# What is TAPPAS?

- TAPPAS is a Java GUI application for the analysis of RNA-Seq data down to the isoform level
- It provides a comprehensive set of data analysis, visualization, filtering, and ad hoc query tools
- It will run on most modern computers, provided they have enough computational resources and storage
- Best of all, TAPPAS is FREE for non-commercial use

Download TAPPAS
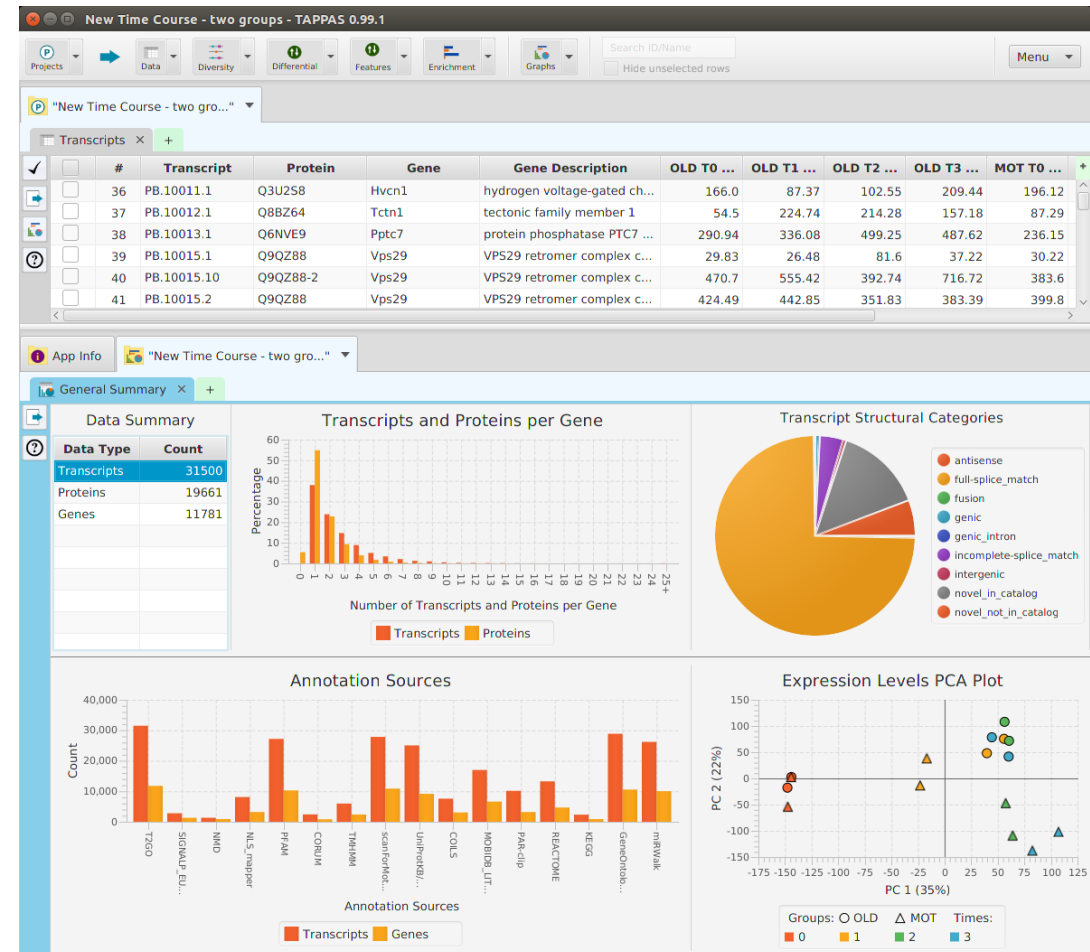
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Use the slide navigation buttons to
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Requirements and Installation

What you need to have:

