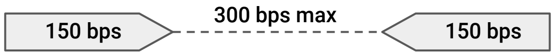
BCB 716 - Sequence Analysis

- A combined problem set 1 and 2 will go out on Thursday
- Your course logins should work now
- Password is your PID

DNA Variant Calling and Analysis

From last time

- **Aligners generate SAM files**
    - An attempt is made to find the closest match for a given read, or read-pair to a reference
    - Alignments are performed independently and in parallel
    - SAM files include
        - the original sequence and quality string from the FASTQ file
        - Initially read pairs are considered together
            - Alignment tolerances
            - Opposite strands
            - Must satisfy a maximum gap distance
        - A placement of the first base that is "normalized" to reference orientation
        - An alignment represented as a CIGAR string
        - Various alignment scores (edit distances, etc.)
- **SAM files are a lot to interpret**
    - Statistic provide a rough idea
    - Localized analysis provides more insights



SAM to BAM

- SAM files tend to be large and difficult to index and manipulate
- Converted into Binary Alignment Maps (BAM files)
- This is done using a toolset called SAMtools
- First to convert a SAM file to a BAM file

```
$ samtools view -S -b CC053.sam -o CC053.bam
$ ls -l CC053.*
-rw-rw-r-- 1 mcmillan its_faculty_psx 5.1G Nov  8 14:57 CC053.bam
-rw-rw-r-- 1 mcmillan its_faculty_psx  24G Nov  8 14:22 CC053.sam
```

- BAM files are smaller, and not simply text, making them easier to search

```
$ samtools view CC053.bam | head -1
A00434:231:H2K7FDSX2:1:1101:10529:1157  99      14      55067154        42
100M    =       55067503        449
GGCTGGAGATGGGGCTGGAGAAGGCGGCTGATCAGGGCTTTCTGAGGGCTCCCTGGAGCCCTCGACTGGCGCCAGGGAAGG
CTCAAGAGGAGGATCTGGG
FFFFFFF:FFFFFFF:FFFFFFFFFF:FFFFFFFFFFFF:FFFFFF:FFFF:FFFFFFFFFFFFFFFFFFFFFFFFFFF:FF
FFFFFFFFFFFFFFFFFFF AS:i:-5 XN:i:0  XM:i:1  XO:i:0      XG:i:0  NM:i:1
MD:Z:77G22      YS:i:-4 YT:Z:CP
```

Sorted and Indexed BAMs

- The reads in a BAM file are roughly in the order they can out of the sequencer
- SAM tools provides a tool to sort the reads genomically

```
$ samtools sort CC053.bam -o CC053.sorted.bam
$ ls -l CC053.*
-rw-rw-r-- 1 mcmillan its_faculty_psx 5.1G Nov  8 14:57 CC053.bam
-rw-rw-r-- 1 mcmillan its_faculty_psx  24G Nov  8 14:22 CC053.sam
-rw-rw-r-- 1 mcmillan its_faculty_psx 3.0G Nov  8 15:11 CC053.sorted.bam
```

- BAM files are even smaller, nearby sequences overlap and compress better
- Last of all we build an index so that the BAM file is easier to search/load

```
$ samtools index CC053.sorted.bam
$ ls -l CC053.*
-rw-rw-r-- 1 mcmillan its_faculty_psx 5.1G Nov  8 14:57 CC053.bam
-rw-rw-r-- 1 mcmillan its_faculty_psx  24G Nov  8 14:22 CC053.sam
-rw-rw-r-- 1 mcmillan its_faculty_psx 3.0G Nov  8 15:11 CC053.sorted.bam
-rw-rw-r-- 1 mcmillan its_faculty_psx 3.0M Nov  8 15:18 CC053.sorted.bam.bai
```

Exercise

Go to the following website:

