

YavAch Package Vignette

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1 Introduction

This package was designed to analyse the Achilles v2.0 and v2.4 datasets from the Broad Institute, however, any other shRNA screens can also be analysed in a similar fashion through building an “RNAi” object. Namely :

```
library(YavAch)
```

```
## Loading required package: ggplot2
```

```
## Loading required package: reshape2
```

```
## Loading required package: plyr
```

```
# The data
```

```
data("Achilles2.4_data") # Achilles v2.4 dataset
```

```
data("Achilles2.4_annotation") # The p53 annotation for the Achilles v2.4 dataset
```

```
# Read in the shRNA data with a row for each hairpin and columns corresponding to cell lines.
```

```
head(Achilles2.4_Data[,1:5])
```

```
##           Name      Gene X697_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE
## 1 AAAAATGGCATCAACCAT RPS6KA1 -0.04112325
## 2 AAACACATTGGGATGTTCT IGF1R  2.19048750
## 3 AAAGAAGAAGCTGCAATATCT TSC1  1.53637450
## 4 AAGCGTGCCGTAGACTGTCCA CHEK1      NaN
## 5 AATCTAAGAGAGCTGCCATCG XRCC5 -1.33028525
```

```
## 6 AATGAAAGCTCACTCTGGATT PIK3CA 1.09965000
## X7860_KIDNEY A1207_CENTRAL_NERVOUS_SYSTEM
## 1 -0.2428750 -0.7204843
## 2 1.8132215 1.0551227
## 3 1.6716550 1.7499833
## 4 NaN NaN
## 5 -2.9123472 -0.9370367
## 6 0.8221555 0.4313193
```

```
# Create a new RNAi object by filling in the corresponding slots
RNAiObject <- new(Class = "RNAi",
  genes = Achilles2.4_Data$Gene,
  sequences = Achilles2.4_Data$Name,
  cancers = colnames(Achilles2.4_Data)[- (1:2)],
  cancersP53 = Achilles2.4_annotation,
  values = Achilles2.4_Data[, - (1:2)])
```

Most of the functions within the package require an “RNAi” object.

2 General Functions

2.1 Variation of shRNAs

```
# object          an RNAi object
# cancerID       a character string indicating the cell line of interest (partial string matching is suf
# geneName       character string specifying the name of the gene of interest (case sensitive)
# type           can be either "all" or "median"
```

```
variation.within.cell.line(object = RNAiObject, cancerID = "SLR24", geneName = "MDM4", type = "all")
```

```
# object          an RNAi object
# entityName      can either be "all" or the name of one of the entity in question (partial string matchi
# geneName       character string specifying the name of the gene of interest (case sensitive)
```

```
variation.within.entity(object = RNAiObject, entityName = "BONE", geneName = "MDM4")
```

```
# object          an RNAi object
# geneName       character string specifying the name of the gene of interest (case sensitive)
# type           one of "value" or "rank"
# statistic      one of "mean" or "median"
```

```
variation.within.entities(object = RNAiObject, geneName = "MDM4", type = "value", statistic = "mean")
```

2.2 Consistency of phenotypes

```
# object          an RNAi object
# entityName      can either be "all" or the name of one of the entity in question (partial string matchi
# geneName       character string specifying the name of the gene of interest (case sensitive)
```

```
# type           one of "line" or "box"

consistency.of.phenotypes(object = RNAiObject, entityName = "BONE", geneName = "MDM4", type = "line")
```

2.3 p53 dependency

```
# object         an RNAi object
# entityName     can either be "all" or the name of one of the entity in question (partial string matching)
# geneName       character string specifying the name of the gene of interest (case sensitive)
# type           one of "line" or "box"

p53.dependency.by.entity(object = RNAiObject, entityName = "Lung", geneName = "MDM4", p53 = "all", type = "line")
```

3 Riger Functions

The RIGER functions require a separate data structure. In this case a simple data.frame is used (the files used for analysing both Achilles datasets are included in the package).

```
data("Achilles_v2.0_GENE") # RIGER data for the Achilles v2.0 dataset
data("Achilles_v2.4_GENE") # RIGER data for the Achilles v2.4 dataset

Achilles2.0 <- Achilles_v2.0_GENE
Achilles2.4 <- Achilles_v2.4_GENE

head(Achilles2.4[,1:5])
```

3.1 Evaluation of RIGER gene score

```
# object         must be an object of the above type
# geneName       character string specifying the name of the gene of interest (case sensitive)
# entityName     can either be "all" or the name of one of the entity in question (partial string matching)

riger.gene.comparison(object = Achilles2.4, geneName = "MDM4", entityName = "all")
```

3.2 Evaluation of RIGER gene score across datasets

```
# object1        must be an object of the above type
# object2        must be an object of the above type
# object1Name    character vector giving the name of the first dataset used in the plot
# object2Name    character vector giving the name of the second dataset used in the plot
# geneName       character string specifying the name of the gene of interest (case sensitive)
# entityName     can either be "all" or the name of one of the entity in question (partial string matching)
# percentage     top and bottom quantiles which should be coloured (number between 1 and 100)
# plotName       character string giving the name of the plot
```

```
riger.gene.comparison.datasets(object1 = Achilles2.0, object2 = Achilles2.4,  
                                object1Name = "Ach1", object2Name = "Ach2",  
                                geneName = "MDM4",  
                                entityName = "Colon",  
                                percentage = 1,  
                                plotName = "Comparing RIGER scores")
```