



MRC  
Biostatistics  
Unit



UNIVERSITY OF  
CAMBRIDGE

# Creating user-friendly documentation to support software development

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# Who is a statistical programmer?

## Key Responsibilities

- Writing efficient and reproducible R scripts.
- Developing and maintaining packages.
- Collaboration (Working closely with biostatisticians, researchers).
- Creating ShinyApps to present results.
- Knowledge Dissemination (Sharing findings through presentations, publications, and workshops).

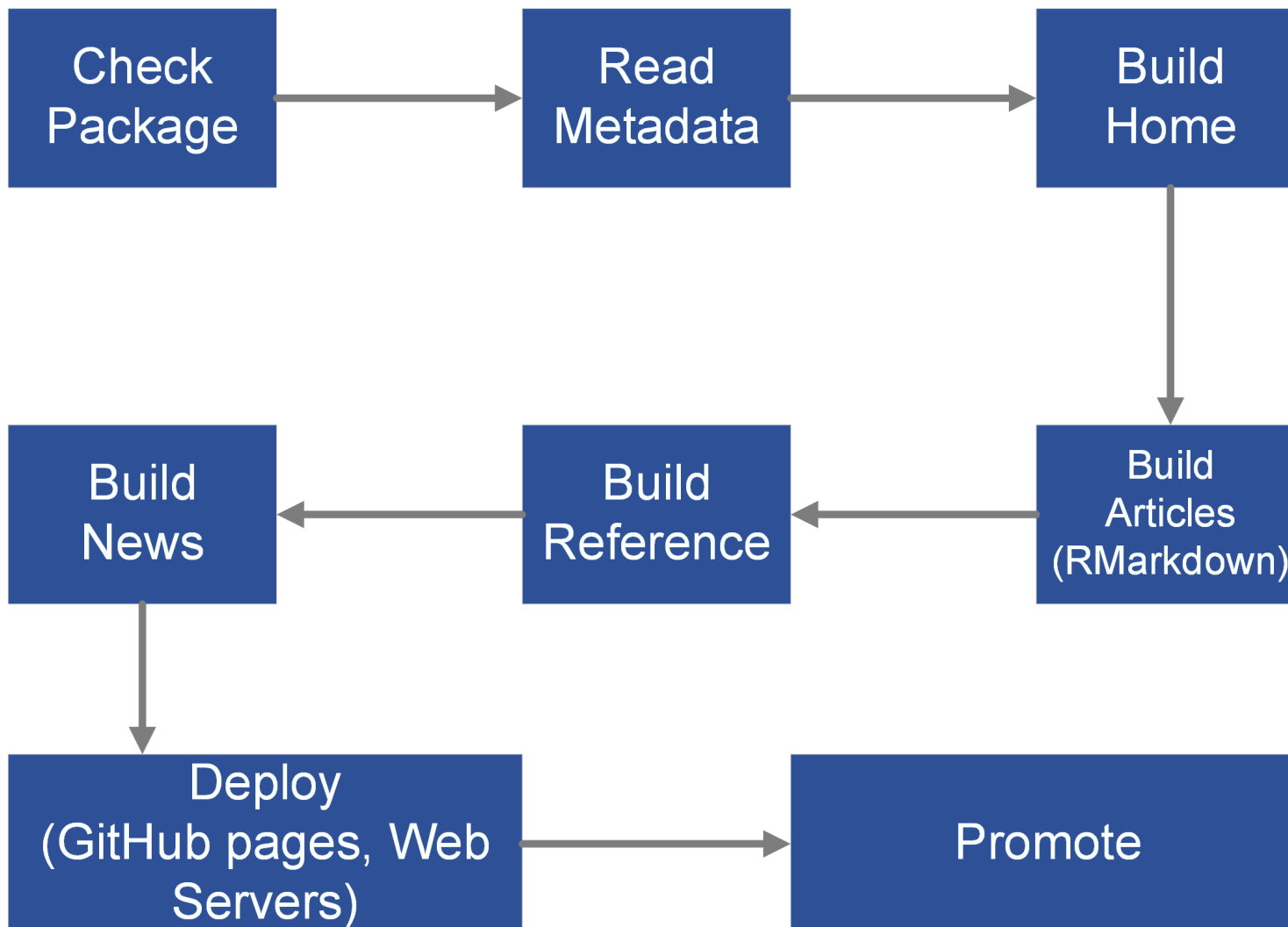
# Goals

- Current development [bringing new functionality](#).
- Create web-documentation [using pkgdown](#).
- New approach [in mastering MAMS R package for end-users](#).

# pkgdown

The **pkgdown** generates a static website from an R package's documentation, making it easier to share and navigate the package's information and resources.

**pkgdown** logic:



# MAMS package documentation

## Details

Currently implemented functions are:

- **`mams()`** : a function allowing to design multi-arm multi-stage studies with normal endpoints,
- **`new.bounds()`** : a function allowing to update the lower and upper boundaries of a multi-arm multi-stage study, typically initially defined by `mams()` , based on observed sample sizes,
- **`mams.sim()`** : a function allowing to simulate multi-arm multi-stage studies given chosen boundaries and sample size, and estimates power and expected sample size,
- **`stepdown.mams()`** : a function allowing to find stopping boundaries for a 2- or 3-stage (stepdown) multiple-comparisons-with-control test,
- **`stepdown.update()`** : a function allowing to update the stopping boundaries of a multi-arm multi-stage study, typically initially defined by `stepdown.mams()` , at an interim analysis as well as allowing for unplanned treatment selection and/or sample-size reassessment,
- **`ordinal.mams()`** : a function allowing to design multi-arm multi-stage studies with ordinal or binary endpoints,
- **`tite.mams()`** : a function allowing to design multi-arm multi-stage studies with time-to-event endpoints.

We refer to Jaki et al (2019) for an overview of the package as well as to Magirr et al (2012) and Magirr et al (2014) for theoretical details.

