

# Package: qgshiny (via r-universe)

August 25, 2024

**Title** A 'shiny' Application for Active Learning Instruction in Introductory Quantitative Genetics

**Version** 0.1.0

**Description** A 'shiny' application for teaching introductory quantitative genetics and plant breeding through interactive simulations. The application relies on established plant breeding and quantitative genetic theory found in Falconer and Mackay (1996, ISBN:0582243025) and Bernardo (2010, ISBN:978-0972072427).

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.0

**Depends** R (>= 3.5.0)

**Imports** stats, shiny, rmarkdown

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

**RemoteUrl** <https://github.com/neyhartj/qgshiny>

**RemoteRef** HEAD

**RemoteSha** 469a581b39f0c731d915a7a6965e8ecd90c76f61

## Contents

run_qgshiny . . . . .	2
-----------------------	---

<b>Index</b>	3
--------------	---

---

`run_qgshiny`

---

*Run the application*

---

## Description

Runs the 'shiny' application interactively.

## Usage

```
run_qgshiny(display.mode = c("normal", "showcase"))
```

## Arguments

`display.mode` The mode in which to display the application. If "showcase", application code is displayed along with the output. If "normal" (default), the code is hidden.

## Examples

```
if (interactive()) {  
  run_qgshiny()  
}
```

# Index

`run_qgshiny`, [2](#)