

# Package ‘SqueakR’

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**Type** Package

**Title** An Experiment Interface for 'DeepSqueak' Bioacoustics Research

**Version** 1.3.0

**Description** Data processing and visualizations for rodent vocalizations exported from 'DeepSqueak'. These functions are compatible with the 'SqueakR' Shiny Dashboard, which can be used to visualize experimental results and analyses.

**URL** <https://osimon81.github.io/SqueakR/>,

<https://github.com/osimon81/SqueakR/>

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**Imports** dplyr, ggcorrplot, ggeasy, gghighlight, ggplot2, ggpubr, googlesheets4, MASS, plotly, RColorBrewer, readxl, report, rlist, rstatix, shiny, shinydashboard, utils

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---

add_timepoint_data	<i>Add Timepoint Data</i>
--------------------	---------------------------

---

### Description

Loads in a specific Excel File, and (optional) selects a time subset of data.

**Usage**

```
add_timepoint_data(data_path, t1 = "", t2 = "")
```

**Arguments**

data_path	The full path to the Excel file exported from DeepSqueak
t1	The start time in the recording (in seconds) to start extracting calls
t2	The end time in the recording (in seconds) to stop extracting calls

**Value**

An object containing the call data (under time constraints if specified)

**Examples**

```
## Not run: add_timepoint_data(
  data_path = "~/inst/extdata/Example_Mouse_Data.xlsx",
  t1 = 3, t2 = 12
)
## End(Not run)
```

---

add_to_experiment	<i>Add Scored Data to Experiment Object</i>
-------------------	---

---

**Description**

Adds summarized timepoint data (acquired by running ‘add\_timepoint\_data()’, followed by ‘score\_timepoint\_data()’) to the created experiment object.

**Usage**

```
add_to_experiment(experiment, added_data)
```

**Arguments**

experiment	The experiment object
added_data	The scored data object to be added to the experiment

**Value**

A list object containing statistics and metadata for the entire experiment. The ‘groups’ and ‘experimenters’ field will auto-populate based on added data using the ‘update\_experiment()’ function.

**Examples**

```
## Not run: add_to_experiment(experiment = experiment, added_data = my_data)
```

analyze\_factor      *Analyze Factor*

---

**Description**

Compares data across experimental groups, plotting the data as a bar graph with error bars.

**Usage**

```
analyze_factor(experiment, analysis_factor)
```

**Arguments**

experiment      The experiment object  
analysis\_factor      A string representing the factor to analyze between groups

**Value**

A bar graph comparing the analysis\_factor between groups

**Examples**

```
## Not run: analyze_factor(experiment = experiment, analysis_factor = "tonality")
```

---

autosqueakRpipeline      *Fully-Automatic Experiment Creation*

---

**Description**

A pipeline function which creates a new experiment object, and adds data and metadata referenced from an external Google Sheets document.

**Usage**

```
autosqueakRpipeline()
```

**Value**

An object containing the full experiment with all data added.

**Examples**

```
## Not run: expt <- autosqueakRpipeline()
```

---

create_experiment	<i>Create New Experiment</i>
-------------------	------------------------------

---

**Description**

Creates an experiment object which will contain all data and metadata. This object will be saved and timestamped by date, so if working with this file over different dates, the object will not be overwritten as a new object will be created (to preserve backups).

**Usage**

```
create_experiment(experiment_name)
```

**Arguments**

experiment_name	The name of the experiment
-----------------	----------------------------

**Value**

A list object containing statistics and metadata for the entire experiment. The 'groups' and 'experimenters' field will auto-populate based on added data using the 'update\_experiment()' function.

**Examples**

```
create_experiment(experiment_name = "My-Project")
```

---

deepsqueak_data	<i>DeepSqueak Example Data</i>
-----------------	--------------------------------

---

**Description**

Data exported from DeepSqueak after processing 'Example Mouse Recording.flac'

**Usage**

```
data(deepsqueak_data)
```

**Format**

A "data.frame" with 714 rows and 17 columns. The definitions of these parameters are sourced from the link in the references section.

