**Convert SRA files to FASTQ files:**

1. Download the SRA toolkit from <http://trace.ncbi.nlm.nih.gov/Traces/sra/sra.cgi?view=software>
2. Decompress:

Tar –zxvf sratoolkit.2.3.4-2-centos\_linux64.tar.gz

1. Convert SRA to fasta by fastq-dump:

./sratoolkit.2.3.4-2-centos\_linux64/bin/fastq-dump /home/pjflaherty/flahertylab/freeze/baker\_yeast/\*.sra

**Fastq to fasta: using fastx toolkit**

<http://hannonlab.cshl.edu/fastx_toolkit/commandline.html#fastq_to_fasta_usage>

**Map reads to reference:**

<http://icb.med.cornell.edu/wiki/index.php/Elementolab/BWA_tutorial>