> **Note:**
> This manual provides the procedure for correct utilization of the Lepis® M0Alpha+™ for microstructural matric analysis. The instructions are to be followed to the letter to ensure that results are complete, precise, accurate, and replicable.

**Prior to initialization, check that:**

a. Computer is plugged in and turned on.

b. Probe is powered and accurately transmitting data. [This should be verified at the beginning of each shift according to the Calibration of Lepis® M0Alpha+™ (Daily) manual, PID **PDSm-4932(f)**.]

c. Probe software is properly synced with spreadsheet program PDS.



**Figure 1.** A popup window will indicate if the probe software is not properly synced with PDS.

**Analysis Preparation**

1. Create a blank sheet in PDS using the MSMa.pds template, and save in the correct location.

2. Select `Count`. In the options popup window, navigate to the `Calibration` text field and input the calibration ID generated by the most recent calibration. [This indicates to PDS where to look for parameters. Alternatively, you can choose `Browse...` in the options and navigate in the file system to the storage location of the calibration data and make your selection from there. Note: This is not the preferred method, but may be employed if necessary.]

3. Ensure that parameters are approximately the same as those in Fig. 2. The only other modifiable parameter in the `Count>Options` menu is Morse Demarcation. Its value is `SILK` by default. If value has been altered, change to `SILK`.
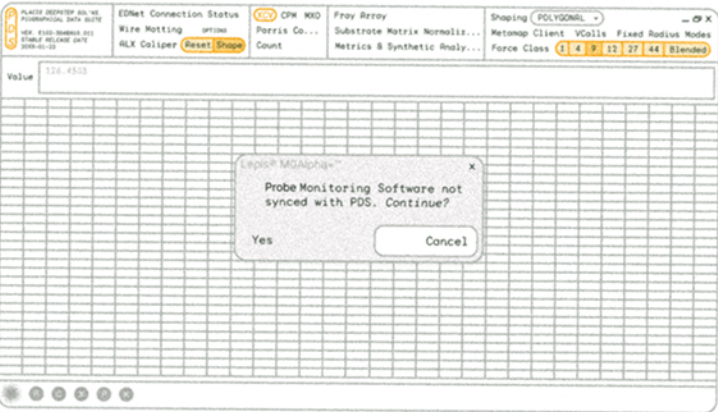
4. Press `Save`.



**Figure 2.** Options popup window for `Count`.

### Acceptable Parameter Ranges

| | |
|---|---|
| XE-4 | 47-60% |
| CMA-C | 3* |
| Chi | 12-fold* |
| Degree | variable |

*Any variation in these parameters is unacceptable. Contact lab manager immediately.

**Troubleshooting**

If XE-4 is lower than 47%: the on-site probe solution gas concentration is insufficient. The probe solution may be low or expired. Instruct the probe team to investigate and add or replace solution as needed.

If XE-4 is higher than 60%: the solution is likely expired. Contact probe team to investigate.

If CMA-C or Chi differ from their values in Fig. 2: either the probe software was improperly synced with PDS, or there is a critical malfunction in the probe itself. Contact lab manager and refer to the PDS Troubleshooting manual, PID **PDSm-4997(a-g)** for further guidance.

Degree will change based on probe positioning and is not a reliable metric for verification.

## Analysis Preparation, cont'd.

5. Toggle `ALX Caliper` to Reset mode, then press `Substrate Matrix Normalization`. Press `Confirm` on the popup asking for verification. Once the operation has run, toggle `ALX Caliper` back to `Shape`.

