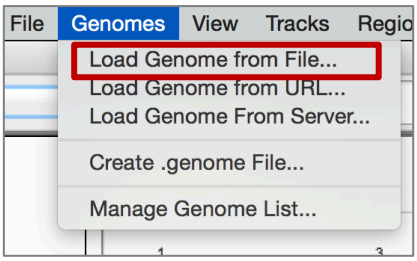
Introduction to the Integrative Genomics Viewer (IGV)

Hands-on exercise: Load genome from file

1. Clear out the data from the previous exercise: Select *File > New Session*

2. Select ***Genomes*** > *Load Genome from File*



Note this is the **Genome** menu, not the File menu

and navigate to the **IGVMarch2017** folder that was pre-installed on the computer, and then to **Data / genome** and open ***chr1.fasta***

The FASTA file contains chromosome 1 from Human hg18.

3. Note in the IGV window: there is no gene track, and no cytoband ideogram in the genome ruler.

IGV hosted genomes package everything together, but you loaded only the FASTA file with the sequence. You can zoom in and out as before, and enter the numeric value of a locus, but you cannot find a gene locus by entering the name in the search box.

4. Load a gene annotation track
Select ***File*** > *Load from File*
and open ***refSeq_chr1.bed*** from the Exercises/LoadGenome folder.

Note this is the **File** menu, not the Genome menu

Now you jump to a locus by entering a gene name in the search box, e.g. CAP9

[Not part of this exercise, but you can use the **UCSC Table Browser** to get a file of gene annotations]

http://genome.ucsc.edu/cgi-bin/hgTables

5. The cytoband cannot be loaded separately into the genome ruler.