

0. Introduction for Quality Control

Quality Control module consists of a suite of tools focused on different levels of quality assessment, including reads quality, alignment quality and RNA modifications quality. Thus, three functions are implemented, including **Assess Reads Quality**, **Assess Alignment Quality** and **Assess RNA modifications Quality**. The details of as follows:

Tool	Description	Input	Output	Time (test data)	Programs	Reference
Assess Reads Quality	This function firstly performs quality control using FastQC and then trims low-quality reads using fastp	Epitranscriptome sequencing reads in FASTQ format	Clean reads in FASTQ format; Reads quality report in HTML format	~40s	FastQC , fastp	Chen et al., 2018, Bioinformatics , Babraham Bioinformatics
Assess Alignment Quality	Assess the quality of read-genome alignments (here reads from MeRIP-Seq experiments)	Reads alignments in SAM/BAM format	Alignment quality report in HTML format	~1 min	trumpet	Zhang et al., 2018, BMC Bioinformatics
Assess RNA Modifications Quality	Quantify RNA modifications signal strength by counting reads and calculating RPKM	RNA modifications in BED format and read alignments in SAM/BAM format	RNA modifications quantification matrix in HTML format	~1 min	DiffBind	Wu et al., 2016, Frontiers in Genetics

1. Assess Reads Quality

In this function, two existing NGS tools **FastQC** (Andrews *et al.*, 2010) and **fastp** (Chen *et al.*, 2018) are integrated to check sequencing reads quality and obtain high-quality reads, respectively.

Input

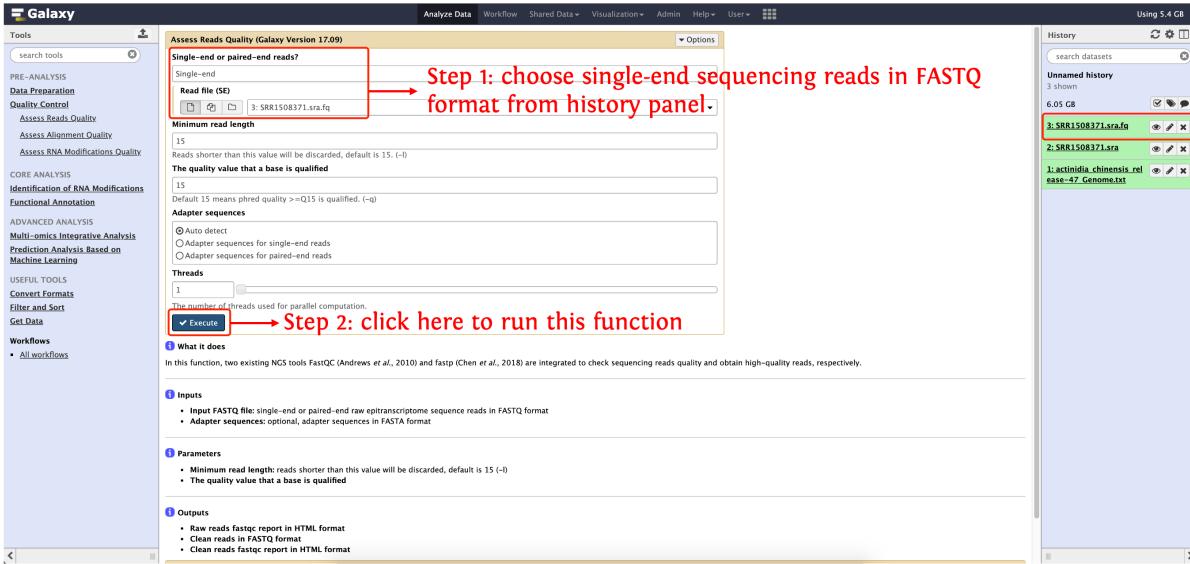
- **Input FASTQ file:** single-end or paired-end raw epitranscriptome sequence reads in FASTQ format
- **Adapter sequences:** optional, adapter sequences in FASTA format

Output

- **Clean reads in FASTQ format**
- **Reads quality report in HTML format**

How to use this function

- The following screenshot shows us how to assess reads quality



2. Assess Alignment Quality

This function is used to generate alignment quality assessment for MeRIP-Seq (methylated RNA immunoprecipitation sequencing) experiments by using an R package "trumpet" (Zhang *et al.*, 2018, *BMC Bioinformatics*).

