

A Step-by-step tutorial for visualizing single-cell RNA-seq datasets from JingleBells at the single cell level in IGV

Let's assume you want to see dataset GSE64002

1. Go to jinglebells.bgu.ac.il, and find the row of GSE64002
2. Press the 'download' link in the row of 'GSE64002'
3. An interface will open with a README file and a bam_files folder. Read the README file to see what bam files you are interested in.
4. Double click the bam_files folder and download the bam and bai files you are interested. Make sure you downloaded to the same place the bam and the bai files. Note the folder you download the files to.
5. Open IGV (If you are unfamiliar with IGV, read the Appendix to see how to use IGV)
6. Select the relevant genome from the genome drop-down list according to the dataset genome version (Column 'Organism (Genome version)' in JingleBells datasets table). If you can't see the genome you need in the genome drop-down list, choose (1) 'More...' from the drop-down or (2) select Genomes->'Load Genome From Server' from the menu bar.
7. Press the File menu and choose 'load from file'. Load the bam file(s) you downloaded from JingleBells repository. Ctrl tab enable choosing multiple files to upload.
8. Alternatively to the upload method described in 7, you can upload by script, see example load2IGV.txt
9. Hover the mouse over each track name, right click the mouse, choose group by, choose tag, and type xi. The reads from each single cell will be group together (Sometimes genomic location should be changed for the groups to be seen).
10. Hover the mouse over each track name, right click the mouse, choose color by, choose tag, and type YC. The reads from each single cell will be colored by the same color (Sometimes genomic location should be changed for the colors to be seen).

11. Blank lines under the top, grey bars, represent reads that are not shown. To see all the reads: View -> Preferences... -> Alignments -> Downsample reads Max read count: 1,000,000

Appendix – IGV basics

1. Register to the IGV site.

<https://www.broadinstitute.org/software/igv/log-in>

User guide:

<https://www.broadinstitute.org/software/igv/UserGuide>

2. Download IGV to your computer, according to your operating system
3. Open IGV