CompGO Introduction

Sam D. Bassett, Ashley J. Waardenberg

Developmental and Stem Cell Biology Lab,
Victor Chang Cardiac Research Institute,
Darlinghurst, Sydney, Australia

1 Introduction

This package contains functions to accomplish several tasks relating to gene ontology enrichment comparison and visualisation given either .bed files or gene lists. It interfaces with rtracklayer and VariantAnnotation to easily annotate .bed files with genes, and with RDAVIDWebService to generate functional annotation charts based on these gene lists. From here, we provide several methods for comparative visualisation, including viewing the GO term hierarchy in two samples using a directed acyclic graph (DAG), performing z-score standardisation (approximately normal using a log odds-ratio (OR) - Equation 1 and 2) of GO terms returned from DAVID and comparing enrichment via pairwise scatterplots with linear fit and Jaccard metrics (Equation 3). We also provide functions to enable large-scale clustering.

$$Z \sim N(log(OR), \sigma^2) \tag{1}$$

$$z_i = \frac{log(OR)}{SE(OR)} \tag{2}$$

$$J_c = \frac{A \cap B}{A \cup B} \tag{3}$$

Please see full vignette for usage instructions, or the user manual for function definitions.

```
> # Not run because it spawns processes at compile time
> #library(CompGO)
> #help.start()
> # Then navigate to CompGO, click on "Package vignettes and other information", and open C
```