- A computer with up-to-date GUI version of Linux or Unix, Mac, or Windows.
- Minimum of 8GB of memory and 4 CPU cores
- Adequate amount, 20GB or more, of unused disk space
- An up-to-date version of the Java Runtime Environment (JRE)
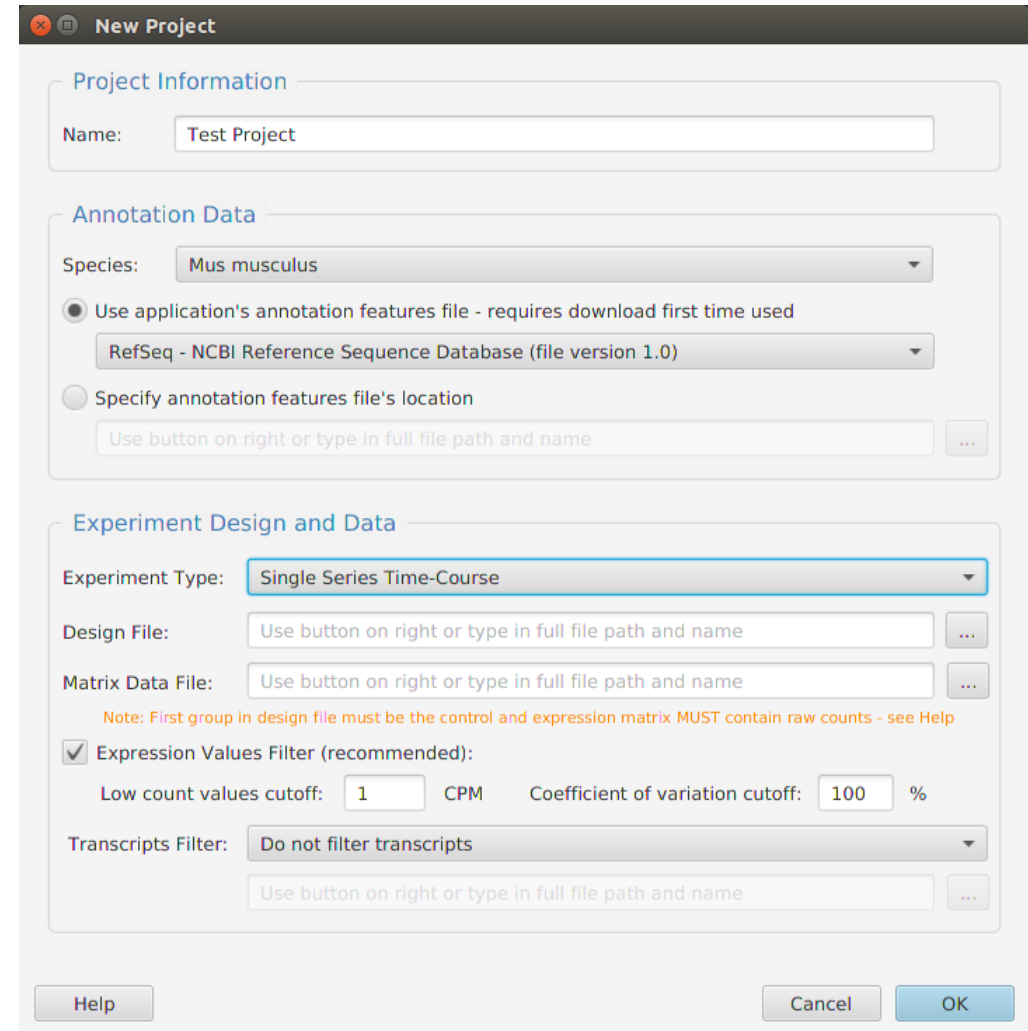- An up-to-date version of R along with a few statistical packages

What you need to do:

- To install, just download the file and decompress it
- To run the application, double click the tappas.jar file
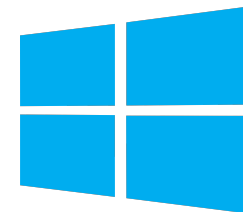
Projects

- TAPPAS is project based: You create a project, input your data, and then work with it
- You need three files to create a project: an experimental design file, a transcript level expression matrix, and the corresponding annotation file
- TAPPAS provides annotation files for multiple species. You may use one of them or provide your own
- Data normalization and filtering options for expression levels and transcripts are provided

Data Analysis

Once you've created a project, TAPPAS provides a large selection of tools to help you analyze your data:

- Differential Splicing Analysis (DSA)
- Annotation Features Differential Splicing Analysis (FDSA)
- Annotation Features Diversity Analysis
- Differential Expression Analysis (DEA)
- Gene Set Enrichment Analysis (GSEA)
- Functional Enrichment Analysis (FEA) including Clustering Analysis


