

# Package ‘AMARETTO’

September 18, 2024

**Type** Package

**Title** Regulatory Network Inference and Driver Gene Evaluation using  
Integrative Multi-Omics Analysis and Penalized Regression

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**Depends** R (>= 3.6), impute, doParallel, grDevices, dplyr, methods,  
ComplexHeatmap

**Description** Integrating an increasing number of available multi-omics cancer data remains one of the main challenges to improve our understanding of cancer. One of the main challenges is using multi-omics data for identifying novel cancer driver genes. We have developed an algorithm, called AMARETTO, that integrates copy number, DNA methylation and gene expression data to identify a set of driver genes by analyzing cancer samples and connects them to clusters of co-expressed genes, which we define as modules. We applied AMARETTO in a pancancer setting to identify cancer driver genes and their modules on multiple cancer sites. AMARETTO captures modules enriched in angiogenesis, cell cycle and EMT, and modules that accurately predict survival and molecular subtypes. This allows AMARETTO to identify novel cancer driver genes directing canonical cancer pathways.

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---

AMARETTO\_CreateModuleData

*AMARETTO\_CreateModuleData*

---

**Description**

AMARETTO\_CreateModuleData

**Usage**

AMARETTO\_CreateModuleData(AMARETTOinit, AMARETTOresults)

**Arguments**

AMARETTOinit List output from AMARETTO\_Initialize().  
 AMARETTOresults List output from AMARETTO\_Run()

**Value**

result

**Examples**

```
data('ProcessedDataLIHC')
AMARETTOinit <- AMARETTO_Initialize(ProcessedData = ProcessedDataLIHC,
                                   NrModules = 2, VarPercentage = 50)
AMARETTOresults <- AMARETTO_Run(AMARETTOinit)
AMARETTO_MD <- AMARETTO_CreateModuleData(AMARETTOinit, AMARETTOresults)
```

---

AMARETTO\_CreateRegulatorPrograms  
*AMARETTO\_CreateRegulatorPrograms*

---

### Description

AMARETTO\_CreateRegulatorPrograms

### Usage

```
AMARETTO_CreateRegulatorPrograms(AMARETTOinit, AMARETTOresults)
```

### Arguments

AMARETTOinit List output from AMARETTO\_Initialize().  
 AMARETTOresults List output from AMARETTO\_Run()

### Value

result

### Examples

```
data('ProcessedDataLIHC')
AMARETTOinit <- AMARETTO_Initialize(ProcessedData = ProcessedDataLIHC,
                                   NrModules = 2, VarPercentage = 50)
AMARETTOresults <- AMARETTO_Run(AMARETTOinit)
AMARETTO_RP <- AMARETTO_CreateRegulatorPrograms(AMARETTOinit,AMARETTOresults)
```

---

AMARETTO\_Download      *AMARETTO\_Download*

---

### Description

Downloading TCGA dataset for AMARETTO analysis

### Usage

```
AMARETTO_Download(CancerSite = "CHOL",
                  TargetDirectory = TargetDirectory)
```

### Arguments

CancerSite TCGA cancer code for data download  
 TargetDirectory Directory path to download data

### Value

result

**Examples**

```
TargetDirectory <- file.path(getwd(),"Downloads/");dir.create(TargetDirectory)
CancerSite <- 'CHOL'
DataSetDirectories <- AMARETTO_Download(CancerSite,TargetDirectory = TargetDirectory)
```

---

```
AMARETTO_EvaluateTestSet
      AMARETTO_EvaluateTestSet
```

---

**Description**

Code to evaluate AMARETTO on a new gene expression test set. Uses output from AMARETTO\_Run() and CreateRegulatorData().

**Usage**

```
AMARETTO_EvaluateTestSet(AMARETTOresults = AMARETTOresults,
  MA_Data_TestSet = MA_Data_TestSet,
  RegulatorData_TestSet = RegulatorData_TestSet)
```

**Arguments**

AMARETTOresults  
AMARETTO output from AMARETTO\_Run().

MA\_Data\_TestSet  
Gene expression matrix from a test set (that was not used in AMARETTO\_Run()).

RegulatorData\_TestSet  
Test regulator data from CreateRegulatorData().