**ID** The number of the call

**Label** The label extracted from DeepSqueak

**Accepted** Whether the call was accepted (as a call)

**Score** The call score, from DeepSqueak

**Begin Time (s)** The time when the call started

**End Time (s)** The time when the call ended

**Call Length (s)** The length of the call

**Principal Frequency (kHz)** The median frequency of the call

**Low Freq (kHz)** The minimum frequency of the call

**High Freq (kHz)** The maximum frequency of the call

**Delta Freq (kHz)** The difference between the maximum and minimum call frequencies

**Frequency Standard Deviation (kHz)** The standard deviation of the call

**Slope (kHz/s)** The slope of the call

**Sinuosity** The call contour path length divided by the distance between start and end of the call

**Mean Power (dB/Hz)**

**Tonality** The signal/noise ratio

**Peak Freq** The frequency at the highest power

**Source**

([DeepSqueak GitHub](#))

**References**

([DeepSqueak Wiki: Export to Excel Page](#))

**Examples**

```
data(deepsqueak_data)
```

---

describe_experiment	<i>Describe Experiment</i>
---------------------	----------------------------

---

**Description**

Lists a condensed summary of data stored in the experiment object.

**Usage**

```
describe_experiment(experiment)
```

**Arguments**

experiment      The experiment object to be saved

**Value**

A list of information about the experiment

**Examples**

```
## Not run: describe_experiment(experiment = experiment_object)
```

---

plotClusters	<i>3D Call Clusters (Custom Label) Plot</i>
--------------	---

---

**Description**

Plots call clusters within a data-point in a 3D Plotly graph, with principal frequency on the x-axis, mean power on the y-axis, and call length on the z-axis.

**Usage**

```
plotClusters(data_path)
```

**Arguments**

data\_path      The path to the raw data

**Value**

3D scatterplot

**Examples**

```
## Not run: plotClusters(data_path = "path")
```

---

plotContours	<i>2D Call Contours</i>
--------------	-------------------------

---

**Description**

Plots call density against principal frequency and call length as a contoured heatmap. Histograms for these variables are displayed across their respective axes.

**Usage**

```
plotContours(data_path)
```

**Arguments**

data_path	The path to the raw data
-----------	--------------------------

**Value**

2D contour plot

**Examples**

```
## Not run: plotContours(data_path = "path")
```

---

plotCorrelations	<i>Plot Correlation Matrix</i>
------------------	--------------------------------

---

**Description**

Plots a box-plot based on principal frequency, grouped by custom labels designated in DeepSqueak.

**Usage**

```
plotCorrelations(
  data_path,
  graph_title = "Correlation Matrix",
  graph_subtitle = "Correlation coefficients labeled."
)
```

**Arguments**

data_path	The full path to the Excel file exported from DeepSqueak
graph_title	The title for the graph (there is a default title if not specified)
graph_subtitle	The subtitle for the graph (there is a default subtitle if not specified)



**Value**

A ggplot2 visualization of the box-plot shown in the viewer window, which can be manually exported.

**Examples**

```
## Not run: plotCorrelations(  
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",  
  graph_title = "myTitle", graph_subtitle = "myDescription"  
)  
## End(Not run)
```

---

plotDeltaHistogram      *Plot Delta Frequency Histogram*

---

**Description**

Plots a distribution of delta frequencies as a histogram.

**Usage**

```
plotDeltaHistogram(  
  data_path,  
  graph_title = "Delta Frequency-Labeled Histogram",  
  graph_subtitle = "Delta Frequency measures the kHz range of each detected call."  
)
```

**Arguments**

`data_path`      The full path to the Excel file exported from DeepSqueak  
`graph_title`    The title for the graph (there is a default title if not specified)  
`graph_subtitle` The subtitle for the graph (there is a default subtitle if not specified)

**Value**

A ggplot2 visualization of the histogram shown in the viewer window, which can be manually exported.

**Examples**

```
## Not run: plotDeltaHistogram(  
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",  
  graph_title = "myTitle", graph_subtitle = "myDescription"  
)  
## End(Not run)
```

---

`plotDensitySplitByCustom`*Plot Density Graph, Splitting Groups by Custom Label*

---

## Description

Plots a density graph, separating each custom label group into a separate plot in the figure.

