Multiphase DA imaging (MPDA)

MPDA is a new approach to quantitative imaging that solves: (i) quantitative per pixel concentrations (equivalent to the older "Correct Yields" matrix method), (ii) better X-ray relative intensities that evolve spatially with composition, and (iii) improved background shapes that adapt with composition changes.

At present it is experimental and triggered by supplying a new .mpdam file in place of the DA matrix file (.dam for PIXE, .damx for SXRF) on the Sort EVT window DA/Cal tab. The .mpdam file is a simple text file containing the following lines:

version (-1 for now)
path to 'phase map' .dai file
path to the "Correct Yields" setup .correct file

For example: file 111163-Q2.mpdam in the Demo/Maia/Rock3/mpdam dir:

```
-1
E:\Demo\Maia\Rock3-partial\mpdam\analysis\111163\111163-phases-Q2.dai
E:\Demo\Maia\Rock3-partial\mpdam\analysis\phases2.correct
```

To use it, you need the following (later we'll have a Wizard to orchestrate these steps):

1. **Identify end-members**
    a. Identify end-members components, and elements that provide a measure of each.
    b. Fit regions that sample the end-members as much as possible, using a yield calculation with composition for the end-member, and make a DA matrix for each.
    c. Also fit a region that samples a background component that will be used as a remainder component called "Rest".
2. **Correct images using the "Correct Yields" method**
    a. Open the "Correct Yields" window and select components, elements that sample each and their matching DA matrices from above, and fill in the composition matrix that relates end-members to their elements.
    b. Also select the DA matrix to be used as the remainder "Rest" component.
    c. Open the .dai image foe for your sample, and click "Correct" to correct concentrations based on the end-member (phase) proportions. Typically, this correction needs 2-3 iterations (press button again).
    d. Save the setup as a .correct file (this path will be referenced from the .mpdam file).
3. **Project end-member or phase maps**
    a. Click in "Mineral" to project the end-member or phase maps.
    b. Save this as your 'phase map' .dai file (this path will be referenced from the .mpdam file).
4. **Create your .mpdam file in an editor**
    a. Use the format above, and the 'phase map' and 'Correct setup' file paths from above.
5. **Select this .mpdam file in Sort EVT (DA/Cal tab)**
    a. Change the file filter to "*.*" and select the .mpdam file.
6. **Start the sort (you can use "cluster" mode for Maia data)**
    a. Normal GeoPIXE functions work the same from there, but you should see better concentrations in images, and better region spectra overlays.

Warnings:

1. Phase maps only work if the data is quantitative so you get realistic phase proportions for each component.