6. Prep the workstation for data reception. Ensure that unnecessary peripherals are safely unplugged, and that browsers and other non-essential applications are closed. This is most crucial during the CPU- and memory-intensive initialization of data transfer. [Modern workstations can handle multiple programs running simultaneously, and have sufficient processing power and memory to perform other operations, but it is still best practice to reduce strain.]
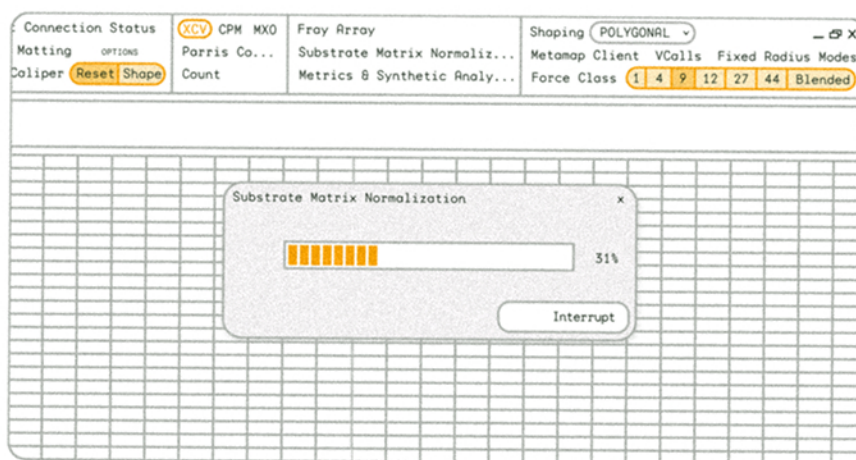


**Figure 3.** A popup window tracks progress of substrate matrix normalization.

## Conducting the Analysis

1. Select `Metrics and Synthetic Analyses` and choose `Microstructural Matric Analysis` from the dropdown menu marked `Analysis Type` in the popup window that appears (Fig. 4).

2. Press Run. The popup window will close, and the data will begin populating the spreadsheet. A new window will appear: `Microstructural Matric Analysis - Monitoring` (Fig. 5). [This may be reopened at any time using the `Monitoring` button in the `Metrics and Synthetic Analyses` window.]

3. Let the experiment run until `Set A`, `Set B`, and `10% Dil.` have equilibrated near 100 š. This may take up to 45 minutes, depending on the composition of the sample. [This ensures that each sample has fully reacted with the probe solution.]

4. Keep an open line of communication with the probe mechanic on duty on-site in case of any issues. In such an event, follow the steps in the Lepis® M0Alpha+™ Probe Troubleshooting & Problem-Solving manual, PID **PDSm-2044(c-bt)**.

5. Once the sets have fully equilibrated, select Interrupt Analysis.

6. Save the file on the central lab server, following lab protocol and the Correct Lab Data Handling - Monitoring Collected Data manual, PID **PDSm-101(a-d)**.

> **Note:**
> This test should be repeated at a frequency of once per hour. Defer to lab protocol if posted; otherwise, perform the experiment at the beginning of each hour.
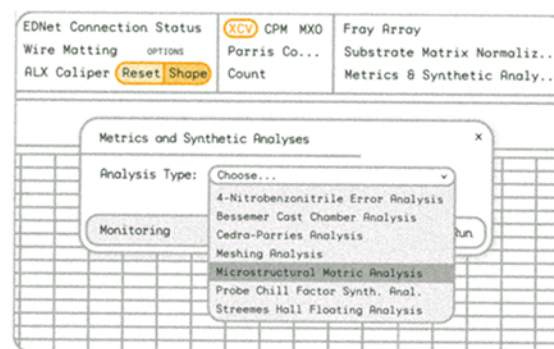


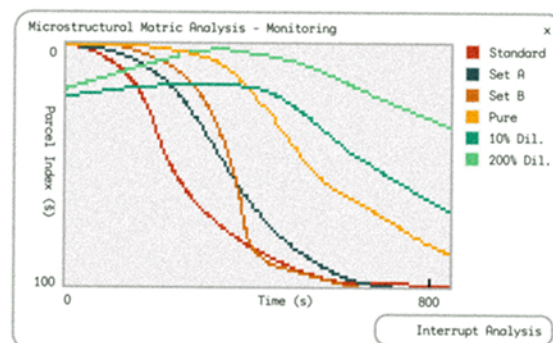**Figure 4.** PDS is natively equipped to perform seven (7) types of substructural analyses.



**Figure 5.** While `Set A` and B have both equilibrated to 100 š, `10% Dil.` has not yet equilibrated.