## Usage

```
plotDensitySplitByCustom(  
  data_path,  
  graph_title = "Call Distribution, Split by Custom Category Labels",  
  graph_subtitle = "Calls are split by custom labels designated in DeepSqueak.",  
  chosen_group = c()  
)
```

## Arguments

<code>data_path</code>	The full path to the Excel file exported from DeepSqueak
<code>graph_title</code>	The title for the graph (there is a default title if not specified)
<code>graph_subtitle</code>	The subtitle for the graph (there is a default subtitle if not specified)
<code>chosen_group</code>	Specifying a particular group to be highlighted in the graph

## Value

A ggplot2 visualization of the density graph shown in the viewer window, which can be manually exported.

## Examples

```
## Not run: plotDensitySplitByCustom(  
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",  
  graph_title = "myTitle", graph_subtitle = "myDescription"  
)  
## End(Not run)
```

---

`plotDensitySplitByDuration`*Plot Density Graph, Splitting Groups by Duration*

---

## Description

Plots a density graph, separating each duration group into a separate plot in the figure.

## Usage

```
plotDensitySplitByDuration(  
  data_path,  
  graph_title = "Call Distribution Grouped by Duration (s)",  
  graph_subtitle = "Duration groups are rounded to the nearest 0.01 second.",  
  chosen_group = c()  
)
```

## Arguments

<code>data_path</code>	The full path to the Excel file exported from DeepSqueak
<code>graph_title</code>	The title for the graph (there is a default title if not specified)
<code>graph_subtitle</code>	The subtitle for the graph (there is a default subtitle if not specified)
<code>chosen_group</code>	Specifying a particular group to be highlighted in the graph

## Value

A ggplot2 visualization of the density graph shown in the viewer window, which can be manually exported.

## Examples

```
## Not run: plotDensitySplitByDuration(  
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",  
  graph_title = "myTitle", graph_subtitle = "myDescription"  
)  
## End(Not run)
```

---

`plotDensitySplitByFrequency`*Plot Density Graph, Splitting Groups by Frequency*

---

## Description

Plots a density graph, separating each frequency group into a separate plot in the figure.

## Usage

```
plotDensitySplitByFrequency(  
  data_path,  
  graph_title = "Call Distribution, Split by Frequency Range (kHz)",  
  graph_subtitle = "Calls are split by frequency ranges of 10 kHz.",  
  chosen_group = c()  
)
```

## Arguments

<code>data_path</code>	The full path to the Excel file exported from DeepSqueak
<code>graph_title</code>	The title for the graph (there is a default title if not specified)
<code>graph_subtitle</code>	The subtitle for the graph (there is a default subtitle if not specified)
<code>chosen_group</code>	Specifying a particular group to be highlighted in the graph

## Value

A ggplot2 visualization of the density graph shown in the viewer window, which can be manually exported.

## Examples

```
## Not run: plotDensitySplitByFrequency(  
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",  
  graph_title = "myTitle", graph_subtitle = "myDescription"  
)  
## End(Not run)
```

---

`plotDensityStackedByCustom`*Plot Density Graph Stacked by Custom Labels*

---

## Description

Plots a density graph, grouped by custom labels set in DeepSqueak, collapsed into a single graph.

## Usage

```
plotDensityStackedByCustom(  
  data_path,  
  graph_title = "Call Distribution Grouped by Custom Category Labels",  
  graph_subtitle = "Calls are grouped by custom categories designated in DeepSqueak.",  
  chosen_group = c()  
)
```

## Arguments

<code>data_path</code>	The full path to the Excel file exported from DeepSqueak
<code>graph_title</code>	The title for the graph (there is a default title if not specified)
<code>graph_subtitle</code>	The subtitle for the graph (there is a default subtitle if not specified)
<code>chosen_group</code>	Specifying a particular group to be highlighted in the graph

## Value

A ggplot2 visualization of the density graph shown in the viewer window, which can be manually exported.

## Examples

```
## Not run: plotDensityStackedByCustom(  
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",  
  graph_title = "myTitle", graph_subtitle = "myDescription"  
)  
## End(Not run)
```

---

`plotDensityStackedByDuration`*Plot Density Graph Stacked by Duration*

---

### Description

Plots a density graph, grouped by duration of each call (rounded to the nearest 0.01 second), collapsed into a single graph.