Input

- **BAM file in IP sample:** alignments in BAM format of immunoprecipitated (IP) RNA samples
- **BAM file in input sample:** alignments in BAM format of input (control) RNA samples
- **Genome annotation in GTF/GFF3 format**

Output

- An HTML report recording the alignment quality.

How to use this function

- **Step 1:** download test data provided by deepEA (https://deepea.nwafu.edu.cn/static/test_data.zip)

- Step 2: upload test data in directory `test_data/Quality_Control/` to history panel

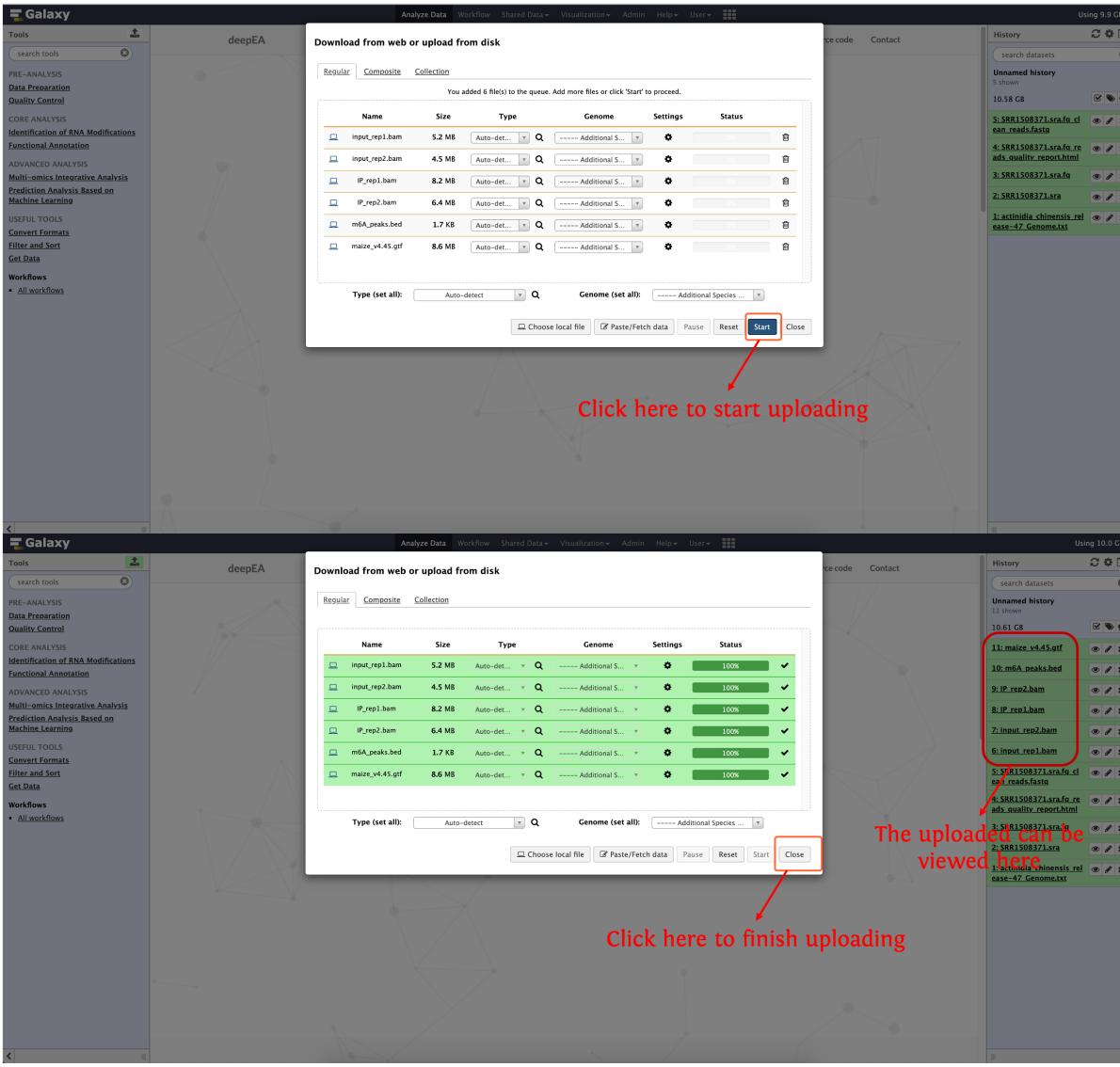
Click this button first to upload local data into deepEA server

