

# Alignment Workshop

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# Find the Data

Find the data we're going to use for this workshop. It's in your home directory

```
cd
```

From there you can go to where the data are:

```
cd workshop_materials/alignment_methods
```

Look at what we have:

```
Ls
```

There are two subdirectories, human and yeast. For now let's look at the yeast data. We'll use the human data in the next session.

```
cd yeast
```

# The Yeast Data

The data we are working with come from the model yeast, *Saccharomyces cerevisiae*. We will look at the sequencing data of one strain, W303, and compare it to the finished sequence of the reference strain, S288C. We have data from two sources: Illumina MiSeq and Pacbio RSII. The Pacbio reads further are raw and error corrected. These are mostly identical read sets, with the error corrected versions of the same reads in the uncorrected, although there are a few error corrected reads for which the original did not seem to be available.

# Optional: Make Data Read Only

Before we start working, you may want to protect yourself against mistakes. You will need to read, but not write to, all of the files in this directory during the exercise. To make sure you don't accidentally delete these data, you can make them read only:

```
chmod 444 *
```

# Decide Where to Work

It is generally good practice to make a directory separate from your raw data to run analyses. You don't have to do this, but if you want to, you are on your own to do this. Throughout this exercise, the full paths to files will not be given. The raw data will always be in `/home/genomics/workshop_materials/alignment_methods` (`~/workshop_materials/alignment_methods`). Any files you create will be wherever you put them, and I will refer to them as, e.g., `<Illumina-S288C.sam>`. This `<name>` notation is a common placeholder for a specific named file (or directory) for which you are assumed to know the path/name but which the writer of the documentation could not know the name. **Do not actually put the `<>` in your commands;** remember that these are file redirects and you will do unfortunate things you did not expect.

Also, **do not copy/paste the commands from this document.** They will not work. You will have to form your own commands. Remember that you can use tab completion to find and confirm files that already exist.

# Prepare to Run BWA

Now we can start working with the data. First, we will align the Illumina data using the program *bwa*. The *bwa* program should already be in your `$PATH`, so you should just be able to type the command and it should work. In order to do alignments, *bwa* requires a special index (the Burrows-Wheeler transform of the data), so we start by making that:

```
bwa index -a bwtsv S288C.fa
```

This should take about 15 seconds. After you are done, there should be 5 additional files in the `alignment_methods` directory of the form “*S288C.fa.\**”. The *S288C.fa*, the actual fasta sequence, is the name prefix, and the extensions are all the various pieces of the index. Note that you will never directly reference these files. You always specify the genome as *S288C.fa*, and *bwa* (or any other program using an index) will know how to find all of its index files based on that. However, if they are not there (or not matched), the program will fail.

# Run BWA

Now we can run bwa. We're going to use the "mem" algorithm to do the alignments:

```
bwa mem S288C.fa Illumina_R1.fastq Illumina_R2.fastq > <Illumina-S288C>.sam
```

This should take about 3 minutes.

# Look at the Files

Now we can look at these files and see what's in them.

We will all do this part together and I will walk you through what is in the files.

```
less S288C.fa
```

```
less Illumina_R1.fastq
```

```
less <Illumina-S288C>.sam
```



# Convert Output to Binary

Our next step is to convert the sam file into binary format. There are two programs we can use to do this, GATK and samtools. The samtools syntax is a little easier, but the GATK tools are more comprehensive, and in some cases you might want to use other functions GATK provides that it can do simultaneously (as we will see here). Pick one of these (it doesn't matter which) and run it. If you have time (now or later), you can go back and do the other one with a different output file name.

Either of these should take about 2 minutes to run. Note the second step which is necessary with samtools!

# Option 1: Run Samtools

Using samtools:

```
samtools sort -o <Illumina.samtools>.bam <Illumina-S288C>.sam
```

```
samtools index <Illumina.samtools>.bam
```

# Option 2: Run GATK

Using GATK:

```
gatk4 SortSam -I <Illumina-S288C>.sam -O <Illumina.picard>.bam -SO  
coordinate --CREATE_INDEX=true
```

# Align the PacBio Data with Minimap2

Now we are going to align the Pacbio reads. The raw Pacbio reads are in PB.fasta, and the error-corrected Pacbio reads are in PBEC.fasta. Align each of these with minimap2.

```
minimap2 -a S288C.fa PB_matched.fasta > <PB-S288C>.sam
```

```
minimap2 -a S288C.fa PBEC_matched.fasta > <PBEC-S288C>.sam
```

These should each take about a minute each to align. Note that the error corrected reads should align faster.

