

CombiTab Quick Start Guide

Version 1.0 — Archaeological Seriation & Combination Table Tool

1. Getting Started

Launch the Application

Run in terminal: `streamlit run combitab.py`

The app opens in your browser with a sidebar (left) and main work area (right).







Load Your Data

1. Click Upload CSV or Excel in the sidebar
2. Select your data file (contexts as rows, artifact types as columns)
3. Or click Load Sample Data to explore with example data

Expected format: First column = context names, other columns = type names, cells = 0/1 or counts.

2. Interface Overview

The main area has six tabs:

Tab	Purpose
 Matrix View	View & sort the combination matrix, manual reordering
 Analysis	Correspondence Analysis, quality metrics, biplot
 Annotations	Add certainty, fragmentation, notes to individual cells
 Column Labels	Assign material groups, mark index types
 Row Labels	Set context types (Grave, Pit, Layer, etc.)
 Export	Save as PNG/SVG/PDF or export data to CSV/Excel

3. Sorting Your Matrix






In the Matrix View tab:

1. Choose a Sort method: Centroid (simple), Correspondence Analysis (statistical), or Iterative
2. Select Sort target: Both rows & columns, Rows only, or Columns only
3. Click Apply Sorting — the matrix reorders automatically

Tip: Use Iterative sorting for best results — it repeats until the ordering stabilizes.

Manual Fine-Tuning

Use the right sidebar to move individual rows/columns:

- Select a row or column from the dropdown
- Click / or / to move it
- Check  Fix position to prevent automatic reordering

4. Quality Metrics

Five metrics appear above the matrix:

- Quality Score — Overall seriation quality (0-1, higher = better)
- Concentration — How close values cluster to the diagonal
- Continuity — Absence of gaps within type distributions

- Avg. Type Continuity — How densely types fill their spans
- Gap Cells — Total number of problematic gap cells

Target: Quality Score > 0.8 indicates a good seriation.

5. Assigning Material Groups

Color-code your artifact types by material:




1. Expand Type Statistics & Material Assignment in Matrix View
2. Edit the Material column directly in the table
3. Click Apply Material Changes when done

Bulk assignment: Type a filter (e.g., "Fibula"), select a material, click Apply Bulk.


Default groups: Ceramic, Metal, Glass, Bone/Antler, Stone, Organic.

6. Interactive Matrix Navigation

With Interactive View enabled (default):

- Scroll to zoom in/out
- Click and drag to pan
- Double-click to reset view
- Hover over cells to see details
- Use toolbar:  Zoom |  Home |  Save image

7. Filtering Large Matrices

Expand  Filter & Focus for these options:

- Filter by Material Group — Show only selected materials
- Focus Mode — Display a range of rows or columns
- Hide Empty — Remove rows/columns with no data

Useful for matrices with 100+ rows/columns.

8. Saving & Exporting

Save Project

Click Export Project (.json) in the sidebar to save everything: data, ordering, metadata, settings.

Reload later with Import Project.

Export Images

In the Export tab, generate publication-ready images:

- PNG — For presentations (adjustable DPI)
- SVG — Vector format for publications
- PDF — Direct document inclusion

Export Data

- CSV — Sorted matrix only
- Excel — Includes metadata sheets and statistics

9. Keyboard Shortcuts

Shortcut	Action
Ctrl + Z	Undo last ordering change
Ctrl + Y	Redo
Ctrl + S	Trigger project export

10. Typical Workflow

- 1. Import** → Upload your CSV/Excel data
- 2. Assign** → Set material groups for artifact types
- 3. Sort** → Apply Iterative CA sorting
- 4. Refine** → Manually adjust problem areas, fix key positions
- 5. Analyze** → Check quality metrics, view CA biplot
- 6. Export** → Save project & export publication images

Need more details? See the full CombiTab Documentation.