BingleSeq: A User-Friendly R Package for Single-Cell RNA-Seq Data Analysis

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Abstract : BingleSeq was developed as a shiny-based, intuitive, and comprehensive application that enables the analysis of single-Cell RNA-Sequencing count data. This was achieved via incorporating three state-of-the-art software packages for each type of RNA sequencing analysis, alongside functional annotation analysis and a way to assess the overlap of differential expression method results. At its current state, the functionality implemented within BingleSeq is comparable to that of other applications, also developed with the purpose of lowering the entry requirements to RNA Sequencing analyses. BingleSeq is available on GitHub and will be submitted to R/Bioconductor.