Pipeline manual

In this study, we performed a lot of computational analysis, including functional gene identification, m6A analysis, orthologous analysis, gene function annotation, gene family identification (pfam), collinearity analysis, transposon identification, CRISPR guide sequences identification, etc.

For the convenience of users, we have compiled some process descriptions for users to download for free. Compared with previous studies, these processes organically integrate the analysis of multiple processes and multiple software. More importantly, these processes can be run in batches, which greatly saves analysis time and improves work efficiency. However, these processes need to be run on a linux server, and some required software needs to be installed in advance. Therefore, those who have a certain basis in bioinformatics research should be easier to use these processes. For processes not involved in this section, please refer to the article or other parts of the website for instructions. Users also can contact us if they have any questions about the website or need help with bioinformatics analysis. We sincerely welcome the users' valuable comments. The following process can be downloaded and used by scientific researchers.

Download:

1. **Pfam_and_TF_analysis**　　2. **Functional_gene_analysis**　　3. **m6A_analysis**　　4. **Synteny_analysis**

5. **CRISPR_analysis**　　6. **Orthologous_and_paralogous_analysis**　　7. **TE_analysis**