BinMat: a molecular genetics tool for processing binary data obtained from fragment analysis in R.

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Abstract

Processing and visualising trends in the binary data obtained from fragment analysis methods in molecular biology can be a time-consuming, and often cumbersome process. Scoring and processing binary data (from methods such as AFLPs, ISSRs, and RFLPs) entails complex workflows that require a high level of computational and/or bioinformatic skills. The application presented here (BinMat) is a free, open-source, and user-friendly R Shiny program that automates the analysis pipeline on one platform. BinMat is presented as a Graphical User Interface (GUI) via the Shiny package in R that is available online across different operating systems. It is also available as an R package. BinMat consolidates replicate sample pairs in a dataset into consensus reads, produces summary statistics, and allows the user to visualise their data as ordination plots and clustering trees without having to use multiple software programs and input files, or rely on previous programming experience.

Hosted file

vanSteenderenBinMat_MER.pdf available at https://authorea.com/users/308074/articles/439070-binmat-a-molecular-genetics-tool-for-processing-binary-data-obtained-from-fragment-analysis-in-r