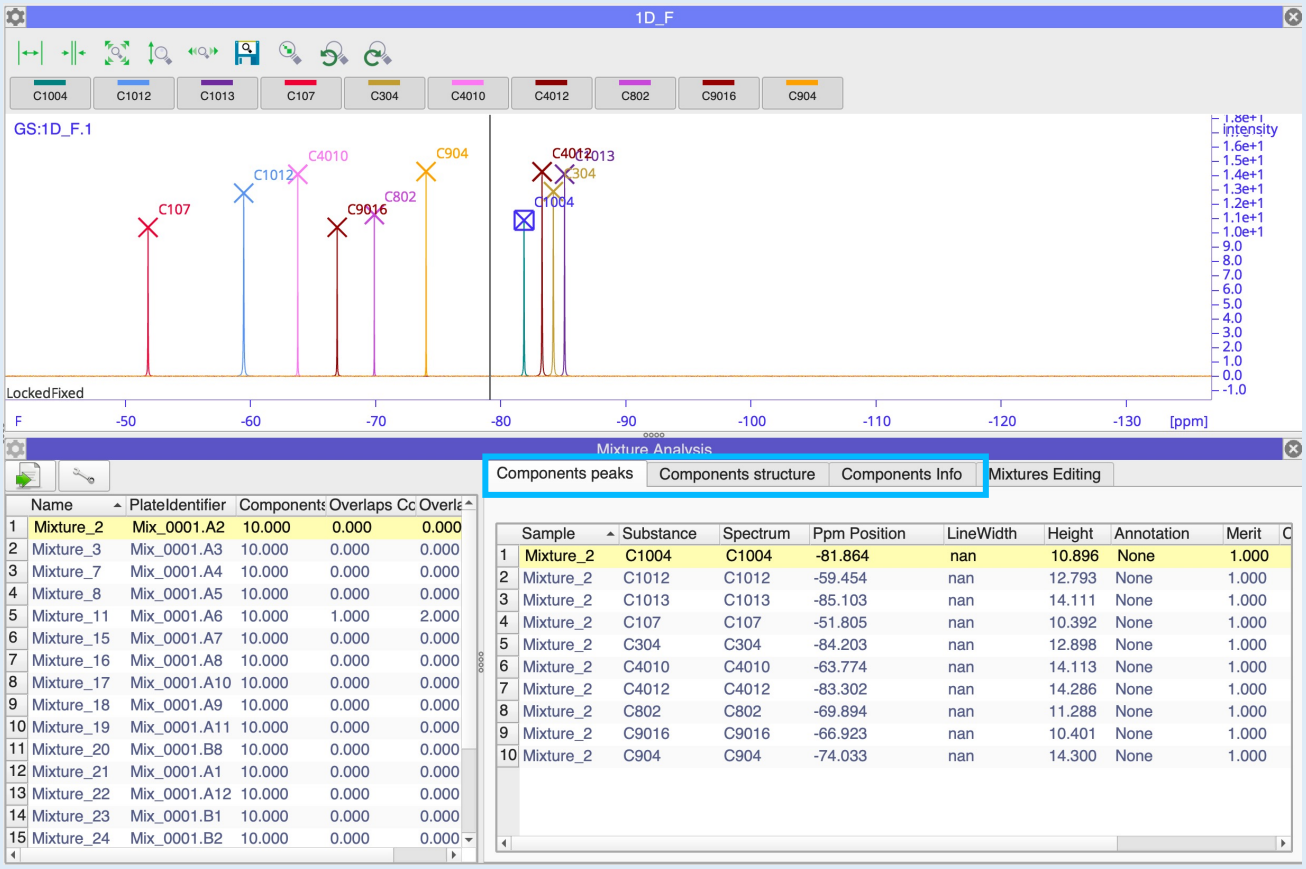
1B Set up Mixture Generation

- Go to **Main Menu → Screen → Generate Mixtures** or use shortcut **GM**

The calculation will be conducted by simulated annealing (SA). You can change the SA parameters by clicking on the gear icon. For the tutorial we will keep the default parameters.

- Choose **Select Number of Components** and se the number to **10.**
  This selection method allows you to choose how many components you want in each mixture. (**Number of Mixtures** allows the creation of a set number of mixtures with components equally distributed among them).
- Leave the **Minimal distance between peaks** at 0.01ppm.
  The algorithm will try to return mixtures where two adjacent peaks from separate spectra are separated by at least the selected value.
- Select the **Spectrum Group** you want to use to create the mixture, in this case: **SG:References**
- Press the **Perform** button to generate your mixtures.

1 Mixture Generation



1D Mixtures Analysis

The module mixture analysis will be opened automatically. If you close it, you can reopen it with **Main Menu → Screen → Mixture Analysis** or shortcut **MI**.

The table on the left-hand side of the module lists all the mixtures with scores. The scores are derived from placing a penalty on the distance between the best-resolved peak and its closest neighbour. The more overlapped the peaks, the higher the score. A score of 0.0 means there are no overlapped peaks in the mixture.

