

# Package: tigreBrowserWriter (via r-universe)

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**Version** 0.1.5

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**Title** 'tigreBrowser' Database Writer

**Depends** R (>= 2.14.0)

**Imports** DBI, RSQLite

**Description** Write modelling results into a database for 'tigreBrowser', a web-based tool for browsing figures and summary data of independent model fits, such as Gaussian process models fitted for each gene or other genomic element. The browser is available at <https://github.com/PROBIC/tigreBrowser>.

**License** AGPL-3

**URL** <https://github.com/PROBIC/tigreBrowserWriter>

**BugReports** <https://github.com/PROBIC/tigreBrowserWriter/issues>

**RoxygenNote** 5.0.1

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

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**RemoteUrl** <https://github.com/trustworthymhelsinki/tigrebrowserwriter>

**RemoteRef** HEAD

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## Contents

closeDb . . . . .	2
initializeDb . . . . .	2
insertAliases . . . . .	3
insertFigureData . . . . .	4
insertFigures . . . . .	5
insertResults . . . . .	6
insertSupplementaryData . . . . .	7
insertZScores . . . . .	8

**Index****9**


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closeDb	<i>Finalise and close the database</i>
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**Description**

Finalise and close the database

**Usage**

```
closeDb(db, experimentSet = "")
```

**Arguments**

db Database object created by [initializeDb](#)  
 experimentSet Name of the experiment set for all the experiments (optional)

**Examples**

```
db <- initializeDb("", "My Dataset")
# ...
closeDb(db)
```

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initializeDb	<i>Create and initialize a database</i>
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**Description**

Create and initialize a database

**Usage**

```
initializeDb(dbPath, datasetName, datasetSpecies = "", datasetSource = "",
  datasetPlatform = "", datasetDescription = "", datasetSaveLocation = "",
  datasetFigureFilename = "")
```

**Arguments**

dbPath Path to the database file to be created. Empty string  
 datasetName Name of the data set  
 datasetSpecies Optional data set metadata: species  
 datasetSource Optional data set metadata: source  
 datasetPlatform  
 Optional data set metadata: platform

```

datasetDescription
    Optional data set metadata: description
datasetSaveLocation
    Optional data set metadata: save location
datasetFigureFilename
    Optional data set metadata: figure file name

```

**Value**

A database object db needed by other tigreBrowserWriter functions

**Examples**

```

## Not run:
# Create a real database to a file
db <- initializeDb("/path/to/the/database.sqlite", "My Dataset")
closeDb(db)

## End(Not run)

# Create a temporary database to be deleted at the end
db <- initializeDb("", "My Dataset")
closeDb(db)

```

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insertAliases	<i>Insert aliases</i>
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**Description**

Insert aliases

**Usage**

```
insertAliases(db, aliasType, aliases, aliasSource = "",
  aliasDescription = "")
```

**Arguments**

```

db          Database object created by initializeDb
aliasType   Name of the alias
aliases     A vector of aliases with names giving the primary identifiers
aliasSource Optional alias metadata: source
aliasDescription
            Optional alias metadata: description

```

**Value**

An updated database object db

**Examples**

```
db <- initializeDb("", "My Dataset")
aliases <- c("aliasA", "aliasB", "aliasC")
names(aliases) <- c("A", "B", "C")
db <- insertAliases(db, "testalias", aliases)
closeDb(db)
```

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insertFigureData	<i>Insert figure data directly to the database</i>
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**Description**

Insert figure data directly to the database

**Usage**

```
insertFigureData(db, experimentName, regulatorName, filenames, name = "",
  description = "", priority = 0)
```

**Arguments**

db	Database object created by <code>initializeDb</code>
experimentName	Experiment name
regulatorName	Regulator name (more detailed experiment identifier)
filenames	A list of file names of PNG figures. names of the list must correspond to the names of the entities the figures are for.
name	Optional figure name
description	Optional figure description
priority	Integer priority used for sorting figures (default: 0)

**Value**

An updated database object db

**Examples**

```
db <- initializeDb("", "My Dataset")
logl <- c(-4.0, -2.0, 0.0)
names(logl) <- c("A", "B", "C")
baselogl <- c(1.0, -1.0, 4.0)
names(baselogl) <- names(logl)
db <- insertResults(db, "testexperiment", "testregulator", "",
  logl, baselineloglikelihoods=baselogl)
# Generate a dummy plot (reused for all data elements for simplicity)
examplefile <- tempfile("plot", fileext=".png")
png(examplefile)
```

```

plot(c(0, 1), c(0, 1))
dev.off()
figures <- list(A=examplefile, B=examplefile, C=examplefile)
db <- insertFigureData(db, "testexperiment", "testregulator",
                      figures)
closeDb(db)

