

Setup - RnaSeq Tutorial

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If you are going to set this up yourself, make sure you understand what the PATH is. Some tutorials for that are here

- <http://www.cyberciti.biz/faq/unix-linux-adding-path/>
- http://www.linfo.org/path_env_var.html (a bit more descriptive)

Bowtie2: <http://bowtie-bio.sourceforge.net/bowtie2/index.shtml>

- cd ~/Programs
- wget <https://sourceforge.net/projects/bowtie-bio/files/bowtie2/2.2.9/bowtie2-2.2.9-source.zip/download>
- unzip download
- rm download
- cd bowtie2-2.2.9
- make
- echo "export PATH=\"\$(pwd):\$PATH\"" >> ~/.bashrc
 - o *This is a shortcut to add bowtie2 to your PATH. Restart terminal before using bowtie2*
 - o *On a Mac, don't use .bashrc, instead use >> ~/.bash_profile*

R: (Required for RSEM)

- sudo apt-get install r-base r-base-dev (For Ubuntu Linux)

Java: (Required for Picard/IGV)

- sudo apt-get install default-jre (For Ubuntu Linux)

RSEM: <http://deweylab.github.io/RSEM/>

- Requires C++, Perl, and R to make
- cd ~/Programs
- wget <https://github.com/deweylab/RSEM/archive/v1.2.31.tar.gz>
- tar -zxvf v1.2.31.tar.gz
- cd RSEM-1.2.31
- make
- make ebseq
- echo "export PATH=\"\$(pwd):\$PATH\"" >> ~/.bashrc

Picard <http://broadinstitute.github.io/picard/>

- Requires Java
- cd ~/Programs
- wget <https://github.com/broadinstitute/picard/releases/download/2.4.1/picard-tools-2.4.1.zip>
- unzip picard-tools-2.4.1.zip
- rm picard-tools-2.4.1.zip
- cd picard-tools-2.4.1
- echo "export PICARD_DIR=\"\$(pwd)\"" >> ~/.bashrc

Tool to convert GTF to Refflat

- Need for **Picard**
- http://hgdownload.cse.ucsc.edu/admin/exe/linux.x86_64/gtfToGenePred (For Linux)
- or
- http://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/gtfToGenePred (On Mac)

Download the Human Genome hg38 from Ensemble:

- <http://www.ensembl.org/info/data/ftp/index.html>
- Row for Human
 - o DNA (FASTA) -> Download
ftp://ftp.ensembl.org/pub/release-84/fastq/homo_sapiens/dna/Homo_sapiens.GRCh38.dna.primary_assembly.fa.gz
 - o Gene Sets (GTF) -> Download
ftp://ftp.ensembl.org/pub/release-84/gtf/homo_sapiens/Homo_sapiens.GRCh38.84.gtf.gz

IGV

- cd ~/Programs
- wget http://data.broadinstitute.org/igv/projects/downloads/IGV_2.3.77.zip
- unzip IGV_2.3.77.zip
- rm IGV_2.3.77.zip
- cd IGV_2.3.77
- echo "export PATH=\"\$PATH:\$PWD\" >> ~/.bashrc"