**Value**

result

**Examples**

```
data('ProcessedDataLIHC')
AMARETTOinit <- AMARETTO_Initialize(ProcessedData = ProcessedDataLIHC,
  NrModules = 2, VarPercentage = 50)

AMARETTOresults <- AMARETTO_Run(AMARETTOinit)
AMARETTOtestReport <- AMARETTO_EvaluateTestSet(AMARETTOresults = AMARETTOresults,
  MA_Data_TestSet = AMARETTOinit$MA_matrix_Var,
  RegulatorData_TestSet = AMARETTOinit$RegulatorData)
```

---

AMARETTO\_ExportResults

*AMARETTO\_ExportResults*

---

### Description

Retrieve a download of all the data linked with the run (including heatmaps)

### Usage

```
AMARETTO_ExportResults(AMARETTOinit, AMARETTOresults, data_address,
  Heatmaps = TRUE, CNV_matrix = NULL, MET_matrix = NULL)
```

### Arguments

|                 |                               |
|-----------------|-------------------------------|
| AMARETTOinit    | AMARETTO initialize output    |
| AMARETTOresults | AMARETTO results output       |
| data_address    | Directory to save data folder |
| Heatmaps        | Output heatmaps as pdf        |
| CNV_matrix      | CNV_matrix                    |
| MET_matrix      | MET_matrix                    |

### Value

result

### Examples

```
data('ProcessedDataLIHC')
TargetDirectory <- file.path(getwd(),"Downloads/");dir.create(TargetDirectory)
AMARETTOinit <- AMARETTO_Initialize(ProcessedData = ProcessedDataLIHC,
  NrModules = 2, VarPercentage = 50)

AMARETTOresults <- AMARETTO_Run(AMARETTOinit)
AMARETTO_ExportResults(AMARETTOinit,AMARETTOresults,TargetDirectory,Heatmaps = FALSE)
```

---

AMARETTO\_HTMLreport

*AMARETTO\_HTMLreport*

---

### Description

Retrieve an interactive html report, including gene set enrichment analysis if asked for.

### Usage

```
AMARETTO_HTMLreport(AMARETTOinit, AMARETTOresults, ProcessedData,
  show_row_names = FALSE, SAMPLE_annotation = NULL, ID = NULL,
  hyper_geo_test_bool = FALSE, hyper_geo_reference = NULL,
  output_address = "./", MSIGDB = TRUE, driverGSEA = TRUE,
  phenotype_association_table = NULL)
```

**Arguments**

AMARETTOinit AMARETTO initialize output  
 AMARETTOresults AMARETTO results output  
 ProcessedData List of processed input data  
 show\_row\_names if True, sample names will appear in the heatmap  
 SAMPLE\_annotation SAMPLE annotation will be added to heatmap  
 ID ID column of the SAMPLE annotation data frame  
 hyper\_geo\_test\_bool Boolean if a hyper geometric test needs to be performed. If TRUE provide a GMT file in the hyper\_geo\_reference parameter.  
 hyper\_geo\_reference GMT file with gene sets to compare with.  
 output\_address Output directory for the html files.  
 MSIGDB TRUE if gene sets were retrieved from MSIGDB. Links will be created in the report.  
 driverGSEA if TRUE, module drivers will also be included in the hypergeometric test.  
 phenotype\_association\_table a Data Frame, containing all modules phenotype association data. Optional.

**Value**

result

**Examples**

```

## Not run:
data('ProcessedDataLIHC')
AMARETTOinit <- AMARETTO_Initialize(ProcessedData = ProcessedDataLIHC,
                                   NrModules = 2, VarPercentage = 50)

AMARETTOresults <- AMARETTO_Run(AMARETTOinit)

AMARETTO_HTMLreport(AMARETTOinit= AMARETTOinit,AMARETTOresults= AMARETTOresults,
                    ProcessedData = ProcessedDataLIHC,
                    hyper_geo_test_bool=FALSE,
                    output_address='./')

## End(Not run)

```

---

AMARETTO\_Initialize    *AMARETTO\_Initialize (version: reorder and filter MA\_Matrix)*

---

**Description**

Code used to initialize the seed clusters for an AMARETTO run. Requires processed gene expressions (rna-seq or microarray), CNV (usually from a GISTIC run), and methylation (from MethylMix, provided in this package) data. Uses the function CreateRegulatorData() and results are fed into the function AMARETTO\_Run().

