

# tPRiors: Bayesian prevalence estimation with elicited priors

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# Expectations

[www.menti.com](https://www.menti.com), code: 8722 4275

- 1 Accessible to non-statisticians / field experts
- 2 Spread true prevalence estimation concept
- 3 Collection of methods + additional analyses

- 1 Accessible to non-statisticians / field experts
- 2 Spread true prevalence estimation concept
- 3 Collection of methods + additional analyses
- 4 Personal: Learn GUI, Shiny, Rshiny, tcl-tk
- 5 Rstudio shiny contest 2021 [Check if interested]
- 6 Manuscript : |tPRiors|

# What's included?

- 8 distinct prevalence models included
- 5 ways to elicit priors (powered by priorGen [Kostoulas 2019])
- 20 modelling set-ups
- $\infty$  modelling strategies
- Single/Multiple populations - Apparent/True prevalence - No zero/Zero prior prevalence - Informative/ Non Informative

**Fast** Clone/Download repository and click Run App through the global.R script  
[github.com/kpatera/tPRiors](https://github.com/kpatera/tPRiors)

**Easy** Through the web - application

- `publicintegratedhealth.shinyapps.io/tPRiors`
- `publicandonehealth.shinyapps.io/tPRiors`
- `kpateras.shinyapps.io/tPRiors`

Chapter 0 -  
PrologueChapter 1 -  
Warming up  
(tPRiors -  
overview)Chapter 2 -  
tPRiors  
specifics -  
Single  
populationChapter 3 -  
tPRiors  
specifics -  
Multiple  
populations

## Epilogue

[Start](#) [Set up](#) [Prior\(s\)](#) [Input & Output](#) [Report](#) [Acks](#)

## Bayesian true prevalence inference via elicited priors

| tPRiors |



Below the user can find a brief description of the shiny application functions and options.

- (a) In tab (Set up) the user following questions can fix the parameters of the analysis (Choose model, priors, special characteristics)
- (b) In tab (Priors) the user can elicitate the prior distribution(s) with the aid of sliders and visual confirmation
- (c) In tab (Model) the user inputs the observed data and Jags sampling characteristics. A basic inference plot is presented. For multiple population the model may take some time to run.
- (d) In tab (Report) the program returns a dynamic output that changes based on (a), (b) and (c).
- (e) In tab (Acks) acknowledgments and useful links can be found.

Settings may still be changed even after a tab has been fixed by the user. Though, we advise users to perform a 'Reset' of [tPRiors] when they want to change a previously fixed setting.

The development of tPRiors was funded by H2020 project unCoVer:Unravelling Data for Rapid Evidence-Based Response. More details can be found in the manuscript, K Pateras and P Kostoulas, tPRiors: An R Shiny tool for generating prior and producing posterior distributions for disease prevalence

4

prior elicitation approaches



8

prevalence model variations



3

preloaded datasets for demonstration



## Set-up page

Start **Set up** Prior(s) Input & Output Report Ack

**Do you have single or multiple populations/clusters**

☐ Single ☒ Multiple

**Do you want to model the true or the apparent prevalence?**

☒ True prevalence ☐ Apparent prevalence

**Do you want to account for zero true prevalence?**

☒ No ☐ Yes

**Would you specify informative priors?**


☒ Yes ☐ No

If No, then the apparent prevalence will be modelled

**Which measure of central tendency or dispersion would you like to use for the true prevalence prior?**

☒ Mean

Reset tPRiors Fix setup!

**Status: 'Not set'**  
Please first select options and press -Fix-



## Prior page

Start

Set up

Prior(s)

Input & Output

Report

Acks

Prevalence

Sensitivity

Specificity

Set a prevalence prior

Specify your prior belief about the Mean True prevalence :

0

0.1

0.2

0.3

0.4

0.5

0.6

0.7

0.8

0.9

1

Is the percentile the upper limit of the Mean ?

☐ Yes ☒ No

Specify the upper or lower limit for the Mean at the specified level of confidence:

0

0.1

0.2

0.3

0.4

0.5

0.6

0.7

0.8

0.9

1

Specify the level of confidence that the true value of the Mean is greater or lower than the percentile value:

0

0.1

0.2

0.3

0.4

0.5

0.6

0.7

0.8

0.9

0.95

1

Caution! Press 'set priors' only when all values are set.

In case 1 slider gets stuck, select 'Patch', wait and select 'Fixed' to continue

☒ Fixed ☐ Patch

Reset tPriors

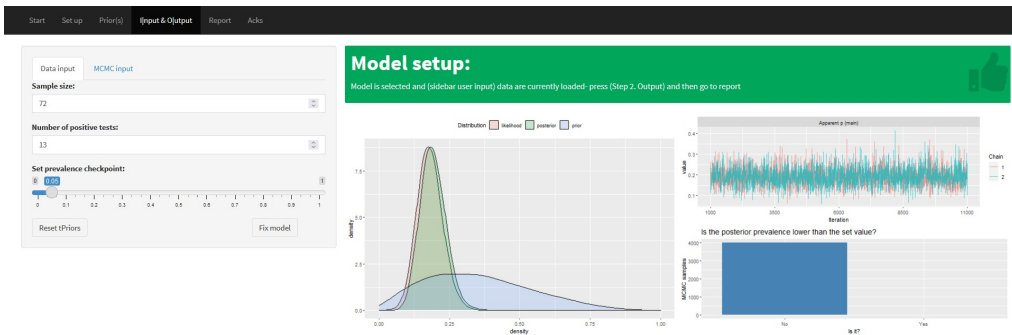
Example

Set prior(s)!

