

Graph tracks

Genome graphs associate numerical data associated with base pair positions. You can open and view genome graph data files in IGB and manipulate them using functions in the **Graph** tab.

Using the **Graph** tab settings, you can display graphs as line graphs or heat graphs, change their scale, convert them to floating (draggable) graphs, and perform mathematical or other types of transformations. You can also compute averages or sums of multiple graphs.

You can create graphs from annotation tracks, such as an RNA-Seq coverage graphs showing the number of read alignments starting at each position.

Examples of genome graphs include:

- Probe intensity values from genome tiling arrays.
- Percentage methylation across chromosomes
- GC content along chromosomes
- Measures of conservation between two genomes

There are two basic types of genomes graphs:

- Position graphs associate scores with single genomic positions.
- Interval graphs associate scores with ranges of genomic positions