

# Benchmarking R packages for Calculation of Persistent Homology

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**Abstract** Several persistent homology software libraries have been implemented in R. Specifically, the Dionysus, GUDHI, and Ripser libraries have been wrapped by the TDA and TDAstats CRAN packages. These software represent powerful analysis tools that are computationally expensive and, to our knowledge, have not been formally benchmarked. Here, we analyze runtime and memory growth for the 2 R packages and the 3 underlying libraries. We find that datasets with less than 3 dimensions can be evaluated with persistent homology fastest by the GUDHI library in the TDA package. For higher-dimensional datasets, the Ripser library in the TDAstats package is the fastest. Ripser and TDAstats are also the most memory-efficient tools to calculate persistent homology.

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