**Usage**

```
AMARETTO_Initialize(ProcessedData = ProcessedData, Driver_list = NULL,
  NrModules, VarPercentage, PvalueThreshold = 0.001,
  RsquareThreshold = 0.1, pmax = 10, NrCores = 1, OneRunStop = 0,
  method = "union", random_seeds = NULL, convergence_cutoff = 0.01)
```

**Arguments**

|                    |  |
|--------------------|--|
| ProcessedData      | List of Expression, CNV and MethylMix data matrices, with genes in rows and samples in columns.  |
| Driver_list        | Custom list of driver genes to be considered in analysis   |
| NrModules          | How many gene co-expression modules should AMARETTO search for? Usually around 100 is acceptable, given the large number of possible driver-passenger gene combinations.   |
| VarPercentage      | Minimum percentage by variance for filtering of genes; for example, 75% would indicate that the CreateRegulatorData() function only analyses genes that have a variance above the 75th percentile across all samples.  |
| PvalueThreshold    | Threshold used to find relevant driver genes with CNV alterations: maximal p-value.  |
| RsquareThreshold   | Threshold used to find relevant driver genes with CNV alterations: minimal R-square value between CNV and gene expression data.  |
| pmax               | 'pmax' variable for glmnet function from glmnet package; the maximum number of variables aver to be nonzero. Should not be changed by user unless she/he fully understands the AMARETTO algorithm and how its parameters choices affect model output.  |
| NrCores            | A numeric variable indicating the number of computer/server cores to use for parallelization. Default is 1, i.e. no parallelization. Please check your computer or server's computing capacities before increasing this number. Parallelization is done via the RParallel package. Mac vs. Windows environments may behave differently when using parallelization. |
| OneRunStop         | OneRunStop   |
| method             | Perform union or intersection of the driver genes evaluated from the input data matrices and custom driver gene list provided.   |
| random_seeds       | A numeric vector of length 2, containing two seed numbers for randomization : 1st for kmeans and 2nd for glmnet  |
| convergence_cutoff | A numeric value (E.g. 0.01) representing the fraction of the total number of genes, in which, The algorithm is considered reaching convergence and will stop, if Nr of Gene-replacements in an iteration falls below this threshold * total number of genes.   |

**Value**

result



**Examples**

```
data('ProcessedDataLIHC')
data('Driver_Genes')
AMARETTOinit <- AMARETTO_Initialize(ProcessedData = ProcessedDataLIHC,
                                   NrModules = 2, VarPercentage = 50)

## Not run:
AMARETTOinit <- AMARETTO_Initialize(ProcessedData = ProcessedDataLIHC,
                                   Driver_list = Driver_Genes[['MSigDB']],
                                   NrModules = 2, VarPercentage = 50)

## End(Not run)
```

---

AMARETTO\_LarsenBased    *AMARETTO\_LarsenBased*

---

**Description**

AMARETTO\_LarsenBased

**Usage**

```
AMARETTO_LarsenBased(Data, Clusters, RegulatorData, Parameters, NrCores,
                     random_seeds, convergence_cutoff)
```

**Arguments**

Data  
Clusters  
RegulatorData  
Parameters  
NrCores  
random\_seeds  
convergence\_cutoff

**Value**

result

---

AMARETTO\_LearnRegulatoryProgramsLarsen  
*AMARETTO\_LearnRegulatoryProgramsLarsen*

---

**Description**

AMARETTO\_LearnRegulatoryProgramsLarsen

**Usage**

AMARETTO\_LearnRegulatoryProgramsLarsen(Data, Clusters, RegulatorData,  
 RegulatorSign, Lambda, AutoRegulation, alpha, pmax, random\_seeds)

**Value**

result

---

AMARETTO\_Preprocess    *AMARETTO\_Preprocess*

---

**Description**

Wrapper code that analyzes process TCGA GISTIC (CNV) and gene expression (rna-seq or microarray) data via one call

**Usage**

AMARETTO\_Preprocess(DataSetDirectories = DataSetDirectories,  
 BatchData = BatchData)

**Arguments**

|                    |                    |
|--------------------|--------------------|
| DataSetDirectories | DataSetDirectories |
| BatchData          | BatchData          |