# Binary Convert the Minimap2 Output

Now convert these into sorted bams also using either samtools or GATK, whichever you prefer.

# Starting IGV

We will spend the rest of the time looking at alignments. For this we will use a tool call IGV (the Integrative Genomics Viewer). To launch IGV, you should be able to either type `igv.sh` or use the shortcut on your desktop. It will pop up a new window, so if you launch it from the command line, you can place it in the background to free that terminal window.

# Loading the Genome

We need to prep some data first.

Load the genome (Menu->Genomes->Load Genome from File...) S288C.fa from the alignment\_methods directory. This should give you a graphical layout of the chromosome lengths at the top of the screen. We also want the annotations, so go to Menu->File->Load from File... and load saccharomyces\_cerevisiae.gff. *You will probably get some warning messages, but just persist and it will load properly in spite of them.*

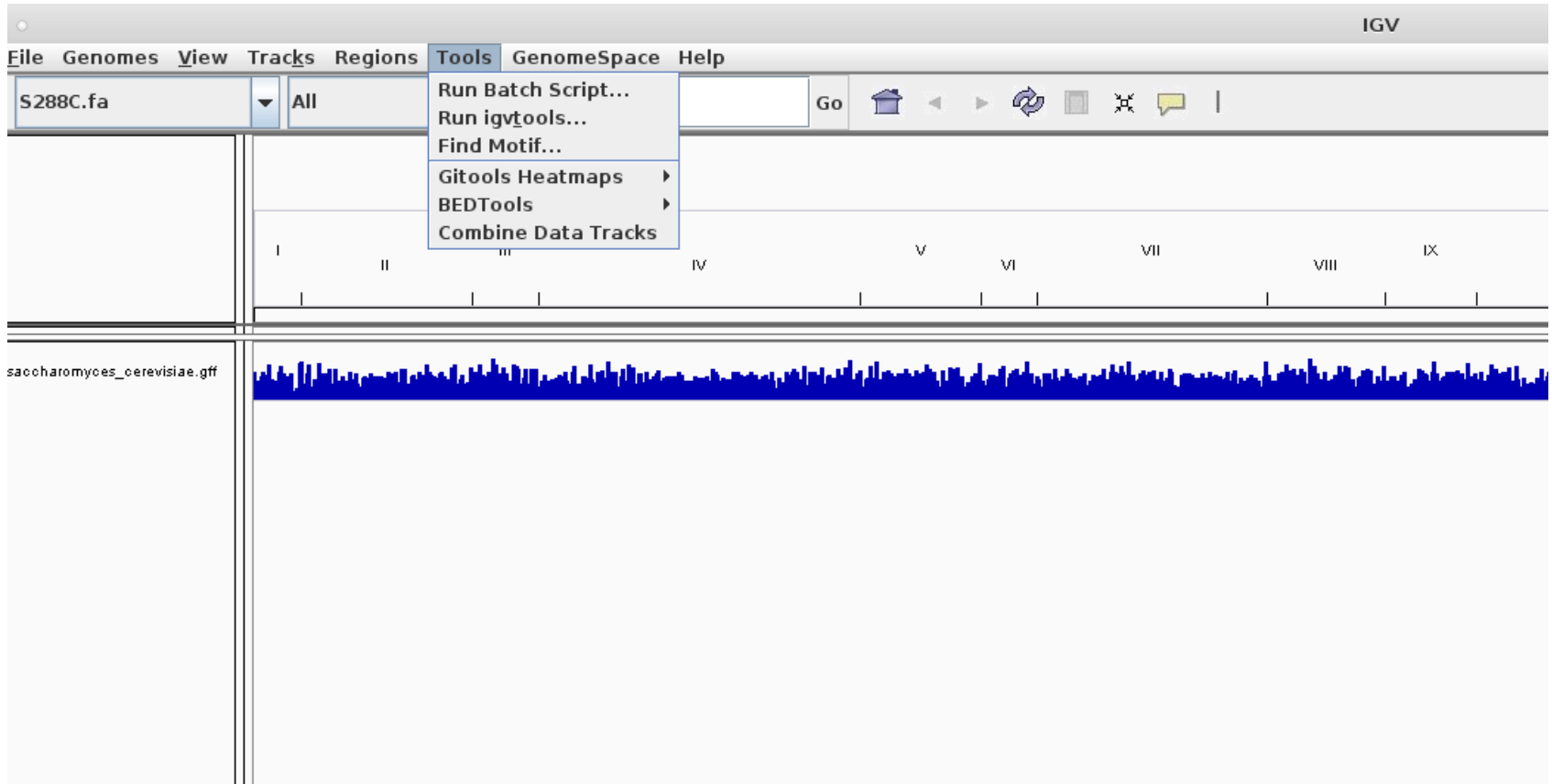
# Computing Coverage

Now we want to use igv-tools to make coverage profiles for our alignments. Go to Menu->Tools->Run igvtools... Now navigate to where you put your bam files for Illumina and the 2 PB runs versus S288C. One at a time, select these as the input file. It will automatically set the output file. It should default to the "Count" function, and we should be fine with the default parameters. Hit run. When it has finished, do the same for the other files until you have done all three, then close that window.

(See screenshot next slide.)



# Computing Coverage



# Computing Coverage

Now navigate to where you put your bam files for Illumina and the two PB versus S288C alignments. One at a time, select these as the input file. It will automatically set the output file. It should default to the “Count” function, and we should be fine with the default parameters. Hit run. When it has finished, do the same for the other files until you have done all three, then close that window.

(See screenshot next slide.)

# Computing Coverage

The screenshot displays a software interface for computing coverage. The main window has a sidebar on the left with various options and a main panel on the right showing a genomic track. A 'Select File' dialog box is open in the center, listing files in the 'alignment\_methods' directory.

**Main Application Window:**

- Command: Count
- Input File: [Empty] **Browse**
- Output File: [Empty] **Browse**
- Genome: /home/genomics/workshop\_data/alignment\_methods/S288C.fa **Browse**
- TDF and Count options
- Zoom Levels: 7
- Window Functions: [Checked]
- Probe to Loci Mapping: [Checked]
- Window Size: 25
- Extension Factor: [Empty]
- Count as Pairs:
- Sort Options
- Temp Directory: [Empty]
- Max Records: 500000
- Messages: [Empty]