Dominic Magin

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Philip Pallmann

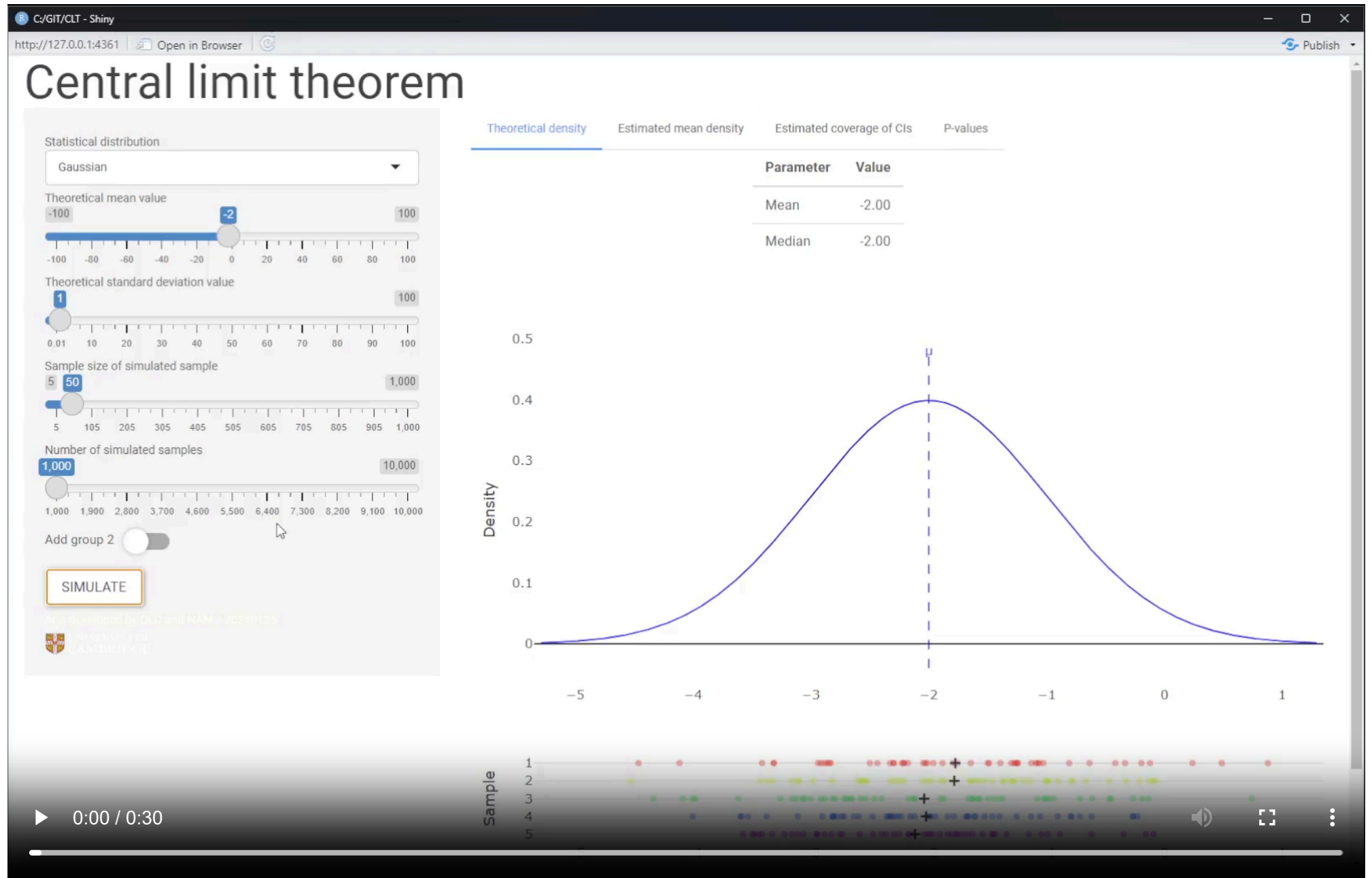
Author

## Dev status

CRAN 2.0.2

downloads 587/month

# Plotly



# webR

▶ Run Code



```
1 a <- rnorm(50)
2 a
```





# About webR

WebR is a version of [R interpreter](#)

WebR's core is based around compiling the open-source R interpreter for [WebAssembly](#)

WebAssembly is a type of code that [can be run in modern web browsers](#) — it is a low-level assembly-like language.

WebAssembly provides [a way to run code on the web](#) with client apps running on the web [that previously couldn't have done so](#).

# webR pros and limitations

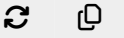
## Pros

- In-browser **near-native** execution speed
- We **don't need** to install R.
- We **don't need** to setup a server.

## Limitations

- Not all packages available **yet**
- Single **core** computations
- Limited local files **access**

# MAMS webR example

[▶ Run Code](#)

```
1 library(MAMS)
2 set.seed(2910)
3 m1 <- mams(K = 3, J = 1, p = 0.65, p0 = 0.55, r = 1, r0 = 1,
4           alpha = 0.05, power = 0.9)
```

# Documentation with embedded webR

# MAMS



## Designing multi-arm multi stage studies

This package allows to design multi-arm multi-stage (MAMS) studies with asymptotically normal endpoints and known variance. It considers normal, binary, ordinal and time-to-event endpoints in which either the single best treatment or all promising treatments are continued at the interim analyses.

## Installation

You can install the latest released version from [CRAN](#) from within R:

```
install.packages("MAMS")
```

## Details

Currently implemented functions are:

- `mams()` : a function allowing to design multi-arm multi-stage studies with normal endpoints,
- `new.bounds()` : a function allowing to update the lower and upper boundaries of a multi-arm multi-stage study, typically initially defined by `mams()`, based on observed sample

### Links

[View on CRAN](#)

### License

[GPL-2](#)

### Citation

[Citing MAMS](#)

### Developers


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### Dev status

CRAN **2.0.2**



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# Questions?