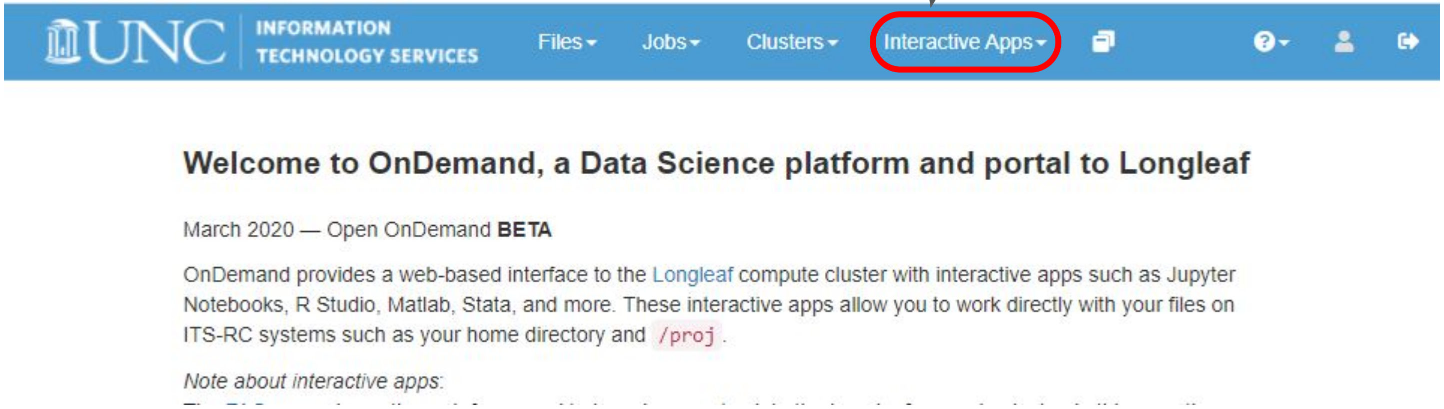
https://ondemand.rc.unc.edu

You will need to authenticate with your ONYEN

Eventually you will get here:

Click here and pick:

longleaf Desktop



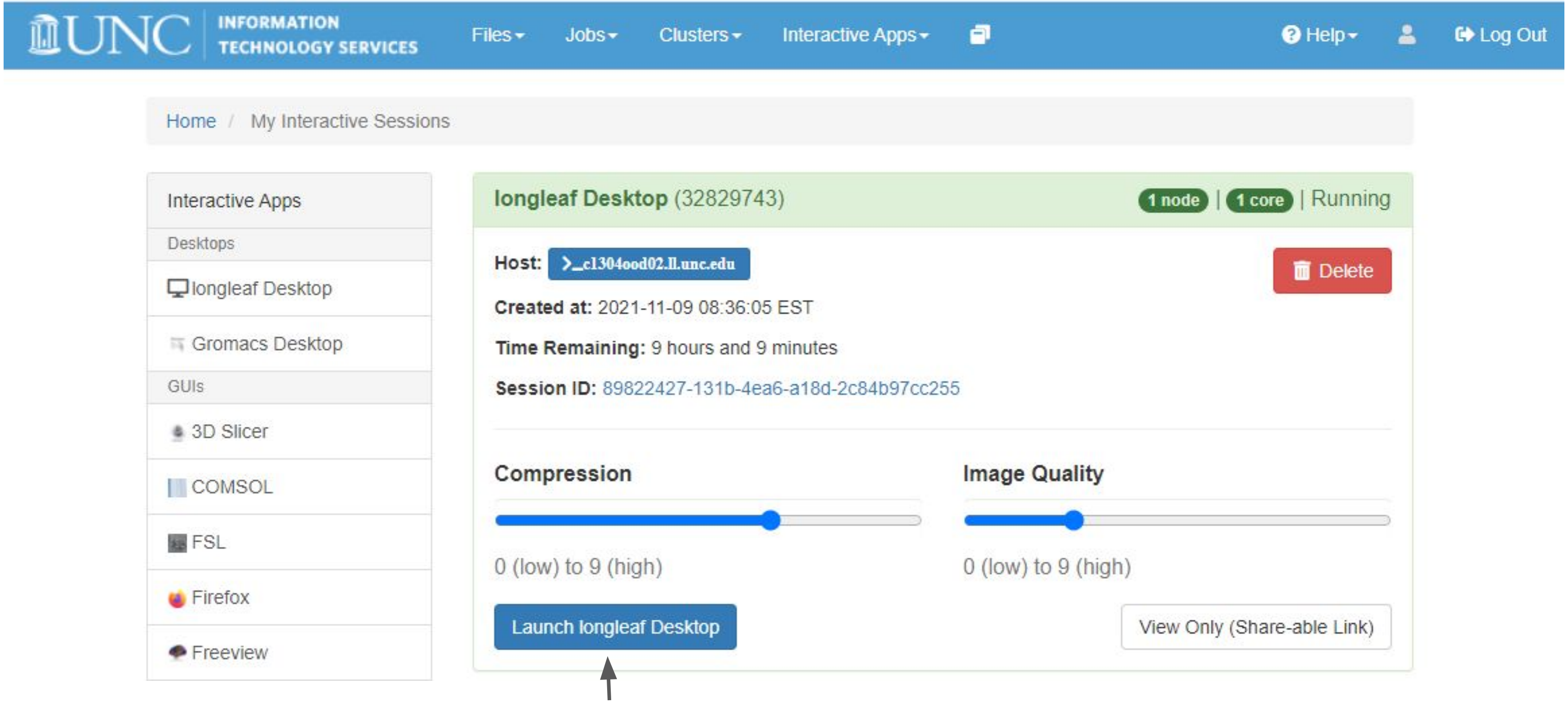
Welcome to OnDemand, a Data Science platform and portal to Longleaf