```

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insertFigures	<i>Insert figure links</i>
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## Description

Insert figure links

## Usage

```

insertFigures(db, experimentName, regulatorName, filename, name = "",
             description = "", priority = 0)

```

## Arguments

db	Database object created by <code>initializeDb</code>
experimentName	Experiment name
regulatorName	Regulator name (more detailed experiment identifier)
filename	URL path to figures. The path can contain the special form <code>\${probe_name}</code> which will be substituted by the name of the entity (gene, ...) by the browser.
name	Optional figure name
description	Optional figure description
priority	Integer priority used for sorting figures (default: 0)

## Value

An updated database object db

## Examples

```

db <- initializeDb("", "My Dataset")
logl <- c(-4.0, -2.0, 0.0)
names(logl) <- c("A", "B", "C")
baselogl <- c(1.0, -1.0, 4.0)
names(baselogl) <- names(logl)
db <- insertResults(db, "testexperiment", "testregulator", "",
                  logl, baselineloglikelihoods=baselogl)
db <- insertFigures(db, "testexperiment", "testregulator",
                  "http://foo.invalid/path/${probe_name}_fit.png")
closeDb(db)

```

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 insertResults

*Insert results*


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## Description

Insert results

## Usage

```
insertResults(db, experimentName, regulatorName, figurePath, loglikelihoods,
  baselineloglikelihoods = NA, experimentDesc = "", loopVariable = 2,
  modelTranslation = FALSE, numberOfParameters = NA, parameterNames = NA,
  experimentProducer = "", experimentTimestamp = "", parameters = NA)
```

## Arguments

db	Database object created by <a href="#">initializeDb</a>
experimentName	Experiment name
regulatorName	Regulator name (more detailed experiment identifier)
figurePath	URL path to figures
loglikelihoods	A vector of log-likelihoods of elements identified by names
baselineloglikelihoods	A vector of baseline log-likelihoods of elements identified by names (optional)
experimentDesc	Optional experiment description
loopVariable	Optional: Loop variable (1=regulator, 2=target (default))
modelTranslation	Optional: For gene regulation models, is translation modelled
numberOfParameters	Optional: Number of parameters
parameterNames	Optional: Parameter names
experimentProducer	Optional: Experiment producer (string)
experimentTimestamp	Optional: Experiment timestamp (string)
parameters	Optional: A vector of parameter values for the model

## Value

An updated database object db

**Examples**

```
db <- initializeDb("", "My Dataset")
logl <- c(-4.0, -2.0, 0.0)
names(logl) <- c("A", "B", "C")
baselogl <- c(1.0, -1.0, 4.0)
names(baselogl) <- names(logl)
db <- insertResults(db, "testexperiment", "testregulator", "",
  logl, baselineloglikelihoods=baselogl)
closeDb(db)
```

---

insertSupplementaryData

*Insert supplementary data*

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**Description**

Insert supplementary data

**Usage**

```
insertSupplementaryData(db, name, suppData, regulatorName = NA, source = "",
  platform = "", description = "")
```

**Arguments**

db	Database object created by <a href="#">initializeDb</a>
name	Name of the supplementary data
suppData	A vector of supplementary data of elements identified by names
regulatorName	Regulator name the data links to (optional)
source	Optional annotation: source
platform	Optional annotation: platform
description	Optional annotation: description

**Value**

An updated database object db

**Examples**

```
db <- initializeDb("", "My Dataset")
suppdata <- c(1, 2, 3)
names(suppdata) <- c("A", "B", "C")
db <- insertSupplementaryData(db, "supptest", suppdata)
boolsupp <- c(TRUE, TRUE, FALSE)
names(boolsupp) <- names(suppdata)
db <- insertSupplementaryData(db, "supptest_bool", boolsupp)
closeDb(db)
```

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insertZScores	<i>Insert data z-scores used for filtering</i>
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**Description**

Insert data z-scores used for filtering

**Usage**

```
insertZScores(db, zscores)
```

**Arguments**

db	Database object created by <a href="#">initializeDb</a>
zscores	A vector of z-scores of elements identified by names

**Value**

An updated database object db

**Examples**

```
db <- initializeDb("", "My Dataset")
zscores <- c(1, 2, 3)
names(zscores) <- c("A", "B", "C")
db <- insertZScores(db, zscores)
closeDb(db)
```

# Index

`closeDb`, [2](#)

`initializeDb`, [2](#), [2–8](#)

`insertAliases`, [3](#)

`insertFigureData`, [4](#)

`insertFigures`, [5](#)

`insertResults`, [6](#)

`insertSupplementaryData`, [7](#)

`insertZScores`, [8](#)