**Select File Dialog:**

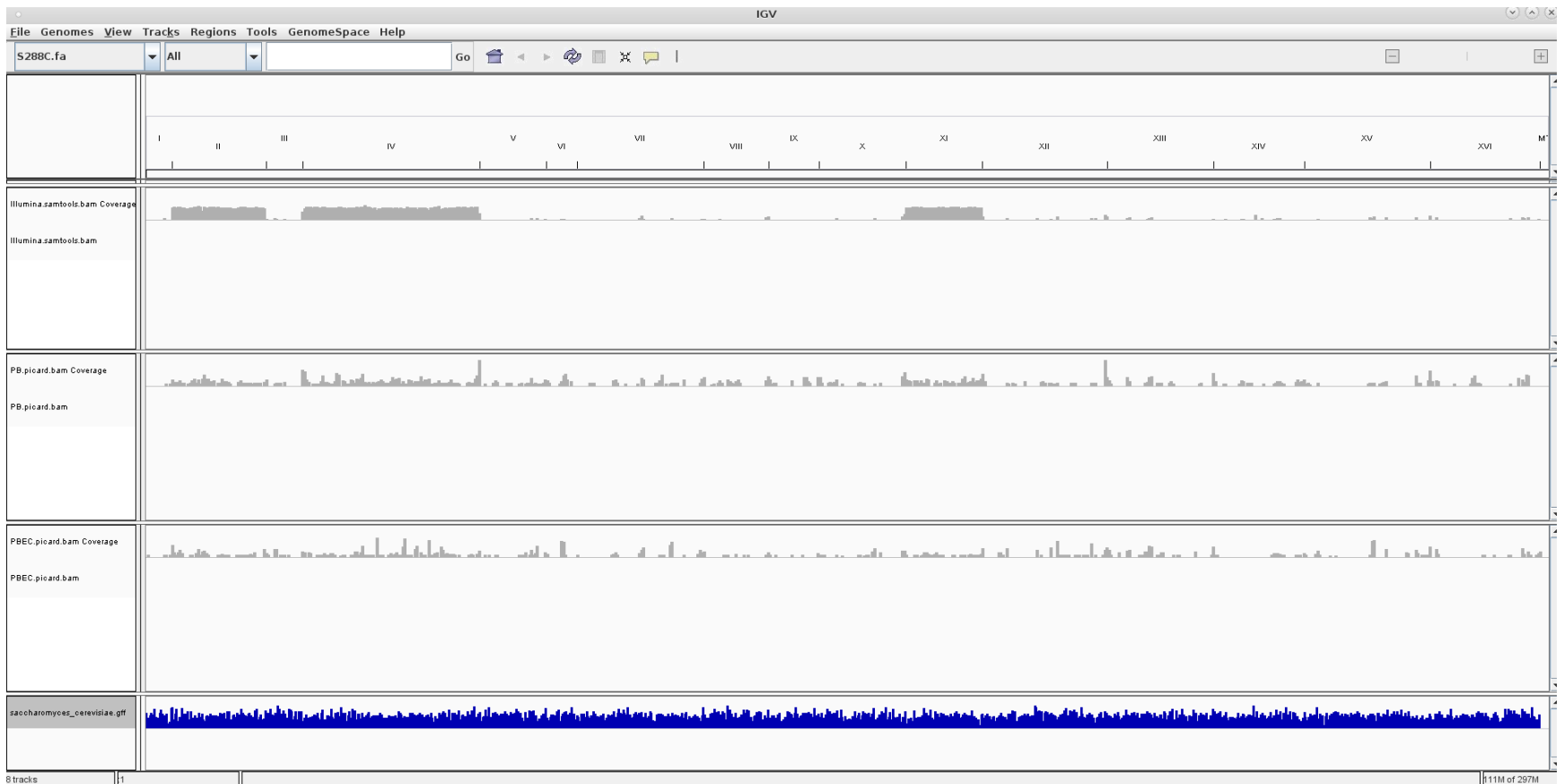
- Look In: alignment\_methods
- Files:
  - illumina.picard.bai
  - illumina.picard.bam
  - illumina.samtools.bam** (Selected)
  - illumina.samtools.bam.bai
  - illumina.samtools.bam.tdf
  - illumina\_R1.fastq
  - illumina\_R2.fastq
  - illumina\_S288.sam
  - PB-S288C.sam
  - PB.fasta
  - PB.picard.bai
  - PB.picard.bam
- File Name: illumina.samtools.bam
- Files of Type: All Files
- Buttons: Select File, Cancel

# Load Sequence Data

Now load the 3 bams. Go back to Menu->File->Load from File... and select the bams (not the .bais or the .tdfs or the .bam.bais, but the .bams themselves; IGV will automatically find the bais and the tdfs).

# Data Loaded

Now you should have something that looks like this:



# Browse!

Navigate around IGV and look at stuff. Some basic browsing:

Click the chromosome numbers to zoom to a chromosome.

Click the “Home” icon to go back to whole genome.

Click and drag in the coordinate window to select a zoom window.

Use the “railroad bars” in the upper right to rescale.

Individual reads will only appear when you are looking at 30kb of genome or less.

You can right-click on the track names to resize or reorder the tracks. You may want to change the compression level of the annotation track so that the different bands don’t stack on top of each other.

The next few pages have some information about places that might be interesting to look at.

# Things to See

You only started with reads that should align to chromosomes II, IV, and XI. (Actually, I messed up on the PacBio reads and typo'd the extract command, so you got II, IV, and IX for PB, so you'll only be able to compare on II & IV.)

The reads have some off-target noise (e.g. I:160000-166000 or III:82000-92000). What looks different about these reads? The PacBio reads also tend to have coverage spikes at the ends of chromosomes.

The next few pages have ranges on each of the chromosomes that seem interesting for various reasons.

# Chromosome II

30000-35000

155000-185000

223000-227000

245000-275000

620000-710000



# Chromosome IV

1-40000

160000-205000

215000-220000

300000-310000

355000-370000

375000-415000

437000-438000

510000-540000

635000-670000

822000-823000

870000-880000

980000-995000

1090000-1105000

1205000-1215000

# Chromosome XI

100000-195000

202000-204000

372000-382000

408000-640000

517000-518000