March 2020 — Open OnDemand **BETA**

OnDemand provides a web-based interface to the Longleaf compute cluster with interactive apps such as Jupyter Notebooks, R Studio, Matlab, Stata, and more. These interactive apps allow you to work directly with your files on ITS-RC systems such as your home directory and `/proj`.

Note about interactive apps:

Wait here for a few seconds



Home / My Interactive Sessions

Interactive Apps

Desktops

- longleaf Desktop
- Gromacs Desktop

GUIs

- 3D Slicer
- COMSOL
- FSL
- Firefox
- Freeview

longleaf Desktop (32829743) 1 node | 1 core | Running

Host: >_c1304ood02.ll.unc.edu

Created at: 2021-11-09 08:36:05 EST

Time Remaining: 9 hours and 9 minutes

Session ID: 89822427-131b-4ea6-a18d-2c84b97cc255

Compression

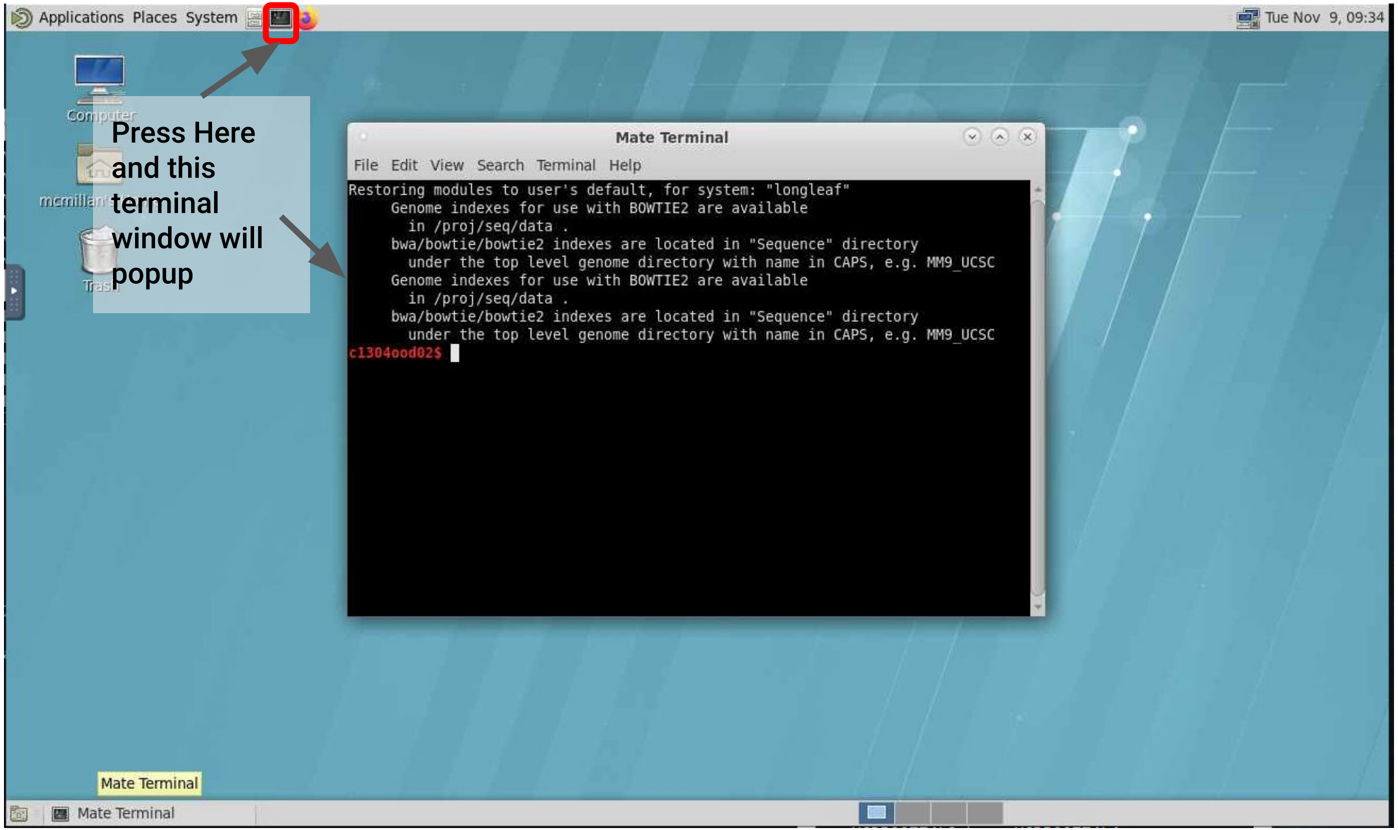
0 (low) to 9 (high)

