# A Method for Analysis of Shared Structure in Large Music Collections using Techniques from Genetic Sequencing and Graph Theory

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Information from many related audio files can be used to find a good estimate of their structure and to improve the quality of the input audio features (e.g. beatwise chord labels)
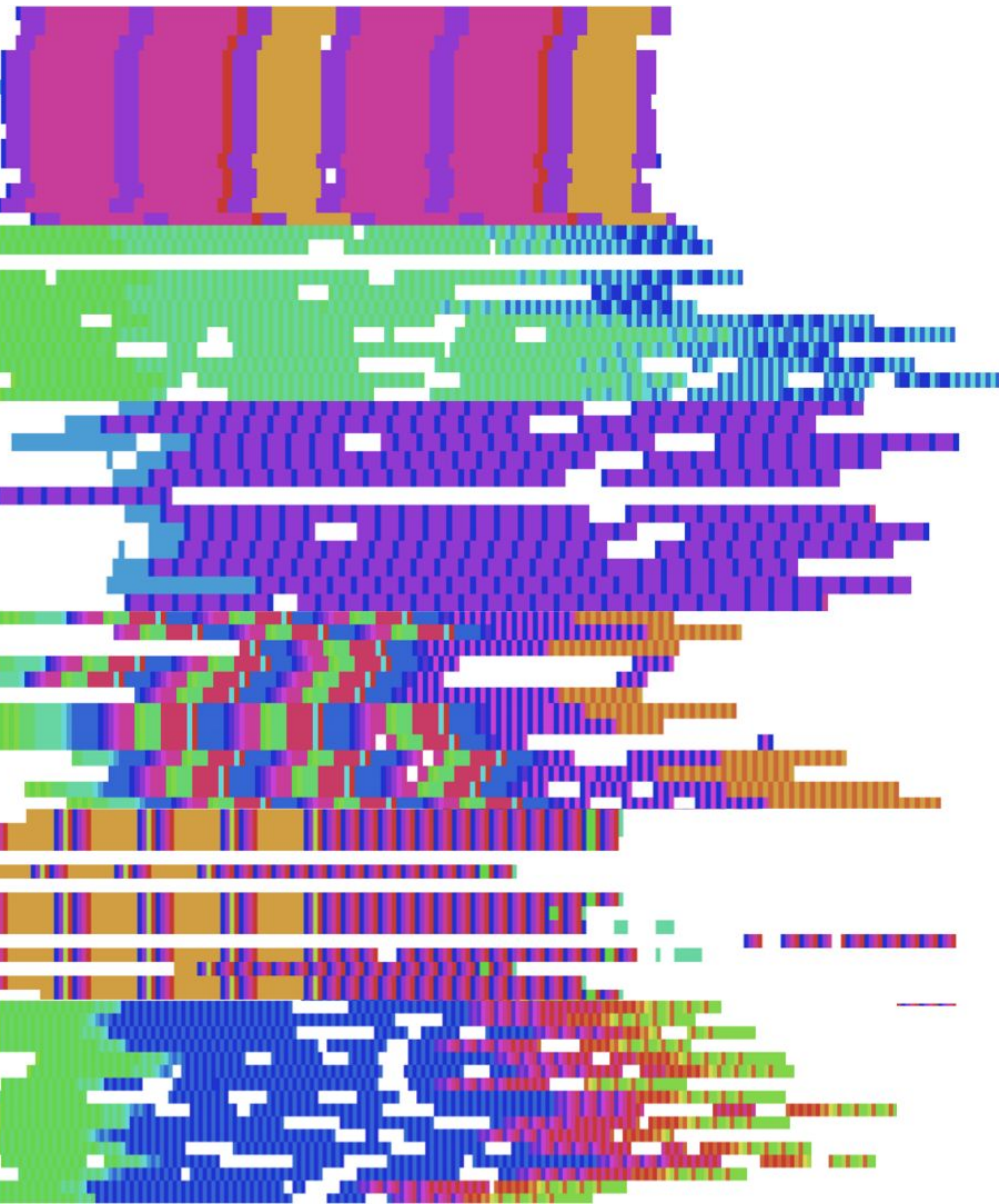

We combine pairwise, self-, and multiple alignments of given feature sequences into graph representations from which we can infer a shared structure
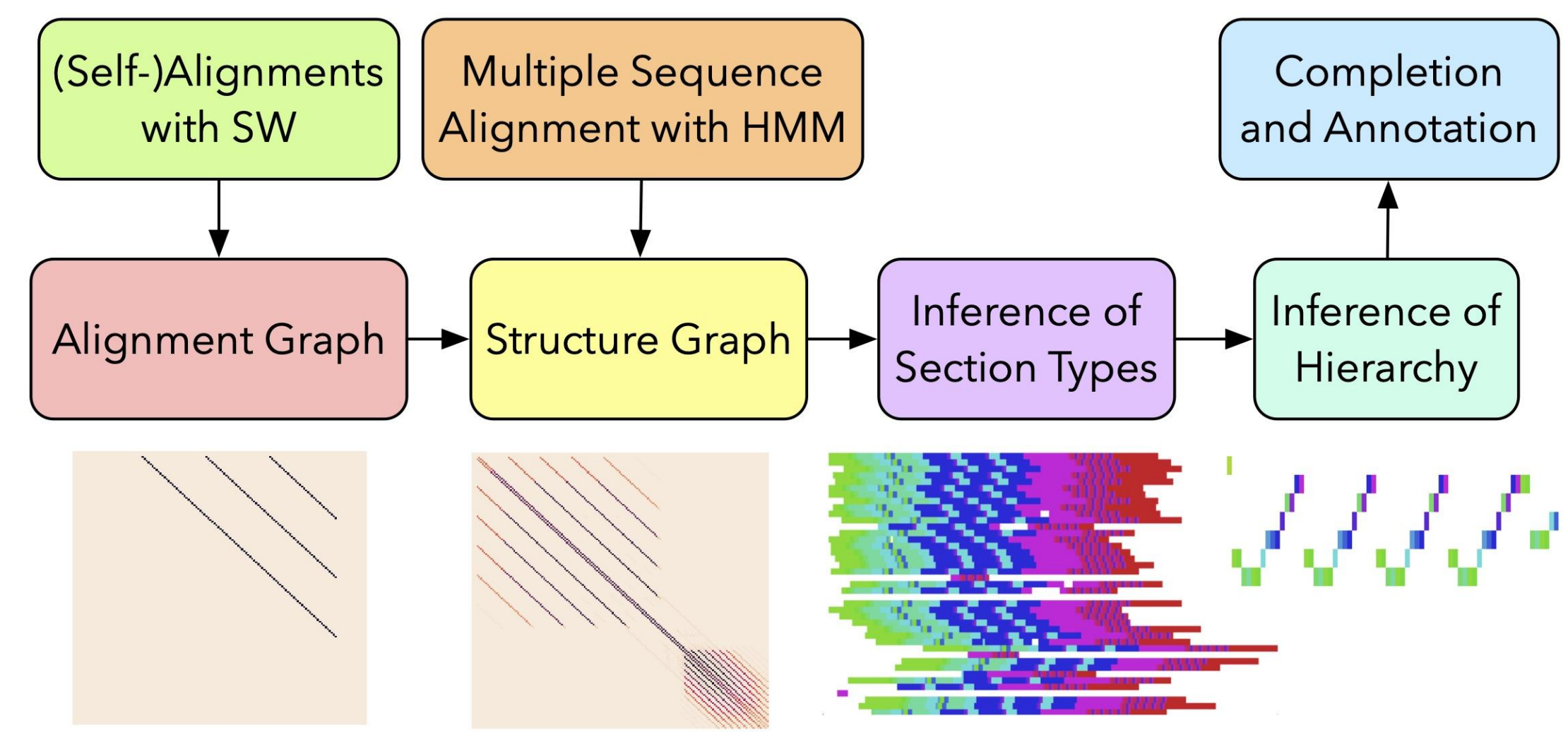