### Usage

```
plotDensityStackedByDuration(  
  data_path,  
  graph_title = "Call Distribution Grouped by Duration (s)",  
  graph_subtitle = "Duration groups are rounded to the nearest 0.01 second.",  
  chosen_group = c()  
)
```

### Arguments

<code>data_path</code>	The full path to the Excel file exported from DeepSqueak
<code>graph_title</code>	The title for the graph (there is a default title if not specified)
<code>graph_subtitle</code>	The subtitle for the graph (there is a default subtitle if not specified)
<code>chosen_group</code>	Specifying a particular group to be highlighted in the graph

### Value

A ggplot2 visualization of the density graph shown in the viewer window, which can be manually exported.

### Examples

```
## Not run: plotDensityStackedByDuration(  
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",  
  graph_title = "myTitle", graph_subtitle = "myDescription"  
)  
## End(Not run)
```

---

plotDensityStackedByFrequency  
*Plot Density Graph Stacked by Frequency*

---

## Description

Plots a density graph, grouped by frequency group collapsed into a single graph.

## Usage

```
plotDensityStackedByFrequency(  
  data_path,  
  graph_title = "Call Distribution Grouped by Frequency Range (kHz)",  
  graph_subtitle = "Calls are grouped by frequency ranges of 10 kHz.",  
  chosen_group = c()  
)
```

## Arguments

data_path	The full path to the Excel file exported from DeepSqueak
graph_title	The title for the graph (there is a default title if not specified)
graph_subtitle	The subtitle for the graph (there is a default subtitle if not specified)
chosen_group	Specifying a particular group to be highlighted in the graph

## Value

A ggplot2 visualization of the density graph shown in the viewer window, which can be manually exported.

## Examples

```
## Not run: plotDensityStackedByFrequency(  
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",  
  graph_title = "myTitle", graph_subtitle = "myDescription"  
)  
## End(Not run)
```

---

plotEthnogram	<i>Plot Ethnogram</i>
---------------	-----------------------

---

**Description**

Plots an ethnogram, representing when detected calls occur through the length of the recording.

**Usage**

```
plotEthnogram(
  data_path,
  graph_title = "Call Ethnogram",
  graph_subtitle = "Calls are indicated by a vertical line."
)
```

**Arguments**

<code>data_path</code>	The full path to the Excel file exported from DeepSqueak
<code>graph_title</code>	The title for the graph (there is a default title if not specified)
<code>graph_subtitle</code>	The subtitle for the graph (there is a default subtitle if not specified)

**Value**

A ggplot2 visualization of the ethnogram shown in the viewer window, which can be manually exported.

**Examples**

```
## Not run: plotEthnogram(
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",
  graph_title = "myTitle", graph_subtitle = "myDescription"
)
## End(Not run)
```

---

plotEthnogramSplitByTonality	<i>Plot Tonality-colored Ethnogram</i>
------------------------------	--

---

**Description**

Plots a tonality ethnogram, representing tonality (clarity) of calls throughout the recording.



**Usage**

```
plotEthnogramSplitByTonality(
  data_path,
  graph_title = "Ethnogram Split By Tonality",
  graph_subtitle = "Tonality: Signal/noise"
)
```

**Arguments**

`data_path`        The full path to the Excel file exported from DeepSqueak  
`graph_title`      The title for the graph (there is a default title if not specified)  
`graph_subtitle`   The subtitle for the graph (there is a default subtitle if not specified)

**Value**

A ggplot2 visualization of the ethnogram shown in the viewer window, which can be manually exported.

**Examples**

```
## Not run: plotEthnogramSplitByTonality(
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",
  graph_title = "myTitle", graph_subtitle = "myDescription"
)
## End(Not run)
```

---

plotPrincipalBoxplot    *Plot Principal Frequency Box-Plot*

---

**Description**

Plots a box-plot based on principal frequency, grouped by custom labels designated in DeepSqueak.

**Usage**

```
plotPrincipalBoxplot(
  data_path,
  graph_title = "Principal Frequency-Labeled Box-Plot",
  graph_subtitle = "Main frequencies where calls labeled in DeepSqueak predominate."
)
```

**Arguments**

`data_path`        The full path to the Excel file exported from DeepSqueak  
`graph_title`      The title for the graph (there is a default title if not specified)  
`graph_subtitle`   The subtitle for the graph (there is a default subtitle if not specified)

**Value**

A ggplot2 visualization of the box-plot shown in the viewer window, which can be manually exported.