**Value**

result

**Examples**

```
## Not run:
TargetDirectory <- "Downloads" # path to data download directory
CancerSite <- 'CHOL'
DataSetDirectories <- AMARETTO_Download(CancerSite,TargetDirectory)
ProcessedData <- AMARETTO_Preprocess(DataSetDirectories,BatchData)

## End(Not run)
```

---

AMARETTO\_ReassignGenesToClusters  
*AMARETTO\_ReassignGenesToClusters*

---

**Description**

AMARETTO\_ReassignGenesToClusters

**Usage**

```
AMARETTO_ReassignGenesToClusters(Data, RegulatorData, Beta, Clusters,  
  AutoRegulation)
```

**Value**

result

---

AMARETTO\_Run                    *AMARETTO\_Run Function to run AMARETTO, a statistical algorithm to identify cancer drivers by integrating a variety of omics data from cancer and normal tissue.*

---

**Description**

AMARETTO\_Run Function to run AMARETTO, a statistical algorithm to identify cancer drivers by integrating a variety of omics data from cancer and normal tissue.

**Usage**

```
AMARETTO_Run(AMARETTOinit)
```

**Arguments**

AMARETTOinit    List output from AMARETTO\_Initialize().

**Value**

result

**Examples**

```
data('ProcessedDataLIHC')  
AMARETTOinit <- AMARETTO_Initialize(ProcessedData = ProcessedDataLIHC,  
  NrModules = 2, VarPercentage = 50)  
AMARETTOresults <- AMARETTO_Run(AMARETTOinit)
```

AMARETTO\_VisualizeModule

*AMARETTO\_VisualizeModule*

---

### Description

Function to visualize the gene modules

### Usage

```
AMARETTO_VisualizeModule(AMARETTOinit, AMARETTOresults, ProcessedData,  
  ModuleNr, show_row_names = FALSE, SAMPLE_annotation = NULL,  
  ID = NULL, order_samples = NULL)
```

### Arguments

AMARETTOinit List output from AMARETTO\_Initialize().  
AMARETTOresults List output from AMARETTO\_Run().  
ProcessedData List of processed input data  
ModuleNr Module number to visualize  
show\_row\_names If TRUE, row names will be shown on the plot.  
SAMPLE\_annotation Matrix or Dataframe with sample annotation  
ID Column used as sample name  
order\_samples Order samples in heatmap by mean or by clustering

### Value

result

### Examples

```
data('ProcessedDataLIHC')  
AMARETTOinit <- AMARETTO_Initialize(ProcessedData = ProcessedDataLIHC,  
  NrModules = 2, VarPercentage = 50)  
  
AMARETTOresults <- AMARETTO_Run(AMARETTOinit)  
  
AMARETTO_VisualizeModule(AMARETTOinit = AMARETTOinit, AMARETTOresults = AMARETTOresults,  
  ProcessedData = ProcessedDataLIHC, ModuleNr = 1)
```

---

|        |               |
|--------|---------------|
| aprior | <i>aprior</i> |
|--------|---------------|

---

**Description**

Following four find empirical hyper-prior values

**Usage**

```
aprior(gamma.hat)
```

**Value**

result

---

|           |                  |
|-----------|------------------|
| BatchData | <i>BatchData</i> |
|-----------|------------------|

---

**Description**

A dataset for conducting batch corection in TCGA samples

**Usage**

```
BatchData
```

**Format**

A data frame with 23263 observations and 3 variables:

**Source**

AMARETTO

---

|         |                |
|---------|----------------|
| Beta.NA | <i>Beta.NA</i> |
|---------|----------------|

---

**Description**

Beta.NA

**Usage**

```
Beta.NA(y, X)
```

**Value**

result

---

|        |               |
|--------|---------------|
| bprior | <i>bprior</i> |
|--------|---------------|

---

**Description**

bprior

**Usage**

bprior(gamma.hat)

**Value**

result

---

|              |                     |
|--------------|---------------------|
| build.design | <i>build.design</i> |
|--------------|---------------------|

---

**Description**

Next two functions make the design matrix (X) from the sample info file

**Usage**

build.design(vec, des = NULL, start = 2)

**Value**

result

---

|               |                      |
|---------------|----------------------|
| cacheResource | <i>cacheResource</i> |
|---------------|----------------------|

---

**Description**

cacheResource

**Usage**

cacheResource(TargetDirectory = TargetDirectory, resource = resource)