Prior setup:

Setup done - Please elicit a prior and press select

## Input & Output page





## Status report:

The report will become available below



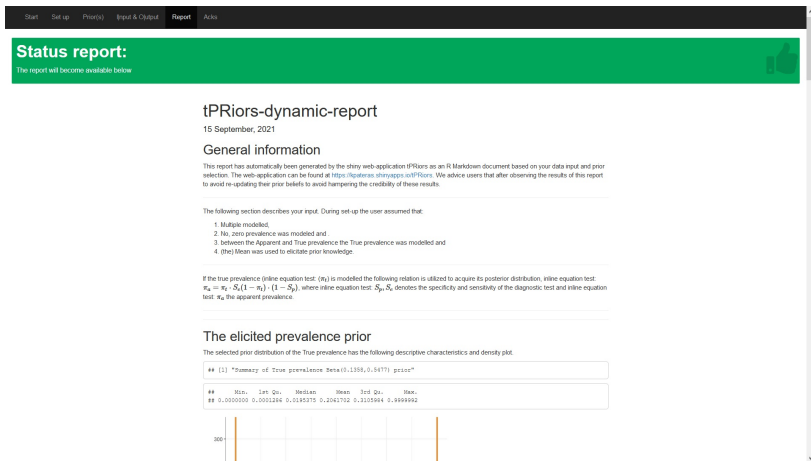
Input

Model

Output



Download data



[Start](#) [Set up](#) [Prior\(s\)](#) [Input & Output](#) [Report](#) [Acks](#)

tPRiors was created using Shiny, JAGS and PriorGen to implement the full hierarchical model for prevalence estimation. tPRiors is powered by the following R packages:

ggplot2

plotly

gridExtra

grid

tidyr

DT

shiny

shinythemes

shinydashboard

shinyjs

shinyWidgets

rmarkdown

R2jags

ggmcmc

PriorGen

# Single population (30-60')

- Prevalence of a moderate adverse event (fatigue) of a vaccine.
- Observed 50 events in a sample of 1000.
- Prior information:
  - 1 A publication stated that average risk for fatigue is low.
  - 2 Experts report that fatigue is observed with very high sensitivity but moderate specificity.
- Fill — > [www.menti.com 5163 1177](https://www.menti.com/51631177)

The screenshot shows the 'Set-up' page of the tPRiors application. The page has a dark header with navigation links: 'Start', 'Set-up', 'Prior', 'Prior & Likelihood', 'Report', and 'Help'. The main content area is divided into two columns. The left column contains four configuration questions, each with radio button options. The right column features a green status box with a checkmark icon.

**Do you have single or multiple populations/batches?**  
☒ Single ☐ Multiple

**Do you want to model the true or the apparent prevalence?**  
☒ True prevalence ☐ Apparent prevalence

**Do you want to account for zero true prevalence?**  
☒ No ☐ Yes

**Would you specify informative priors?**  
☒ Yes ☐ No  
Please, first the apparent prevalence will be modelled

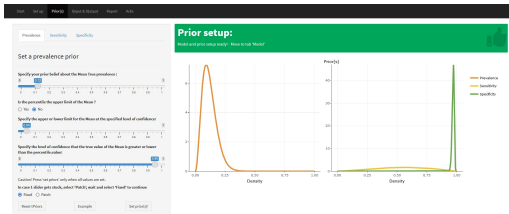
**Which measure of central tendency or dispersion would you like to use for the true prevalence prior?**  
☒ Mean ☐ Median ☐ Mode ☐ Percentile

Buttons at the bottom: 'Next (Priors)' and 'Exit (Help)'.

**Status: 'Set'**  
Your prior assumptions that 1. Single will be modelled, 2. No, zero prevalence will be modelled, 3. No True prevalence will be modelled and 4. No informative priors will be modelled.

- 1 Single - True - No zero - Informative - Mean.
- 2 If Apparent ( $Se=Sp=1$ ), if also Non-informative, then 3 prior prevalence choices available.
- 3 Currently, selected measure applies to all priors.

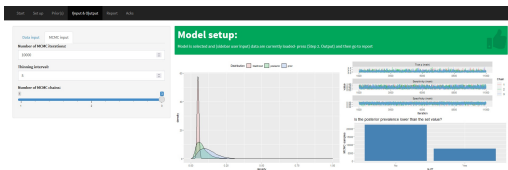
## Prior page



- 1 Does not currently support raw hyper-parameter values
- 2 Some prior specifications can be non-appropriate
- 3 Caution! If "Set" is selected, change values slowly to avoid technical errors. Use the fix if needed or reset.



## Input &amp; Output page



- 1 Messing with MCMC input should not change inference.
- 2 Change input data to check the dynamics of posterior, prior, likelihood.

## Further analyses

- 1 Check ESS, diagnostics, extra plots,
- 2 Check models, input data, output data
- 3 Use ggmmcmc for clearer diagnostic plots

# Multiple populations (30-60')

- Check manuscript Pateras & Kostoulas 2022 (|tPRiors|)
- Replicate the multiple population results via the Dementia\_updated.xls dataset.

- Tips
  - Set-up: Multiple - True - NonZero - Informative
  - Priors: Conditions applied, caution how to set values
  - I&O : Necessary step to check 'Step 2. Output' before moving to report!
- Exercise goals
  - ... to produce the posterior study-level boxplot.
  - ... to save all information for reproducibility.
  - ... to re-produce the posterior study-level boxplot of your peer.

- Pateras, K. and Kostoulas, P. |tPRiors|: a tool for prior elicitation and obtaining posterior distributions of true disease prevalence. BMC Med Res Methodol 22, 91 (2022).
- Bagipulo et al. A Systematic Review and Meta-Analysis on the Prevalence of Dementia in Europe (2018)
- Kostoulas P. priorGen, R package (2019)