**Guide: Salmon for quantifying transcript abundance from RNA-seq data in Ubuntu**

Salmon is a fast and accurate pseudoalignment tool that estimates transcript abundance without explicitly aligning reads to a reference genome. Installing Salmon in Ubuntu is a simple process that can be completed using the following steps:

1. Update Ubuntu's package repository and install Salmon using the apt-get command in the terminal:

sudo apt-get update

sudo apt-get install salmon

1. If the above command does not work or if you want to install the latest version of Salmon manually, download the compressed file from the Salmon GitHub release page using wget and extract it:

wget -q https://github.com/COMBINE-lab/salmon/releases/download/v1.10.0/salmon-1.10.0\_linux\_x86\_64.tar.gz

tar zxf salmon-1.10.0\_linux\_x86\_64.tar.gz

1. Add the Salmon executable to your system's PATH by exporting the path to the bin directory of the extracted Salmon folder. Replace path/to in the command below with the path to the bin directory of the extracted Salmon folder:

export PATH=$PATH:path/to/salmon-1.10.0\_linux\_x86\_64/bin

1. Verify that Salmon is installed and working correctly by running the following command in the terminal:

salmon --version

This should display the version number of Salmon.

1. Once Salmon is installed, go to the working directory where your RNA-seq data is located using the cd command. For example, if your data is located in the directory /mnt/e/salmon\_test, run the following command to navigate to that directory:

cd /mnt/e/salmon\_test

1. Build an index of the reference transcriptome using the salmon index command. For example, to build an index of the transcriptome file ref\_index.fasta and save it in a directory called test\_index, run the following command:

salmon index -t ref\_index.fasta -i test\_index

1. Once the index is built, use the salmon quant command to quantify the expression levels of the RNA-seq reads. You can write a shell script to run the salmon quant command on multiple files in batch mode. For example, create a file called salmon\_quant\_batch.sh and add the following code to it:

#!/bin/bash

for file in \*.fastq.gz

do

salmon quant -i test\_index -l A -r "$file" -o "${file%.fastq.gz}\_quant"

done

This shell script will loop through all the FASTQ files in the directory, and run the salmon quant command on each file, with output saved in a directory named after the input file.