

# Quantification

In RNA-seq data analysis, after alignment, the most common step is to estimate gene or/and transcript expression abundance, the expression level is represented by read counts. There are three options in this step:

- [Quantify to annotation model \(Partek E/M\)](#)
- [Quantify to transcriptome \(Cufflinks\)](#)
- [Quantify to reference \(Partek E/M\)](#)
- [Quantify regions](#)
- [HTSeq](#)
- [Count feature barcodes](#)
- [Salmon](#)