Data analysis is provided for case-control and single or multiple time-course experiments. Alternative splicing information is important for understanding RNA-Seq data: in addition to gene level data analysis, TAPPAS tools provide data analysis at the isoform level.
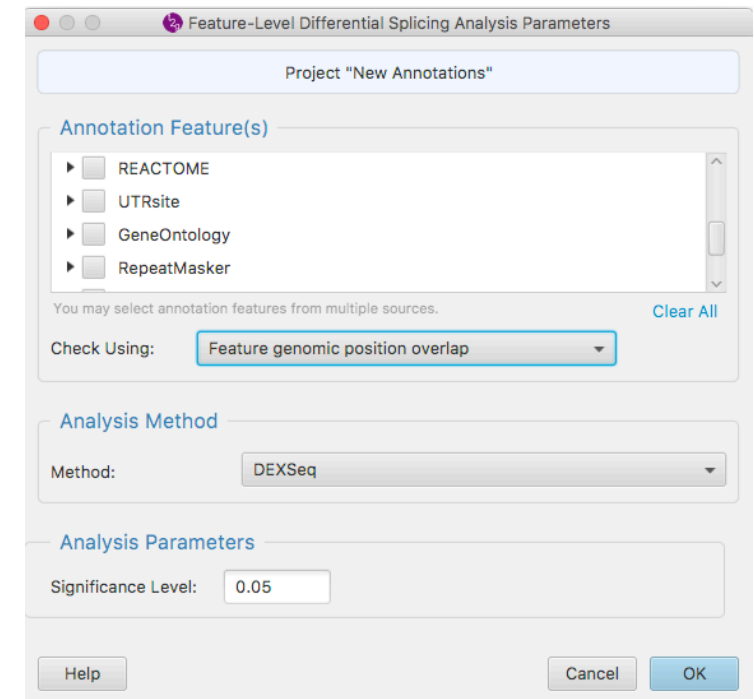
Data Visualization

TAPPAS provides a comprehensive set of data visualization tools to help you recognize patterns and better understand the data :

- Summary plots and charts
- Distribution charts
- Annotation features visualization for genes, transcripts, and proteins
- Expression data density and PCA plots
- Cluster network graphs
- GO terms directed acyclic graphs
- Venn Diagrams
- Miscellaneous data visualization
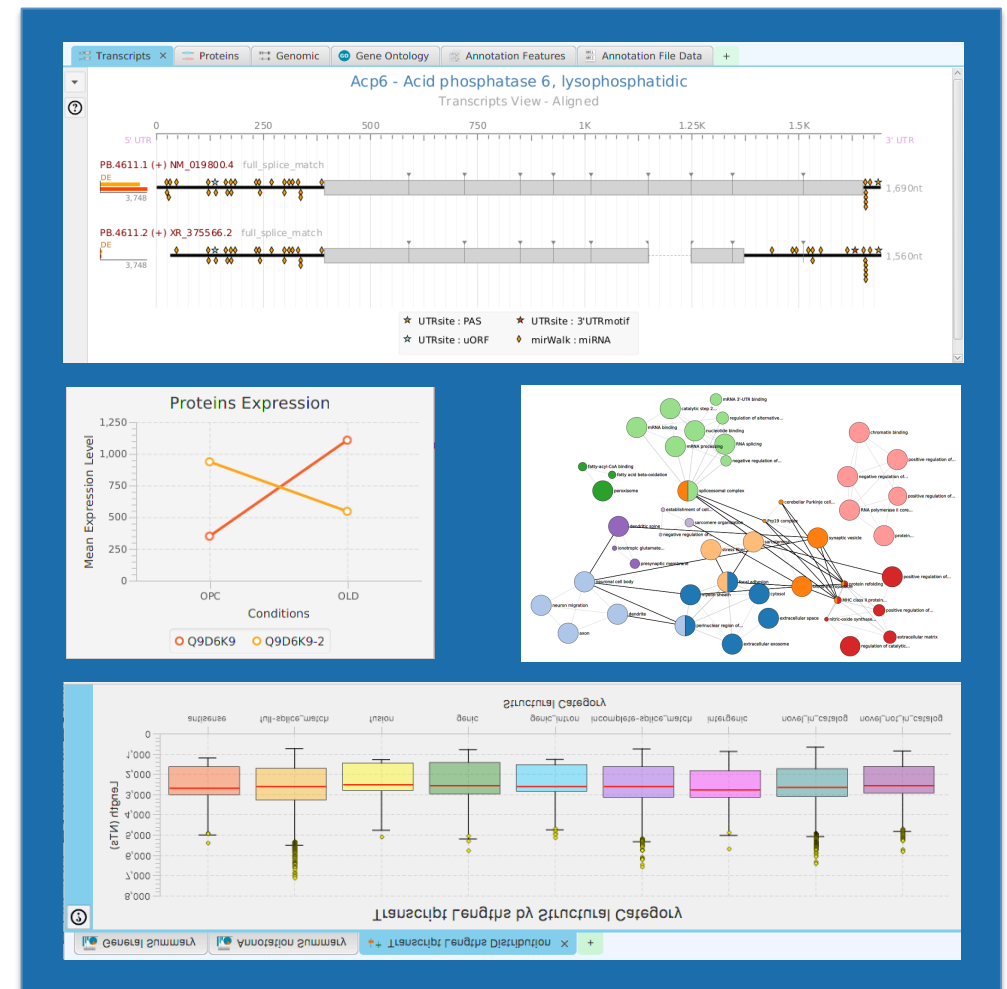
Other Features