Image Quality

0 (low) to 9 (high)

**Wait for this button to appear.
Then press it**

Eventually you'll get here



Press Here and this terminal window will popup

```
Restoring modules to user's default, for system: "longleaf"
     Genome indexes for use with BOWTIE2 are available
       in /proj/seq/data .
     bwa/bowtie/bowtie2 indexes are located in "Sequence" directory
       under the top level genome directory with name in CAPS, e.g. MM9_UCSC
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       in /proj/seq/data .
     bwa/bowtie/bowtie2 indexes are located in "Sequence" directory
       under the top level genome directory with name in CAPS, e.g. MM9_UCSC
c1304ood02$ 
```

Now type a few commands at the command line

- **Install an initial set of bioinformatic modules:**

```
$ cp /proj/mcmillanlab/BCB716F21/loadModules .
$ loadModules
$ module list


Currently Loaded Modules:
1) samtools/1.9    3) bowtie2/2.4.1    5) minimap2/2.17
2) bwa-mem2/2.2.1  4) igv/2.8.7
```

- **Today we'll discuss IGV**

Integrative Genomics Viewer (IGV)

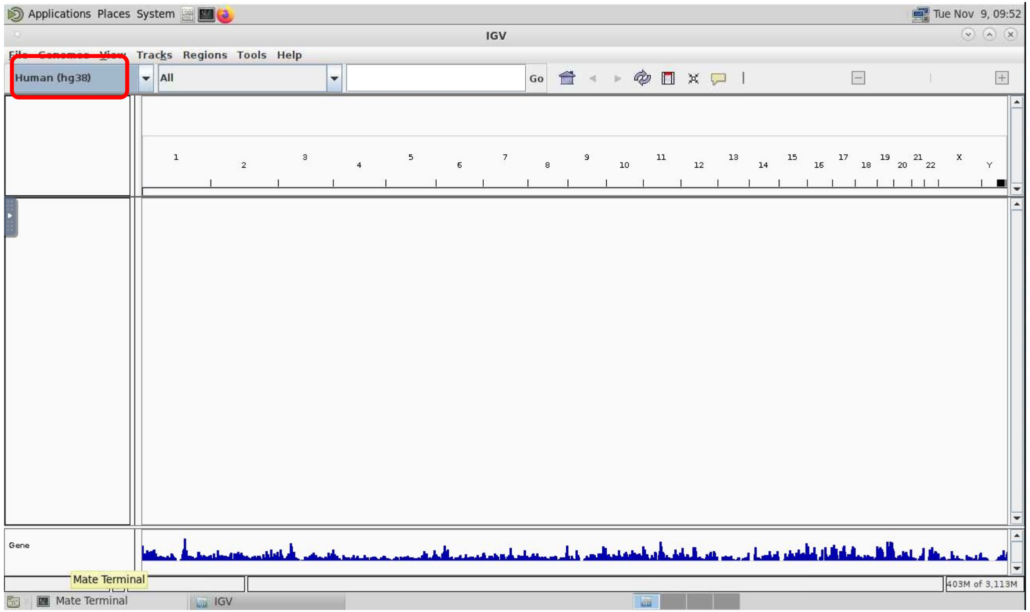
- **I typed:**

```
$ igv &      # starts the viewer as a background process
```

