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SEQprocess: A pipeline tool for processing of next generation sequencing data with modularized customization

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Next-Generation Sequencing (NGS) technology is now widely used in biomedical research field. The application of NGS technologies includes the identification sequence variants of DNA or RNA and the quantitation of RNA abundances or DNA copy numbers. Previously several softwares for NGS data processing pipelines have been released. However, the softwares do not cover the recently updated GDC pipelines which is a standardized pipeline used in the processing of the TCGA data. Moreover, there is no comprehensive tools that handle the recent clinical applications of NGS technology such as cell-free DNA, small RNA, and exosomal RNA sequencing data. Here, we developed a SEQprocess that can provide NGS processing pipelines covering the GDC pipeline as well as the new data for clinical applications. SEQprocess is implemented in an R program to provide an automated and user friendly interfaces. SEQprocess also provide a flexible customization framework by modularizing the multiple NGS processing steps that can be easily included or excluded in the process. In addition, SEQprocess automatically generate a report that summarize the processing steps, which will ensure reproducibility of the NGS data analysis.

Biography

Ji Hye Choi has completed her Doctor of Science Degree majoring in Biomedical Informatics and Convergence Medicine from Ajou University of Medicine, Suwon, Republic of South Korea in August 2017 and currently is a Research Fellow at the same university. Her research interests are Genomics, Bioinformatics and System Biology. She has authored more than five papers in reputed journals including *Cancer Research, Nature communication, Experimental & Molecular Medicine, Oncotarget and BMC Bioinformatics*.

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