There are three main threads of development in this source tree.

1. The R programs at the top level and in the R/ subdirectory comprise a set of functions and example usage for the qualitative assessment of RNA-SEQ profiles.
2. The files under inst/shiny are an attempt to make the analysis more accessible by embedding it in a Shiny app. Shiny is an R package that makes interactive applications available in web browsers.
3. The Python script under inst/python is a script that will read a series of BAM file and a feature annotation file (in GTF format) and will produce a text file containing read depths across the selected features. The output of this script can be read into the supplied R functions for analysis.

## The R functions

The R functions are collected in a package called 'qarp', which is an acronym for Quantiative Analysis of RNA-seq Profiles. With these functions you can analyze RNA-SEQ profile data genome-wide to detect translational changes that might otherwise go unnoticed.