

# 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 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 "\*.mpdam" 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.