

# Package: classifyBLCA (via r-universe)

November 3, 2024

**Title** What the Package Does (One Line, Title Case)

**Version** 0.0.0.9000

**Description** What the package does (one paragraph).

**License** GPL (>= 3)

**Encoding** UTF-8

**Language** en

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.1

**Imports** broom, dplyr, rlang, stats

**Depends** R (>= 2.10)

**LazyData** true

**Repository** <https://kaiaragaki.r-universe.dev>

**RemoteUrl** <https://github.com/KaiAragaki/classifyBLCA>

**RemoteRef** HEAD

**RemoteSha** eb6eff4fa4a9c06bc6a76e009474c197053df215

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centroids\_consensus      *Centroids for the BLCA Consensus Classes*

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**Description**

A data.frame containing the centroid coordinates for the six consensus classes of muscle-invasive bladder cancer

**Usage**

```
centroids_consensus
```

**Format**

An object of class tbl\_df (inherits from tbl, data.frame) with 857 rows and 9 columns.

**Author(s)**

Aurelie Kamoun

**References**

<https://www.biorxiv.org/content/10.1101/488460v2>

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centroids\_tcga      *Centroids for the BLCA TCGA Classes*

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**Description**

A data.frame containing the centroid coordinates for the five TCGA classes of muscle-invasive bladder cancer

**Usage**

```
centroids_tcga
```

**Format**

An object of class tbl\_df (inherits from tbl, data.frame) with 1264 rows and 7 columns.

**Author(s)**

Gordon Robertson

**References**

<https://doi.org/10.1016/j.cell.2017.09.007>

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centroids\_uromol2021    *Centroids for the BLCA UROMOL2021 Classes*

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**Description**

A data.frame containing the centroid coordinates for the four UROMOL2021 classes of non-muscle-invasive bladder cancer

**Usage**

```
centroids_uromol2021
```

**Format**

An object of class tbl\_df (inherits from tbl, data.frame) with 1942 rows and 7 columns.

**Author(s)**

Sia Lindskrog

**References**

<https://www.nature.com/articles/s41467-021-22465-w>

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classify\_blca    *Calculate centroid correlation for samples*

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**Description**

Calculate centroid correlation for samples

**Usage**

```
classify_blca(  
  df,  
  gene_id = c("entrez", "ensembl", "hgnc"),  
  classifier = c("tcga", "uromol2021", "consensus"),  
  tidy = FALSE  
)
```

**Arguments**

<code>df</code>	A data.frame containing RNA expression with unique genes as rows and samples as columns. RNA-seq data must be log-transformed.
<code>gene_id</code>	Character specifying the type of gene identifiers used for the row names or first column of <code>df</code> .
<code>classifier</code>	Classifier to be used.
<code>tidy</code>	Logical. If TRUE, assumes the first column contains the gene identifiers. Otherwise, assumes IDs are row names

**Details**

If using the TCGA classifier, you must provide either Entrez IDs or HGNC symbols. The original centroids provided for the TCGA classifier only included Entrez and HGNC, and the conversion from Entrez to Ensembl is ambiguous. Therefore, conversion and selection of unique genes must be performed by the user on a case-by-case basis, perhaps using the expression value of the gene as a guide for which genes to keep.

**Value**

A tibble containing:

**estimate** Pearson correlation of a given sample to the given class centroid

**conf.low, conf.high** low and high end of 95% confidence interval

**nearest** centroid for which the sample has the highest correlation to

**statistic** t-statistic

**parameter** degrees of freedom

**sep\_lvl** (Highest Correlation - 2nd Highest Correlation)/median(Distance to highest correlation)

**Author(s)**

Aurelie Kamoun

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