

StarTrek:Application Examples

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Introduction

In this vignette, we demonstrate the application of **StarTrek** as tool for pathways analysis integrating different data types. For basic use of the **StarTrek** package, please refer to the vignette Working with StarTrek package.

In many cases, **StarTrek** is used as tool to measure pathway activity and pathway cross-talk. However, **StarTrek** can also be combined with other tools (within or out of the scope of R and Bioconductor [Gentleman et al., 2004, Carey et al., 2005]), to build exible analysis pipelines. In this vignette we demonstrate the cooperation between **StarTrek** and other tools with several examples.

Case Study n°1

To install use the code below.

```
path<-getKEGGdata(KEGG_path="Carb_met")
tumo<-SelectedSample(Dataset=Data_CANCER_normUQ_filt,typesample="tumor")[,1:100]
norm<-SelectedSample(Dataset=Data_CANCER_normUQ_filt,typesample="normal")[,1:100]
score_euc_dist<-dev_std_crtlk(dataFilt=Data_CANCER_normUQ_filt,path)
nf <- 60
res_class<-svm_classification(TCGA_matrix=score_euc_dist,nfs=nf,normal=colnames(norm),tumour=colnames(t
```

References