The table also lists the number of components and overlapped peaks present in each mixture. It can be sorted into ascending or descending order by clicking on the table column header.

When you select a mixture on the left hand side, the spectra of the mixture's components/substances will show in the SpectrumDisplay.

You can further inspect the mixture components on the left hand side using several tabs:

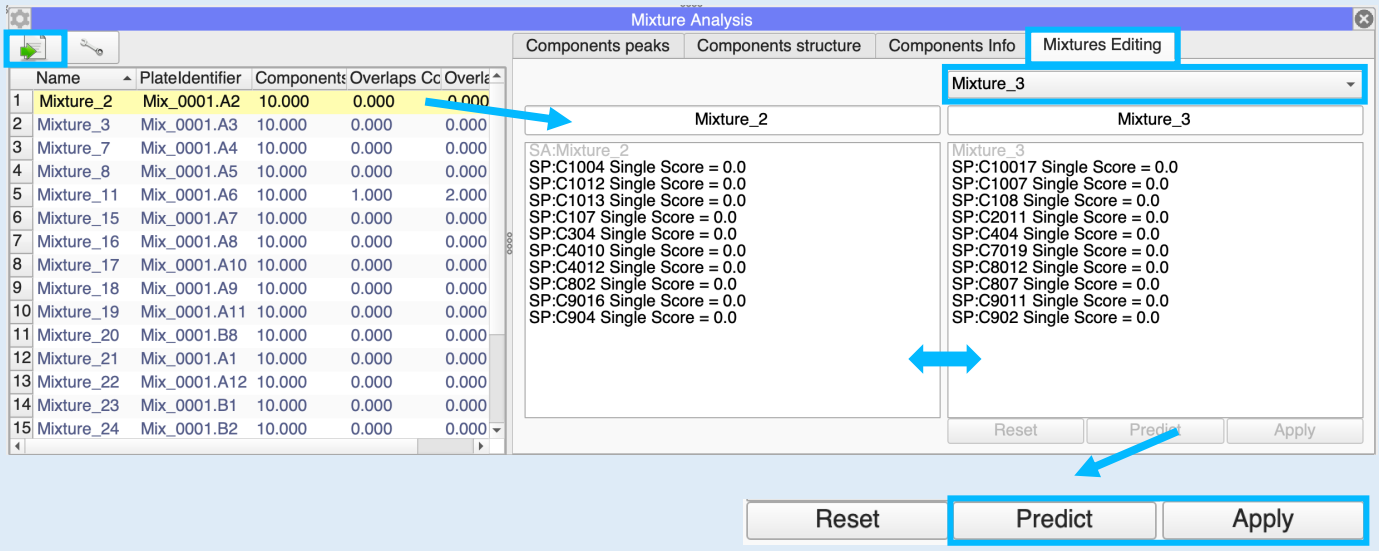
Component Peaks provides a peak list of the mixture components.

- Click on a peak to select the peak and navigate to it in the SpectrumDisplay.

Components Structure visualises the compound structures if SMILES have been provided.

Components Info provides additional physical information about the components.

1 Mixture Generation



1E Mixtures Editing

The **Mixtures Editing** tab will allow you to move components between mixtures by hand to try to improve scores or create new mixtures.

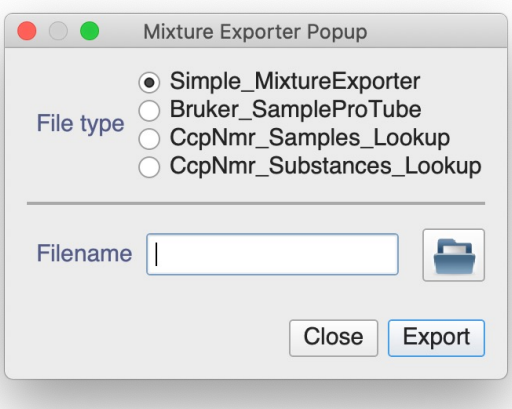
The left panel will show the selected mixture and its components.

- Select an option from the pulldown menu on the right, e.g. **New empty mixture** or any other mixture.
- **Drag and drop** the components between the windows
- Click the **Predict** button to recalculate the scores, then **Apply** to get the new mixtures.

Once you are happy with your mixtures you can export them to an Excel file using the export button  in the top left corner.

You can save the data in variety of different formats, including for a Bruker SamplePro Tube pipetting robot and as CCCPN lookup files for when you set up your screening projects.

If you require an alternative format (e.g. for a different type of robot), then please contact us, as we can probably set this up relatively easily for you.



Contact Us

Website:
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Suggestions and comments:
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Issues and bug reports:
https://forum.ccpn.ac.uk/

Cite Us

Mureddu, L. et al. CcpNmr AnalysisScreen, a new software programme with dedicated automated analysis tools for fragment-based drug discovery by NMR. J. Biomol. NMR (2020)

Skinner, S. P. et al. CcpNmr AnalysisAssign: a flexible platform for integrated NMR analysis. J. Biomol. NMR 66, (2016)