UCSC Genome Browser, Table Browser, and BLAT:
- UCSC GB

- primarily used for eukaryotic organisms(97euks/49 mammals) and prioritizes updates to primates/model organisms
- includes assembly data, precomputed comparative genomic data, mRNA, EST, RefSeq gene alignments, and links to the NCBI Map Viewer/Ensembl

-UCSC Genes: track found in most chr. viewers in the GB, gene prediction set based on RefSeq, GenBank, and Uniprot(consistenly import data from RefSeq = accurate)

-Conservation Track: Displayed graphically for 100 species, and can +/- species based on a specific selection

- PhastCons: genome alignments among few limited species can be downloaded as Multiple Alignment Format (MAF) files, and uses alginments by blastz. Conservation scores computed using phastCons, which is based on a 2-state phylogenetic HMM.

- Other tracks include SNPs, gene expression data, ENCODE project data, etc.

- Track Display:

- Hide: not shown
- Dense: shown, all features on 1 line
- Full: shown, all features on separate lines
- Squish: shown, 50% height of 'full' but with same info
- Pack: shown, displays separately and labeled, but not all features have their own tracks

- BLAT: analagous to Splign, used to align sequences to an entire genome and determine gene models, lacks a graphical display

- Table Browser: good tool to download data off of UCSC, output filters to narrow fields and is de-limited.

Galaxy
- Comparative Genomics: ID all DNA sequences in a genome that are functional, as selection often preserves functional genes. Can determine the functional role of these sequences through comparing them to known sequences, and can also be used to determine evolutionary history of an organism based on genes/DNA sequences shared.

- Galaxy: open source, easy interface, usegalaxy.org. Can be installed locally or used on a cloud as well. Integrates command line computational tools and database information, initially designed for people with little programming experience. Maintained by the "Galaxy Community". Data conversion is accomplished by Galaxy to allow for manipulation.

IGV
Integrative Genomic Viewer (dev'd by the Broad Institute, a collab between MIT and Harvard). Designed to handle large scale genomic datasets, similar to other GBs but is available for local download to be run outside of a web browser. Most GBs are high-res small reads/ low-res wide reads, so bigWig and bigBed data file formats are needed.

- Initial projects were developed to meet the needs of larger projects like the Cancer Genome Atlas and the 1000 genomes project, with a goal to make data visualization easier for trained and untrained biologists using bioinformatics.