Profile HMMs are used to find simultaneous alignments of multiple sequences (MSA)
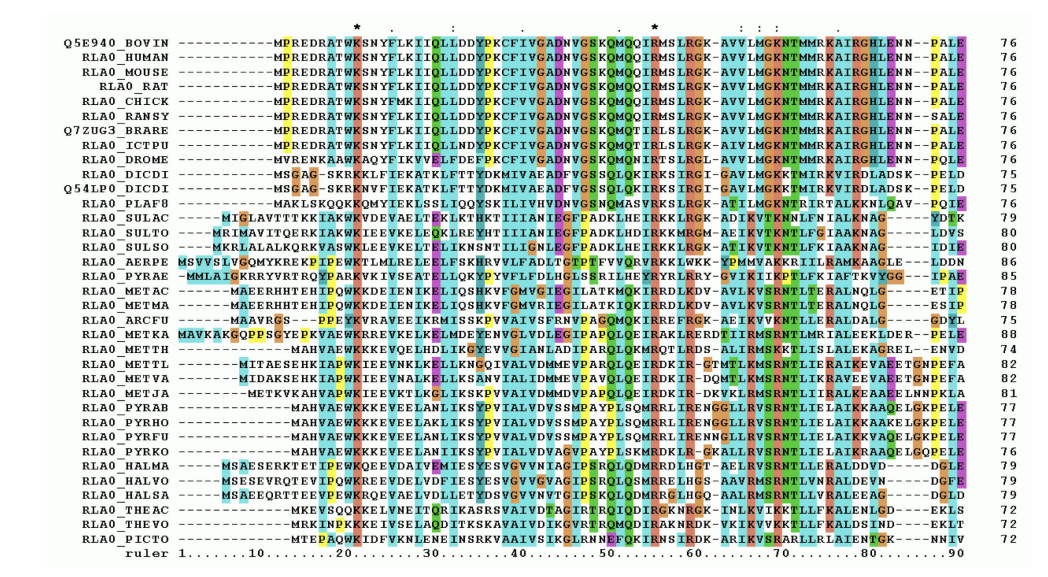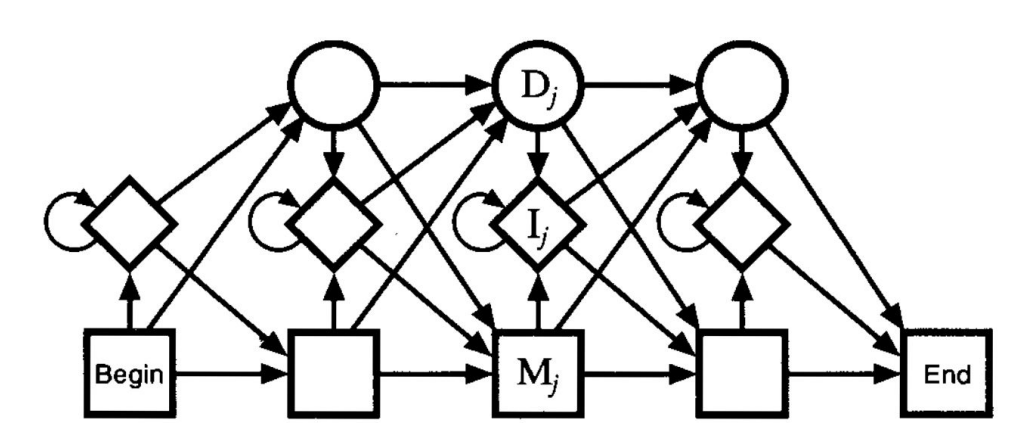
The MSA are used to label the time segments in the alignment graph and identically labeled segments are collapsed. Some segments may remain unlabeled but are likely connected to labeled ones
