Multi-segment Reconstruction with Invariant Features

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ABSTRACT

Multi-segment reconstruction (MSR) problem consists of recovering a signal from noisy segments with unknown positions of the observation windows. One example arises in DNA sequence assembly, which is typically solved by matching short reads to form longer sequences. Instead of trying to locate the segment within the sequence through pair-wise matching, we propose a new approach that uses shift-invariant features to estimate both the underlying signal and the distribution of the positions of the segments. Using the invariant features, we formulate the problem as a constrained nonlinear least-squares. The non-convexity of the problem leads to its sensitivity to the initialization. However, with clean data, we show empirically that for longer segment lengths, random initialization achieves exact recovery. Furthermore, we compare the performance of our approach to the results of expectation maximization and demonstrate that the new approach is robust to noise and computationally more efficient.