- **After some machinations, and maximizing**

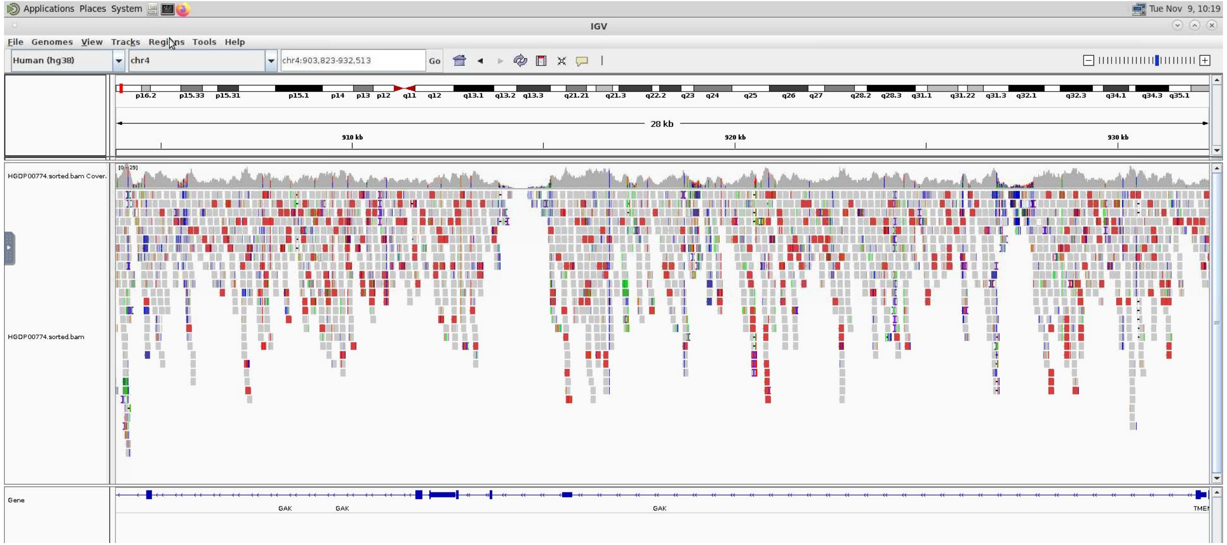
First, you'll need to make sure you are using the correct genome.

I'll use Human (hg38)


Applications Places System
Tue Nov 9, 09:52
IGV
File Genomes View Tracks Regions Tools Help
Human (hg38)
All
Go
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
Gene
Mate Terminal
403M of 3,113M
Mate Terminal
IGV