Then click this button to choose local file

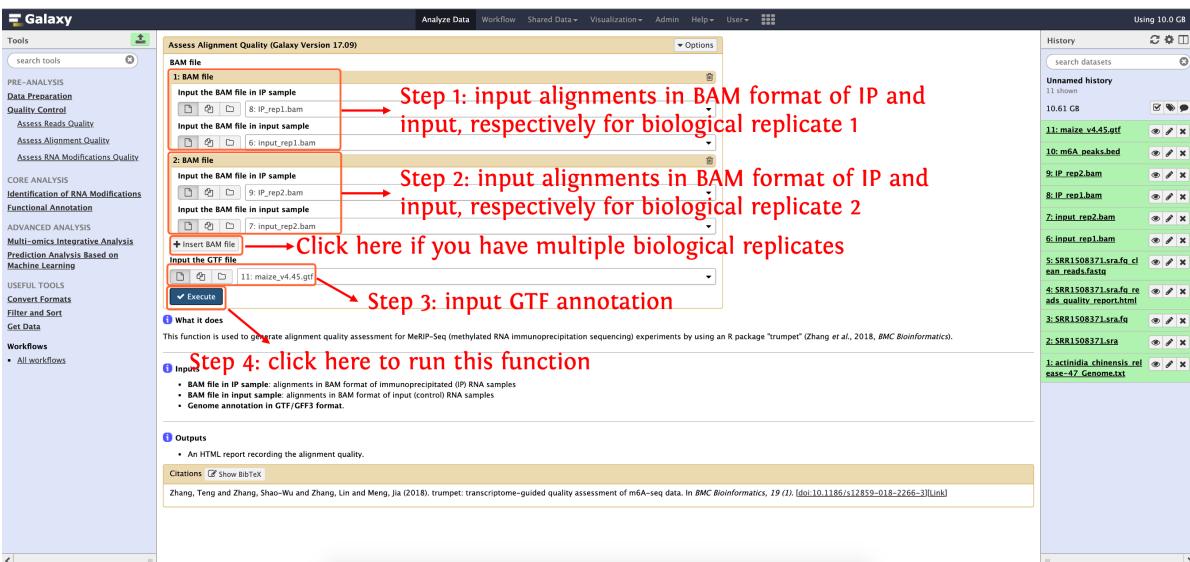
Then choose test data provided by deepEA

**Show More
Click here**

input_rep1.bam
Document - 5.9 MB
Tags Add Tags...
Created 2020/7/28
Modified 2020/7/28
Cancel Open



- Step 3: input the corresponding file as the following screenshot shows to run this function:



3. Assess RNA Modifications Quality

This tool aims to quantify RNA modifications (e.g. m6A, m1A) signal strength by counting reads and calculating RPKM in binding site intervals using an R package Diffbind (Wu *et al.*, 2016, *Frontiers in Genetics*)

Input

- RNA modifications in BED format
- IP alignments in BAM format
- input alignments in BAM format

Output

- An interactive HTML document recording each RNA modification region's RPKM

How to use this function

- Please see the following screenshots to run this function, test data used in the screenshot is available in `test_data/Quality_Control/`

