

tPRiors: Bayesian prevalence estimation with elicited priors

Konstantinos Pateras

1. University of Thessaly, Department of Public and One Health
2. University of Utrecht, Department of Biostatistics and Data Science

kostas.pateras@gmail.com
www.kpateras.eu

September 1, 2022

Expectations

www.menti.com, code: 8378 1377

Chapter 0 -
Prologue

Chapter 1 -
Warming up
(tPRiors -
overview)

Chapter 2 -
tPRiors
specifics -
Single
population

Chapter 3 -
tPRiors
specifics -
Multiple
populations

Epilogue

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

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

Epilogue

- 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?

Chapter 0 - Prologue

Chapter 1 - Warming up (tPRiors - overview)

Chapter 2 - tPRiors specifics - Single population

Chapter 3 - tPRiors specifics - Multiple populations

Epilogue

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

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

Epilogue

Fast Clone/Download repository and click Run App through the global.R script github.com/kpatera/tPRiors

Easy Through the web - application


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

Starting page

[Start](#)
[Set up](#)
[Priors](#)
[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 Responses. 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) Export & Output Report Help

Status: 'Not set'

Please first select options and press 'Fix'

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!

Prior page

Start
Set up
Prior(s)
Report & Output
Report
About

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 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

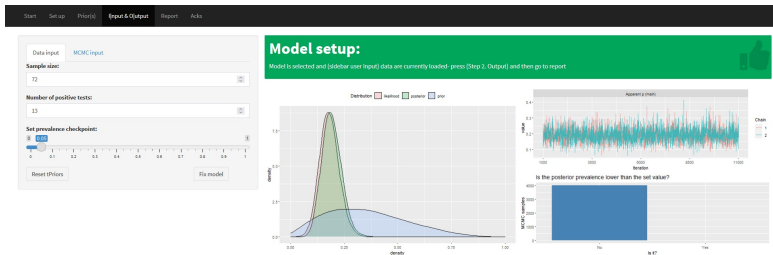
Reset tPriors Example Set prior(s)?

Prior setup:

Setup done - Please click a prior and press select



Input & Output page



Report page


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

Status report:
The report will become available below

Input

Model


Output

 Download data

Calculation in progress. This may take a while...

Report page

Start
Set up
Priors
Input & Output
Report
Notes

Status report:
The report will become available below


tPRiors-dynamic-report

15 September, 2021

General information

This report has automatically been generated by the shiny web-application tPRiors as an R Markdown document based on your data input and prior selection. The web-application can be found at <https://konstantinos.shinyapps.io/tPRiors/>. We advice users that after observing the results of this report to avoid re-updating their prior beliefs to avoid hampering the credibility of these results.

The following section describes your input. During set-up the user assumed that:

1. Multiple modelled.
2. No zero prevalence was modeled and.
3. between the Apparent and True prevalence the True prevalence was modelled and
4. (the) Mean was used to elicitate prior knowledge.


If the true prevalence (inline equation test: π_x) is modelled the following relation is utilized to acquire its posterior distribution, inline equation test: $\pi_x = \pi_y - S_p(1 - \pi_y) - (1 - S_p)$, where inline equation test: S_p, S_e denotes the specificity and sensibility of the diagnostic test and inline equation test: π_y the apparent prevalence.

The elicited prevalence prior

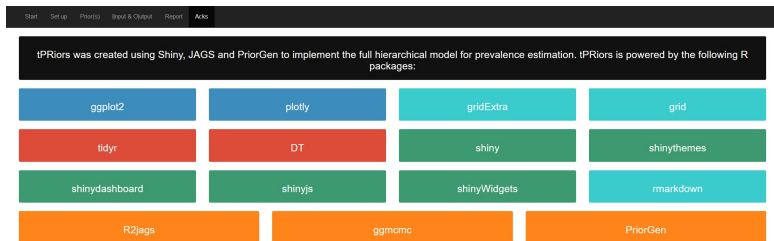
The selected prior distribution of the True prevalence has the following descriptive characteristics and density plot.

```
## [1] "Summary of True prevalence Beta(0.1350,0.5477) prior"
```

##	Min.	1st Q.	Median	Mean	2nd Q.	Max.
##	0.0000000	0.0001284	0.195375	0.2042702	0.3195994	0.9999992



Acks page



Single population (30-60')

Chapter 0 -
Prologue

Chapter 1 -
Warming up
(tPRiors -
overview)

Chapter 2 -
tPRiors
specifics -
Single
population

Chapter 3 -
tPRiors
specifics -
Multiple
populations

Epilogue

- 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.

Set-up page

Set up | Prior D. Input | Report | Help

Do you have single or multiple population(s) 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

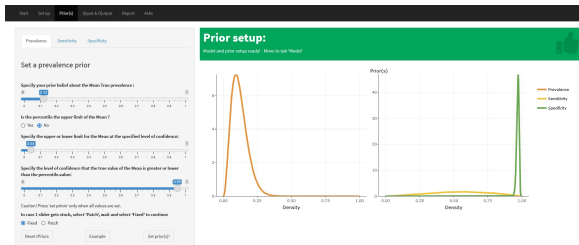
Would you specify information priors?
☒ Yes ☐ No
 If No, then the apparent prevalence will be modelled.

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

Status: 'Set'
 Your input assumes that: 1. Single will be modelled, 2. No, zero prevalence will be modelled, 3. the True prevalence will be modelled and 4. No informative prior(s) will be modelled.

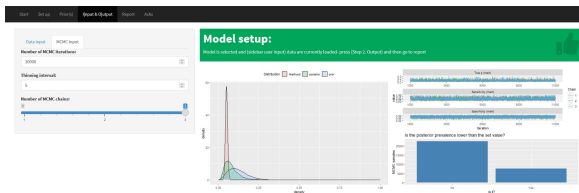
- 1 Single - True - No zero - Informative - Mean.
- 2 If Apparent ($Se=Sp=1$), if also Non-informative, then 3 prior prevalence choices available.
- 3 Currently, selected measure applies to all priors.

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 & 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

Chapter 0 -
Prologue

Chapter 1 -
Warming up
(tPRiors -
overview)

Chapter 2 -
tPRiors
specifics -
Single
population

Chapter 3 -
tPRiors
specifics -
Multiple
populations

Epilogue

- 1 Check ESS, diagnostics, extra plots,
- 2 Check models, input data, output data
- 3 Use ggmmcmc for clearer diagnostic plots
- 4 [www.menti.com 3855 2899](https://www.menti.com/join/38552899)

Multiple populations (30-60')

Chapter 0 -
Prologue

Chapter 1 -
Warming up
(tPRiors -
overview)

Chapter 2 -
tPRiors
specifics -
Single
population

Chapter 3 -
tPRiors
specifics -
Multiple
populations

Epilogue

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

- Tips

- 1 Set-up: Multiple - True - NonZero - Informative
- 2 Priors: Conditions applied, caution how to set values
- 3 I&O : Necessary step to check 'Step 2. Output' before moving to report!

- 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.

Bibliography

Chapter 0 -
Prologue

Chapter 1 -
Warming up
(tPRiors -
overview)

Chapter 2 -
tPRiors
specifics -
Single
population

Chapter 3 -
tPRiors
specifics -
Multiple
populations

Epilogue

- 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)