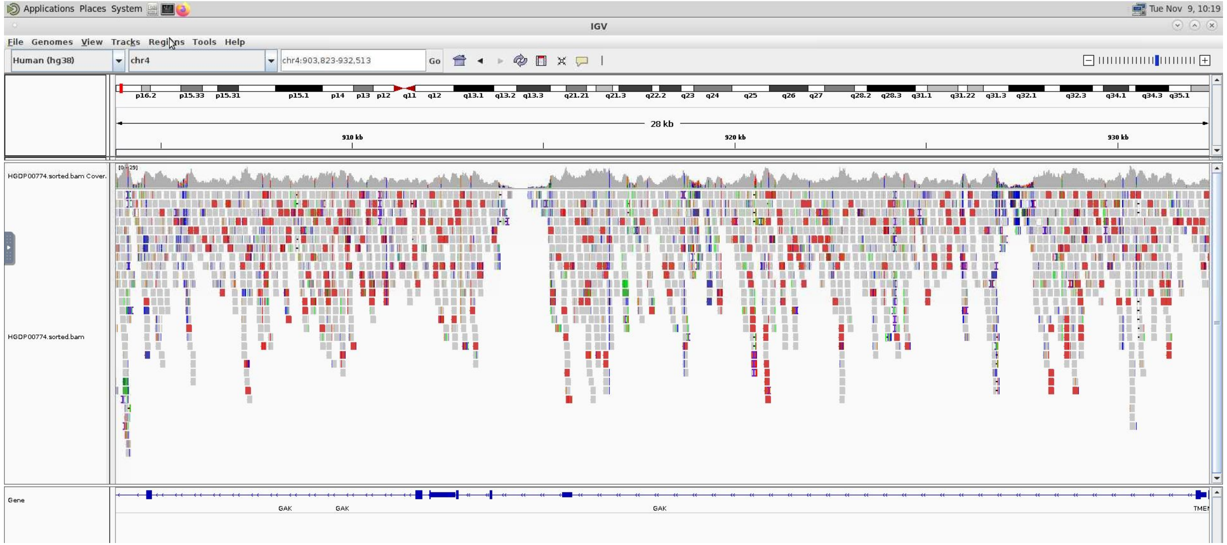
Visualizing BAM files

- The Interactive Genome Viewer (IGV) is a standard tool for visualizing sorted BAM files with index files
- You won't see any reads until you get to a window smaller than 30 kb (configurable, but)
- Coverage above
- Alignments below


Applications Places System
Tue Nov 9, 10:19
IGV
File Genomes View Tracks Regions Tools Help
Human (hg38)
chr4
chr4:903,823-932,513
Go
p16.2 p15.33 p15.31 p15.1 p14 p13 p12 q11 q12 q13.1 q13.2 q13.3 q21.21 q21.3 q22.2 q23 q24 q25 q26 q27 q28.2 q28.3 q31.1 q31.22 q31.3 q32.1 q32.3 q34.1 q34.3 q35.1
28 kb
910 kb
920 kb
930 kb
[0 - 29]
HGDP00774.sorted.bam Cover.
HGDP00774.sorted.bam
Gene
GAK
GAK
GAK
TMEI

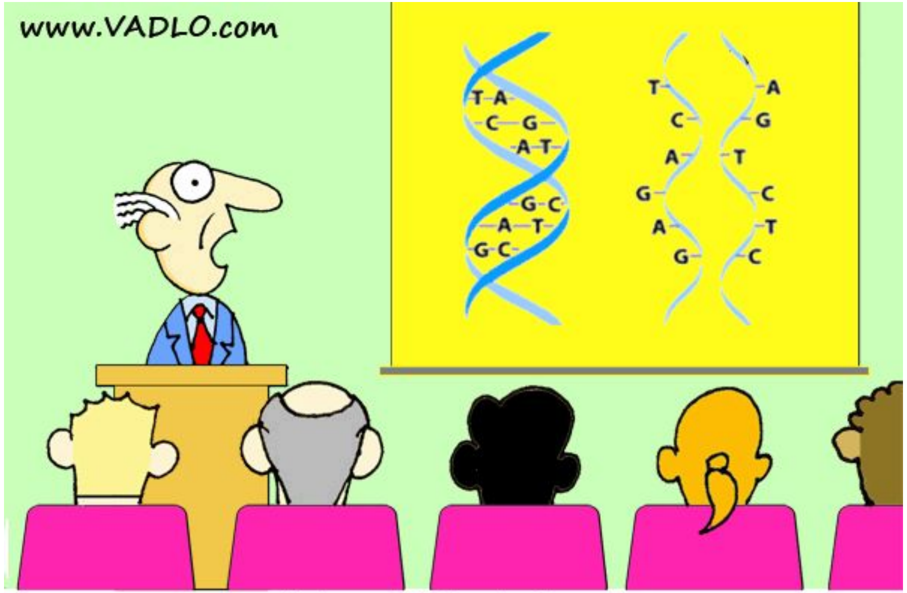
Visualizing BAM files

- The reads are labelled with variants and INDELS that differ from the reference
- Red reads are separated from mates by a larger gap than expected


Applications Places System
Tue Nov 9, 10:19
IGV
File Genomes View Tracks Regions Tools Help
Human (hg38)
chr4
chr4:903,823-932,513
Go
p16.2 p15.33 p15.31 p15.1 p14 p13 p12 q11 q12 q13.1 q13.2 q13.3 q21.21 q21.3 q22.2 q23 q24 q25 q26 q27 q28.2 q28.3 q31.1 q31.22 q31.3 q32.1 q32.3 q34.1 q34.3 q35.1
28 kb
910 kb
920 kb
930 kb
[0 - 29]
HGDP00774.sorted.bam Cover.
HGDP00774.sorted.bam
Gene
GAK
GAK
GAK
TMEI

Next Time

Visualizing, Interpreting, and Analyzing Alignment outputs



“Then Crick asked me,
‘Watson, should we name them A,C,T,G or A,B,C,D?”