**Examples**

```
## Not run: plotPrincipalBoxplot(  
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",  
  graph_title = "myTitle", graph_subtitle = "myDescription"  
)  
## End(Not run)
```

---

plotSummaryPDF

*Export PDF*

---

**Description**

Plots a density graph, separating each frequency group into a separate plot in the figure.

**Usage**

```
plotSummaryPDF(data_path, save_path = tempdir(), experimenter = "Anon")
```

**Arguments**

data_path	The full path to the Excel file exported from DeepSqueak
save_path	The full path to the directory where the PDF will be saved (default is the current working directory)
experimenter	The name of the experimenter for naming the save file (default is "Anon")

**Value**

A PDF containing a series of relevant ethnograms and density graphs assessing the recording.

**Examples**

```
## Not run: plotSummaryPDF(  
  data_path = "inst/extdata/Example_Mouse_Data.xlsx",  
  save_path = tempdir(), experimenter = "experimenter_name"  
)  
## End(Not run)
```

---

plotSunburstAnimals     *Sunburst Plot for Animal Distribution*

---

**Description**

Plots interactive sunburst plot for animal distribution across experimental groups. Currently only valid for between-groups studies.

**Usage**

```
plotSunburstAnimals(experiment)
```

**Arguments**

experiment     The experiment object

**Value**

Sunburst distribution plotting animal distribution

**Examples**

```
## Not run: plotSunburstAnimals(experiment = experiment)
```

---

plotSunburstExperimenters  
                          *Sunburst Plot for Experimenter Distribution*

---

**Description**

Plots interactive sunburst plot for experimenter distribution across experimental groups. Currently only valid for between-groups studies.

**Usage**

```
plotSunburstExperimenters(experiment)
```

**Arguments**

experiment     The experiment object

**Value**

Sunburst distribution plotting experimenter contribution

**Examples**

```
## Not run: plotSunburstExperimenters(experiment = experiment)
```

---

plotSurface	<i>3D Surface Plot for Call Datasets</i>
-------------	--

---

**Description**

Plots interactive 3D plot for density of detected calls against call length (s) and principal frequency (kHz), using bivariate kernel density estimation provided via the MASS package

**Usage**

```
plotSurface(data_path, res = 60)
```

**Arguments**

data_path	The path to the call data
res	The resolution to render surface plot (default is 60)

**Value**

3D surface plot for the selected call dataset

**Examples**

```
## Not run: plotSurface(data_path = "path")
```

---

remove_experiment_data	<i>Remove Data from Experiment File</i>
------------------------	---

---

**Description**

Removes the data object of interest from the experiment according to a data\_id. Removing the data with data\_id = 12 removes the 12th dataset added to the experiment.

**Usage**

```
remove_experiment_data(experiment, data_id)
```

**Arguments**

experiment	The experiment object
data_id	The number of the data file to be removed

**Value**

The experiment file, with the rejected call data removed.

**Examples**

```
## Not run: experiment <- remove_experiment_data(experiment = experiment_object, data_id = 12)
```

---

save_experiment	<i>Save Experiment Locally</i>
-----------------	--------------------------------

---

**Description**

Saves the experiment as an .RData file in a specified location.

**Usage**

```
save_experiment(experiment, save_path)
```

**Arguments**

experiment	The experiment object to be saved
save_path	The full path where the experiment object will be saved locally

**Value**

The experiment object, saved as "[NAME\_OF\_EXPERIMENT] ([SAVE\_DATE]).RData" to the specified location.

**Examples**

```
## Not run: save_experiment(experiment = experiment_object, save_path = tempdir())
```

score\_timepoint\_data *Score Timepoint Data*

---

### Description

Transforms data into a list of mean, standard deviation, and range of several call metrics.

