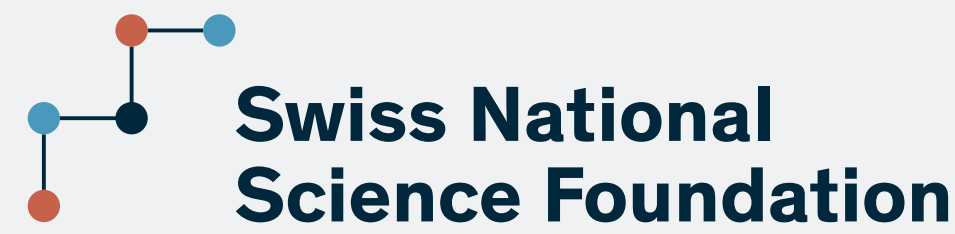


**EPFL**

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## Basic Principle

- The **DiMCAT** workflow starts with initializing a **Dataset** object:
  - either an empty one, loading a **Package** into the **Inputs Catalog**;
  - or one that had been serialized together with its **Outputs**.
- Having copied a given **Dataset** object, a **PipelineStep** may
  - add **Feature** or **Result** resources to the **Outputs**;
  - perform transformations on **Resources** added by previous Steps.



## Slicing

**Fig. 3:** This truncated heatmap shows the relative frequencies (in %) of transitions between the ten most frequent local keys in *my corpora*. Keys are given as Roman numerals pertaining to a major scale. Percentages following y-axis labels correspond to the proportion of key segments in the given key. Black bars represent the relative entropy of each (complete) row.

## Statement of Need

## The Reproducible Slice-Group-Analyze Pipeline

## Analyzing & Transforming

**Fig. 4:** Sankey plot displaying the transition masses between chordal roots of all 4-grams terminating on a Perfect Authentic Cadence.

Figure 1 consists of two panels, (a) and (b), each displaying a heatmap of the 1000 Genomes Project data. The heatmaps show the relationship between different populations and genetic markers. The populations are listed on the left of each panel, and the genetic markers are listed on the right. The color of each cell in the heatmap represents a value, with a color scale ranging from 0.00 (blue) to 0.99 (red). Panel (a) shows the 1000 Genomes Project data, and panel (b) shows the 1000 Genomes Project data. The heatmaps are arranged in a grid, with the populations listed on the left and the genetic markers listed on the right. The color of each cell indicates the value of the relationship between the population and the marker.

**CODE**