**Value**

result

---

|                |                       |
|----------------|-----------------------|
| ComBat_NoFiles | <i>ComBat_NoFiles</i> |
|----------------|-----------------------|

---

**Description**

ComBat\_NoFiles

**Usage**

```
ComBat_NoFiles(dat, saminfo, type = "txt", write = FALSE,
  covariates = "all", par.prior = TRUE, filter = FALSE, skip = 0,
  prior.plots = FALSE)
```

**Value**

result

---

|                  |                         |
|------------------|-------------------------|
| computeGisticURL | <i>computeGisticURL</i> |
|------------------|-------------------------|

---

**Description**

computeGisticURL

**Usage**

```
computeGisticURL(url = NULL, acronym = "CHOL")
```

**Value**

result

---

|                     |                            |
|---------------------|----------------------------|
| CreateRegulatorData | <i>CreateRegulatorData</i> |
|---------------------|----------------------------|

---

**Description**

Determine potential regulator genes.

**Usage**

```
CreateRegulatorData(MA_matrix = MA_matrix, CNV_matrix = NULL,
  MET_matrix = NULL, Driver_list = NULL, PvalueThreshold = 0.001,
  RsquareThreshold = 0.1, method = "union")
```

**Value**

result

---

|            |                   |
|------------|-------------------|
| design.mat | <i>design.mat</i> |
|------------|-------------------|

---

**Description**

design.mat

**Usage**

```
design.mat(saminfo)
```

**Value**

result

---

|              |                     |
|--------------|---------------------|
| Driver_Genes | <i>Driver_Genes</i> |
|--------------|---------------------|

---

**Description**

A list of cancer driver genes described in literature.

**Usage**

```
Driver_Genes
```

**Format**

List

**Source**

AMARETTO

---

|               |                      |
|---------------|----------------------|
| filter.absent | <i>filter.absent</i> |
|---------------|----------------------|

---

**Description**

filters data based on presence/absence call

**Usage**

```
## S3 method for class 'absent'
filter(x, pct)
```

**Value**

result



---

```
FindTranscriptionallyPredictive_CNV
      FindTranscriptionallyPredictive_CNV
```

---

**Description**

Function to identify which genes CNV significantly predict expression of that gene.

**Usage**

```
FindTranscriptionallyPredictive_CNV(MA_matrix, CNV_matrix,
      PvalueThreshold = 0.001, RsquareThreshold = 0.1)
```

**Value**

result

---

```
geneFiltering      geneFiltering
```

---

**Description**

Function to filter gene expression matrix

**Usage**

```
geneFiltering(Type, MAdat, Percentage)
```

**Value**

result

---

```
GeneSetDescription      GeneSetDescription
```

---

**Description**

GeneSetDescription

**Usage**

```
GeneSetDescription(filename, MSIGDB)
```

**Arguments**

|          |  |
|----------|--|
| filename | The name of the gmt file.  |
| MSIGDB   | If True, the gene set description column will be provided from MSIGDB. |

**Value**

result

---

|                  |                         |
|------------------|-------------------------|
| get_firehoseData | <i>get_firehoseData</i> |
|------------------|-------------------------|

---

**Description**

Downloading TCGA dataset via firehose

**Usage**

```
get_firehoseData(TargetDirectory = "./",
  TCGA_acronym_uppercase = "LUAD", dataType = "stddata",
  dataFileTag = "mRNAseq_Preprocess.Level_3", FFPE = FALSE,
  fileType = "tar.gz",
  gdacURL = "http://gdac.broadinstitute.org/runs/", untarUngzip = TRUE,
  printDisease_abbr = FALSE)
```

**Value**

result

---

|                |                       |
|----------------|-----------------------|
| GmtFromModules | <i>GmtFromModules</i> |
|----------------|-----------------------|

---

**Description**

GmtFromModules

**Usage**

```
GmtFromModules(AMARETTOinit, AMARETTOresults, driverGSEA)
```

**Arguments**

|                 |   |
|-----------------|---|
| AMARETTOinit    | List output from AMARETTO_Initialize().   |
| AMARETTOresults | List output from AMARETTO_Run().  |
| driverGSEA      | if TRUE , module driver genes will also be added to module target genes for GSEA. |

**Value**

result

---

 HyperGTestGeneEnrichment

*Hyper Geometric Geneset Enrichment Test*


---

### Description

Calculates the p-values for unranked gene set enrichment based on two gmt files as input and the hyper geometric test.

