Analysis Pipeline

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Abstract

The package implements a pipeline for the quantification and differential expression of RNA-Seq data. The pipeline is designed to simplify the analysis as much as possible, thus requiring minimal user input.

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Pre-processing

Index files

Index files for the kallisto pipeline are already provided in the package. These files are listed using the kallisto.idx function:

{r} #availableReferences()

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When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

{r} #summary(cars)

You can also embed plots, for example:

`{r, echo=FALSE} #plot(cars) #`

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.