Using JavaFX as its platform, TAPPAS provides the rich set of features expected from a modern GUI application:

- Data tables with customizable columns, sorting, and filtering
- Ability to export all application data and images to file
- Resizable windows and zooming
- Context-sensitive help and menus
- Data drill downs
- Display customization
- Individual project tabs
- And lots of other features…
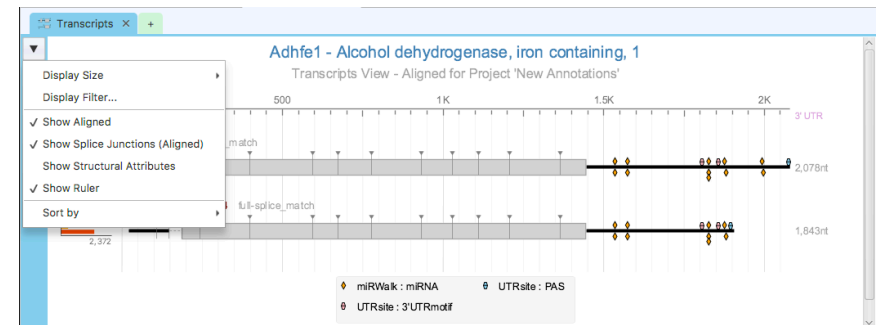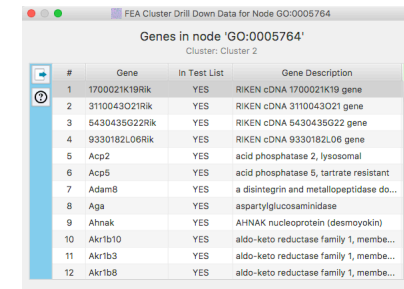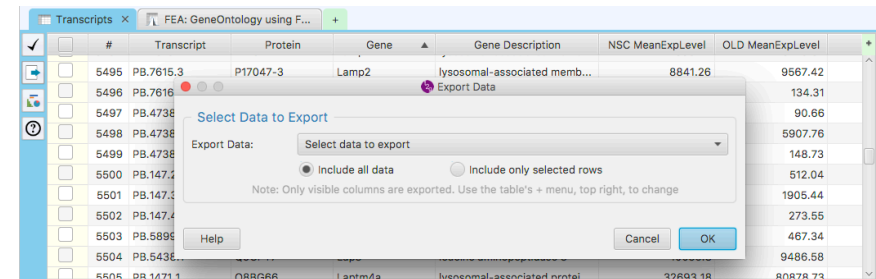
And much more…

Hopefully, by now you have a good idea of what TAPPAS has to offer. If you would like to find out more, here are some suggestions:

- Download the application and try it out using one of our demo expression matrices and annotation files. Better yet, use your own data
- Check out the Overview section for more in-depth information regarding application features and data analysis
- Read the original TAPPAS research paper and get all the biological and technical details

Download TAPPAS

Check Out Overview

Read Research Paper

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