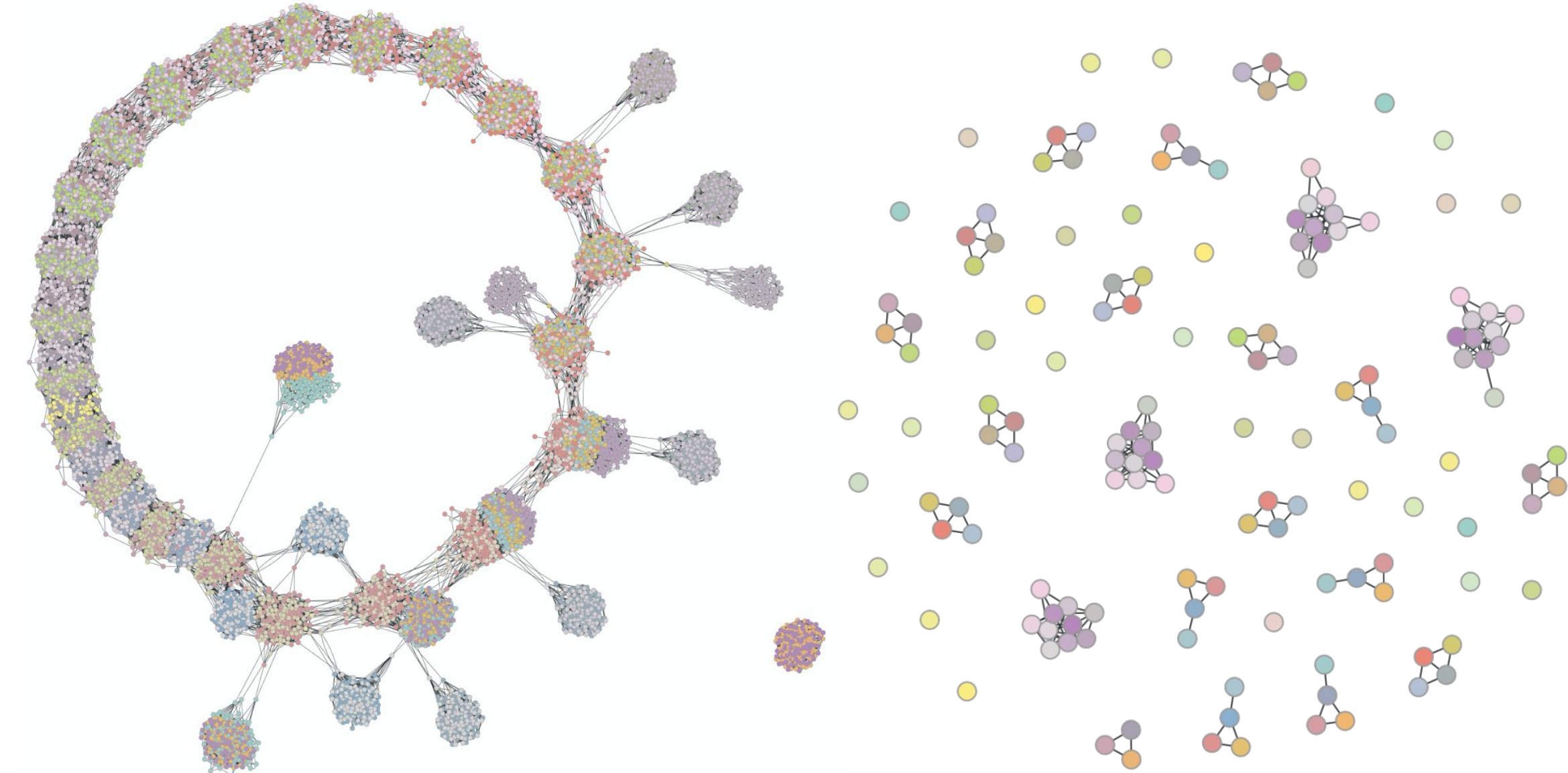
Connected components yield section labels which can be organized into hierarchical structures. Each section type is associated with a feature sequence obtained via the statistical mode of the involved segments
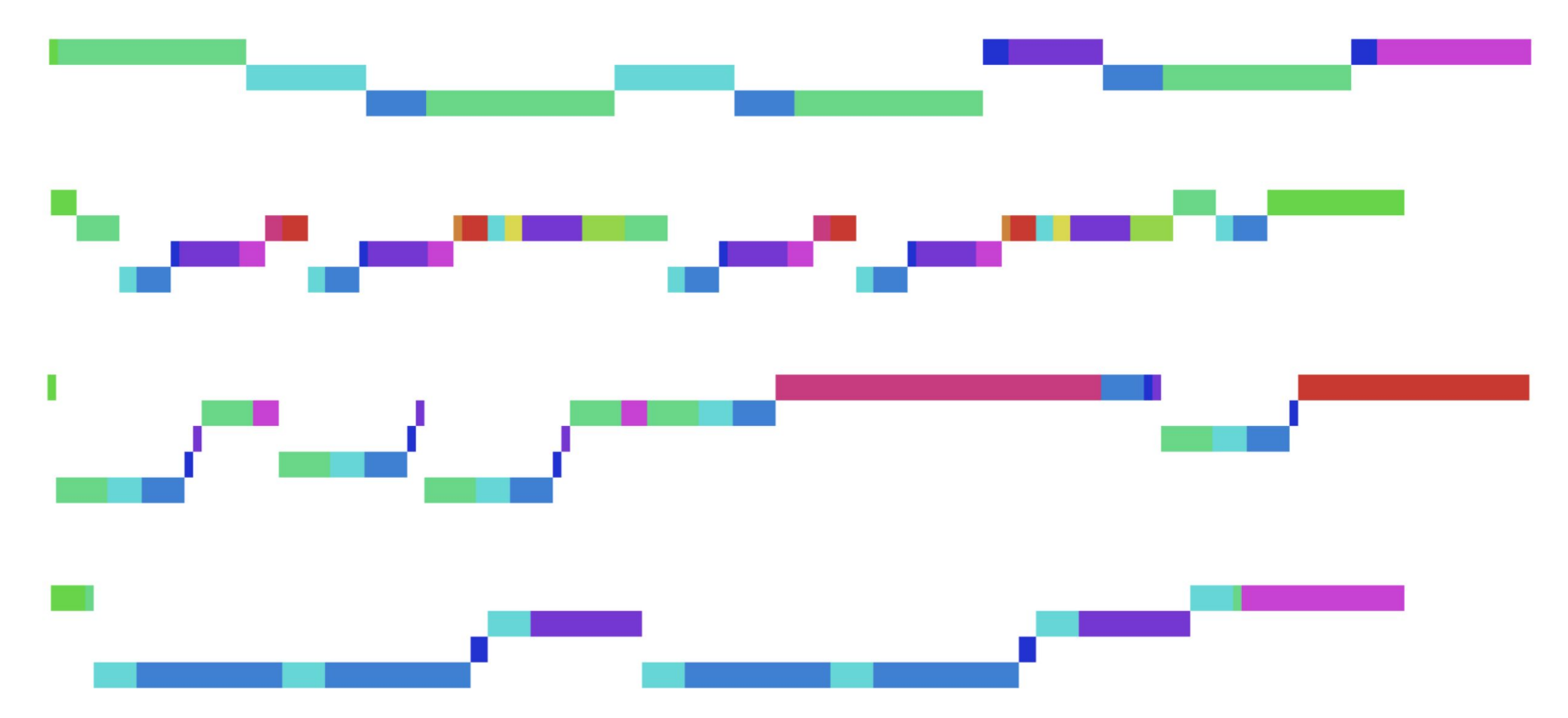
Dataset with 2167 live performances of 15 songs
https://github.com/grateful-dead-live/fifteen-songs-dataset

Distribution over the 15 songs of proportion of ground truth annotations correctly matched with beatwise chord sequences
(a) raw features, (b) annotated versions, (c) shared structure