

Supplementary Information for “Characterizing core morphology and scar patterning within a unified spherical harmonic framework”

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Guide to the Interactive HTML Outputs

Overview

This folder contains a set of interactive HTML files, all generated by the analysis scripts included in the online repository, designed to allow readers to visually inspect the primary analytical pipeline of this study. Each file is a standalone web page: open it in any modern browser by double-clicking, no server, internet connection, or additional software is required.

All interactive files live under analysis/output/html/:

```
analysis/output/html/
├── scar_alignment_svd.html
├── scar_alignment_lin2024.html
├── kde_sphere_interactive/
│   ├── kde_sphere_EXP.html
│   ├── kde_sphere_IM.html
│   └── kde_sphere_SDG.html
├── reconstruction_interactive/
│   ├── interactive_EXP.html
│   ├── interactive_IM.html
│   ├── interactive_SDG.html
│   ├── interactive_EXP_CoIA_axes.html
│   └── interactive_SDG_CoIA_axes.html
```

Three dataset codes appear throughout the filenames:

- **IM:** the idealized digital core models.
- **EXP:** the experimental knapped cores.
- **SDG:** the archaeological Sandinggai cores.

The sections below describe what each file shows and how to read it, together with the script that generates it.

Alignment diagnostics

These two pages visualise, specimen by specimen, the orientation standardisation that is applied to the raw flaking scar vectors before any SPHARM analysis. In both pages a dropdown at the top selects the specimen, every panel is a fully rotatable/zoomable 3D plot, and a short caption beneath each panel states what that step does.

[scar_alignment_svd.html](#)

Generated by align_svd.R. This is the alignment used for the main analysis. It shows the four step SVD pipeline as four side-by-side panels:

- **Step 0: Raw data.** Scar start/end points in their original coordinates, with the SVD-fitted best-fit plane and its normal.
- **Step 1: Rotate.** The best-fit plane normal (the third right singular vector of the unit scar direction vectors) is rotated onto the Z-axis, so the plane lies flat in XY.
- **Step 2: Translate.** The centroid of all scar endpoints is moved to the origin, removing positional bias between specimens.
- **Step 3: Rotate XY.** The dominant in-plane scar direction (first singular vector of the XY projections) is rotated onto the X-axis, so every specimen shares a common reference frame.

[scar_alignment_lin2024.html](#)

Generated by align_lin2024.R. This page documents the alternative alignment of Lin et al., 2024, used in the rotational-invariance validation rather than the main pipeline. It has three panels:

- **Step 0: Direction vectors / reference normal.** Unit direction vectors are computed from scar endpoints; the morphological plane normal (Norm_X/Y/Z, measured externally in Geomagic Wrap software) serves as the reference orientation.
- **Step 1: Rotate.** A Rodrigues rotation aligns the measured morphological normal with the Z-axis, placing the best-fit plane in XY.
- **Step 2: Translate.** The longest scar is identified and its rotated start-point is moved to (0, 0), anchoring the origin while preserving the absolute spatial relationships between scars.

Scar vector density on the sphere

[kde_sphere_interactive/kde_sphere_{EXP,IM,SDG}.html](#)

Generated by `spherical_kde_interactive_export.py`, one file per dataset. Each page renders the von Mises–Fisher kernel density estimate (KDE) of a specimen’s flaking-scar direction vectors on a single unit sphere, coloured by density. This is the spherical density that the SP-SPHARM descriptors are computed from, shown here as a directly inspectable surface.

Only the raw direction vectors are embedded; the KDE itself is recomputed in the browser, so the density responds live to the bandwidth control.

Controls:

- **Specimen dropdown**, grouped by core type.
- **Bandwidth slider (bw)**: recomputes the KDE on the fly; the concentration parameter is $\kappa = 1/bw^2$.
- **Type Mean**: pools the direction vectors of every specimen of the selected type and re-fits the KDE, giving a per-type average pattern.
- **Scars**: toggles the scatter of individual scar vector points over the density surface.
- **Contours**: overlays iso-density contour lines.
- **2D Map**: an equirectangular density map.
- **Graticule**, **view presets**, **material** selector, **Info** panel, a density **colour bar**, and PNG export.

SPHARM reconstructions

[reconstruction_interactive/interactive_{EXP,IM,SDG}.html](#)

Generated by `spharm_interactive_export.py`, one file per dataset. Each page is a dual viewport: the Morphology reconstruction (M-SPHARM, left) and the Scar pattern reconstruction (SP-SPHARM, right) for the same specimen, with synchronised rotation and zoom. The surfaces are synthesised in the browser in real time from the stored spherical-harmonic coefficients (up to degree $l = 20$).

Controls:

- **Specimen dropdown**, grouped by core type.
- **Degree slider ($l \leq$)** with a **play button**: rebuilds the surface using only harmonics up to the chosen degree, and animates $l = 1 \rightarrow 20$ to show how detail accumulates as higher frequencies are added.
- **Type Mean**: averages the coefficients across all specimens of the selected type and reconstructs that mean shape.
- **Colormap**: shades the surface by radial deviation from its mean radius (blue = inward, red = outward), with a colour bar.

- **Wire** (wireframe), **material** selector, **view presets**, **Info** panel, plus **PNG** screenshot and **OBJ** mesh export.

[reconstruction_interactive/interactive_{EXP,SDG}_CoIA_axes.html](#)

Generated by the `export_axis_interactive_html()` routine in `spharm_reconstruction.py` (reusing the viewer above). These pages exist only for the two datasets that have a co-inertia analysis (CoIA): **EXP** and **SDG**.

Instead of individual specimens, the dropdown steps through synthetic average shapes sampled along the CoIA axes that summarise the covariation between the morphology block and the scar pattern block. For each of *Morph Axis 1/2* and *Scar Axis 1/2*, the axis is sampled at a sequence of positions (across a robust percentile range); at each position a Gaussian-kernel-weighted mean of the coefficients is reconstructed. The Info panel reports the axis, the axis coordinate of the current step, the kernel bandwidth, and the effective sample size behind each averaged shape.