### Usage

```
HyperGTestGeneEnrichment(gmtfile, testgmtfile, NrCores,
  ref.numb.genes = 45956)
```

### Arguments

|                |  |
|----------------|--|
| gmtfile        | The gmt file with reference gene set.  |
| testgmtfile    | The gmt file with gene sets to test. In our case, the gmt file of the modules. |
| NrCores        | Number of cores used for parallelization.                                      |
| ref.numb.genes | The total number of genes teste, standard equal to 45 956 (MSIGDB standard).   |

### Value

result

---

 int.eprior

*int.eprior*


---

### Description

Monte Carlo integration function to find the nonparametric adjustments

### Usage

```
int.eprior(sdat, g.hat, d.hat)
```

### Value

result

---

|                     |               |
|---------------------|---------------|
| <code>it.sol</code> | <i>it.sol</i> |
|---------------------|---------------|

---

**Description**

Pass in entire data set, the design matrix for the entire data, the batch means, the batch variances, priors (m, t2, a, b), columns of the data matrix for the batch. Uses the EM to find the parametric batch adjustments

**Usage**

```
it.sol(sdat, g.hat, d.hat, g.bar, t2, a, b, conv = 1e-04)
```

**Value**

result

---

|   |          |
|---|----------|
| L | <i>L</i> |
|---|----------|

---

**Description**

likelihood function

**Usage**

```
L(x, g.hat, d.hat)
```

**Value**

result

---

|                 |                        |
|-----------------|------------------------|
| Lambda_Sequence | <i>Lambda_Sequence</i> |
|-----------------|------------------------|

---

**Description**

Lambda\_Sequence

**Usage**

```
Lambda_Sequence(sx, sy)
```

**Value**

result

---

|            |                   |
|------------|-------------------|
| list.batch | <i>list.batch</i> |
|------------|-------------------|

---

**Description**

Makes a list with elements pointing to which array belongs to which batch

**Usage**

```
list.batch(saminfo)
```

**Value**

result

---

|               |                      |
|---------------|----------------------|
| MsigdbMapping | <i>MsigdbMapping</i> |
|---------------|----------------------|

---

**Description**

A dataset containing all MSIGDB pathways and their descriptions. .

**Usage**

```
MsigdbMapping
```

**Format**

List

**Source**

AMARETTO

---

|                  |                               |
|------------------|-------------------------------|
| plot_run_history | <i>Title plot_run_history</i> |
|------------------|-------------------------------|

---

**Description**

Title plot\_run\_history

**Usage**

```
plot_run_history(AMARETTOinit, AMARETTOresults)
```

**Arguments**

AMARETTOinit    AMARETTO initialize output  
 AMARETTOresults    AMARETTO results output

**Value**

plot

**Examples**

```
data('ProcessedDataLIHC')
AMARETTOinit <- AMARETTO_Initialize(ProcessedData = ProcessedDataLIHC,
                                   NrModules = 2, VarPercentage = 50)

AMARETTOresults <- AMARETTO_Run(AMARETTOinit)

plot_run_history(AMARETTOinit,AMARETTOresults)
```

---

postmean

*postmean*

---

**Description**

postmean

**Usage**

```
postmean(g.hat, g.bar, n, d.star, t2)
```

**Value**

result

---

postvar

*postvar*

---

**Description**

postvar

**Usage**

```
postvar(sum2, n, a, b)
```

**Value**

result

---

|                   |                          |
|-------------------|--------------------------|
| Preprocess_MAdata | <i>Preprocess_MAdata</i> |
|-------------------|--------------------------|

---

**Description**

Preprocess\_MAdata

**Usage**

```
Preprocess_MAdata(CancerSite = CancerSite, MAEO_ge = MAEO_ge,  
BatchData = BatchData)
```

**Value**

result

---

|        |               |
|--------|---------------|
| printf | <i>printf</i> |
|--------|---------------|

---

**Description**

Wrapper function for C-style formatted output.

**Usage**

```
printf(...)
```

**Value**

result

---

|                   |                          |
|-------------------|--------------------------|
| ProcessedDataLIHC | <i>ProcessedDataLIHC</i> |
|-------------------|--------------------------|

---

**Description**

A list of dataframes of processed toy example dataset from TCGA-LIHC.