### Usage

```
score_timepoint_data(data_subset, group, animal, id, experimenter)
```

### Arguments

data_subset	The object created in 'add_timepoint_data()' which will be scored
group	The experimental group (i.e. "Control") these data correspond to
animal	The animal or animal group ID for these data
id	The full name of the experiment, including the extension.
experimenter	The experimenter who recorded these results

### Value

A list object containing statistics and metadata for each file.

### Examples

```
## Not run: score_timepoint_data(  
  data_subset = my_subsetted_data, group = "Control",  
  experimenter = "Experimenter 1", animal = "4207", id = "Data_sheet.xlsx"  
)  
## End(Not run)
```

---

semisqueakRpipeline *Semi-Automatic Experiment Creation*

---

### Description

A pipeline function which creates a new experiment object and adds data by prompting the user for metadata (for every file that is added).

### Usage

```
semisqueakRpipeline()
```

**Value**

An object containing the full experiment with all data added.

**Examples**

```
## Not run: expt <- semisqueakRpipeline()
```

---

squeakrANOVA

*Generate ANOVA tables for Detected Calls*

---

**Description**

Aggregates raw data tables for all data added to experiment object, and calculates and displays ANOVA statistics.

**Usage**

```
squeakrANOVA(experiment, analysis_factor)
```

**Arguments**

experiment      The experiment object  
analysis\_factor      A string representing the factor to analyze between groups

**Value**

A table comparing the analysis\_factor between groups

**Examples**

```
## Not run: squeakrANOVA(experiment = experiment, analysis_factor = "Delta_Freq")
```

squeakRDashboard      *Launch SqueakR Dashboard*

---

**Description**

Run the SqueakR Shiny Dashboard locally to interface with experimental data.

**Usage**

```
squeakRDashboard()
```

**Value**

A Shiny Dashboard

**Examples**

```
## Not run: squeakRDashboard()
```

---

squeakrSummary      *Summary Statistics for Experiment*

---

**Description**

Aggregates raw data for experiment and summarizes descriptive statistics of the current results, grouped by experimental groups.

**Usage**

```
squeakrSummary(experiment)
```

**Arguments**

experiment      The experiment object

**Value**

Text which summarizes experiment data split by group

**Examples**

```
## Not run: squeakrSTATS(experiment = experiment)
```



---

unblind_all_ids	<i>Decode Experiment IDs</i>
-----------------	------------------------------

---

**Description**

Creates a vector of the original call file names, indexed by the order they are listed in the experiment. This allows experimenters to unblind themselves to the data they collect

**Usage**

```
unblind_all_ids(experiment)
```

**Arguments**

experiment	The experiment object
------------	-----------------------

**Value**

A vector representing the original call file names

**Examples**

```
## Not run: decode_experiment_ids(experiment)
```

---

unblind_data_id	<i>Find Matching Experiment ID</i>
-----------------	------------------------------------

---

**Description**

Finds the index of a dataset matching a supplied file name in the experiment.

**Usage**

```
unblind_data_id(experiment, filename)
```

**Arguments**

experiment	The experiment object
filename	The full name of the file, including the extension

**Value**

A number or numbers representing index or indices where that file appears in the experiment

**Examples**

```
## Not run: unblind_data_id(experiment, "my_data1.xlsx")
```

---

unblind_data_name	<i>Find Matching Experiment Name</i>
-------------------	--------------------------------------

---

**Description**

Finds the name of a dataset matching a supplied index in the set of data

**Usage**

```
unblind_data_name(experiment, id)
```

**Arguments**

experiment	The experiment object
id	The dataset number to be unblinded

**Value**

The name of the original file, corresponding to the data at the requested index

**Examples**

```
## Not run: unblind_data_name(experiment, 2)
```

---

update_experiment	<i>Updates Experiment Object Metadata</i>
-------------------	---

---

**Description**

Auto-populates ‘groups’, ‘experimenters’, and ‘animals’ fields in experiment object by checking experimental data (within the experiment object) for new data.

**Usage**

```
update_experiment(experiment)
```

**Arguments**

experiment	The experiment object
------------	-----------------------

**Value**

A list object containing statistics and metadata for the entire experiment. The ‘groups’, ‘experimenters’, and ‘animals’ fields will auto-populate based on added data using the ‘update\_experiment()’ function.

*update\_experiment*

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### **Examples**

```
## Not run: update_experiment(experiment)
```

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