**Usage**

```
ProcessedDataLIHC
```

**Format**

List

**Source**

AMARETTO

---

|         |                |
|---------|----------------|
| readGMT | <i>readGMT</i> |
|---------|----------------|

---

**Description**

readGMT

**Usage**

```
readGMT(filename)
```

**Arguments**

filename

**Value**

result

---

|          |                 |
|----------|-----------------|
| read_gct | <i>read_gct</i> |
|----------|-----------------|

---

**Description**

Function to turn a .gct data files into a matrix format

**Usage**

```
read_gct(file_address)
```

**Arguments**

file\_address    Address of the input gct file.

**Value**

result

**Examples**

```
data_matrix<-read_gct(file_address="")
```



---

|                 |                        |
|-----------------|------------------------|
| Save_CancerSite | <i>Save_CancerSite</i> |
|-----------------|------------------------|

---

**Description**

Save\_CancerSite

**Usage**

```
Save_CancerSite(CancerSite, TargetDirectory, DataSetDirectories,  
ProcessedData)
```

**Value**

result

---

|                                    |   |
|------------------------------------|---|
| TCGA_BatchCorrection_MolecularData | <i>TCGA_BatchCorrection_MolecularData</i> |
|------------------------------------|---|

---

**Description**

TCGA\_BatchCorrection\_MolecularData

**Usage**

```
TCGA_BatchCorrection_MolecularData(GEN_Data = GEN_Data,  
BatchData = BatchData, MinInBatch = MinInBatch)
```

**Value**

result

---

|                              |                                     |
|------------------------------|-------------------------------------|
| TCGA_GENERIC_BatchCorrection | <i>TCGA_GENERIC_BatchCorrection</i> |
|------------------------------|-------------------------------------|

---

**Description**

TCGA\_GENERIC\_BatchCorrection

**Usage**

```
TCGA_GENERIC_BatchCorrection(GEN_Data = GEN_Data,  
BatchData = BatchData)
```

**Value**

result

TCGA\_GENERIC\_CheckBatchEffect  
*TCGA\_GENERIC\_CheckBatchEffect*

---

**Description**

TCGA\_GENERIC\_CheckBatchEffect

**Usage**

TCGA\_GENERIC\_CheckBatchEffect(GEN\_Data, BatchData)

**Value**

result

---

TCGA\_GENERIC\_CleanUpSampleNames  
*TCGA\_GENERIC\_CleanUpSampleNames*

---

**Description**

TCGA\_GENERIC\_CleanUpSampleNames

**Usage**

TCGA\_GENERIC\_CleanUpSampleNames(GEN\_Data = GEN\_Data, IDlength = 12)

**Value**

result

---

TCGA\_GENERIC\_GetSampleGroups  
*TCGA\_GENERIC\_GetSampleGroups*

---

**Description**

TCGA\_GENERIC\_GetSampleGroups

**Usage**

TCGA\_GENERIC\_GetSampleGroups(SampleNames)

**Value**

result

---

TCGA\_GENERIC\_MergeData

*TCGA\_GENERIC\_MergeData*

---

**Description**

TCGA\_GENERIC\_MergeData

**Usage**

TCGA\_GENERIC\_MergeData(NewIDListUnique, DataMatrix, MergeMethod)

**Value**

result

---

TCGA\_Load\_GISTICdata *TCGA\_Load\_GISTICdata*

---

**Description**

TCGA\_Load\_GISTICdata

**Usage**

TCGA\_Load\_GISTICdata(GisticDirectory)

**Value**

result

---

TCGA\_Load\_MolecularData

*TCGA\_Load\_MolecularData*

---

**Description**

TCGA\_Load\_MolecularData

**Usage**

TCGA\_Load\_MolecularData(MAEO\_ge)

**Value**

result

---

|          |                 |
|----------|-----------------|
| trim.dat | <i>trim.dat</i> |
|----------|-----------------|

---

**Description**

Trims the data of extra columns, note your array names cannot be named 'X' or start with 'X.'

**Usage**

```
trim.dat(dat)
```

**Value**

result

---

|           |                  |
|-----------|------------------|
| write_gct | <i>write_gct</i> |
|-----------|------------------|

---

**Description**

write\_gct

**Usage**

```
write_gct(data_in, file_address)
```

**Value**

result

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