Chapter 0 Prologue

Chapter 1 -Warming up (tPRiors overview)

tPRiors specifics -Single population

Chapter 3 tPRiors specifics -Multiple

Epilogue

tPRiors: Bayesian prevalence estimation with elicited priors

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Plans within and after training

1 www.menti.com, code: 7651 6327

Warming to (tPRiors overview)

Chapter 2 tPRiors specifics -Single population

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Enilogue

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

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- 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]

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- 1 Developed with R and Shiny
- 2 No heavy IT skills required
- 3 1st draft in 2-3 months

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tPRiors
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population

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- 1 Developed with R and Shiny
- 2 No heavy IT skills required
- 3 1st draft in 2-3 months
- 4 Increased learning curve on topic

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What's included?

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

How to work with tPRiors?

- Install with devtools
- Download repository and click Run App through the global.R script [Fastest]
- Use https://publicintegratedhealth.shinyapps.io/tPRiors

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Starting page



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 [876]oral when they seant to change a previously fixed setting.

The development of PNSox was funded by MXXXV project unCollection-welling Data for Rapid Evidence-Based Response, More details can be found in the manuscript, K Patents and P Kratzulas, PNSorc An R Shiny tool for generating prior and producing posterior distributions for disease prevalence





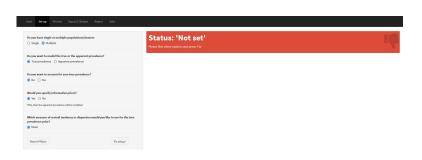


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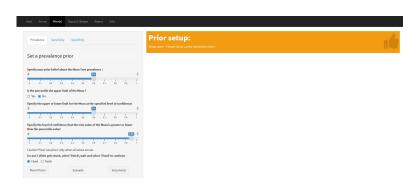
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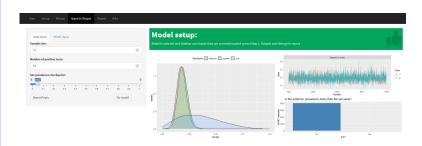
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E. 9.

Input & Output page



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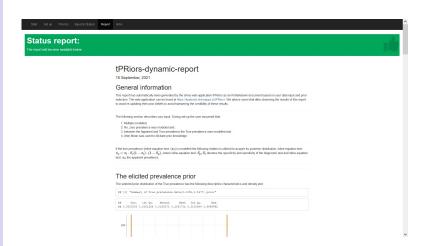
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Report page



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Chapter 3 tPRiors specifics -Multiple populations

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Single population toy-example

- Prevalence of a moderate adverse event (fatigue) of a vaccine.
- 2 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.

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



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- 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.

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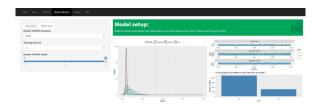
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Input & Output page



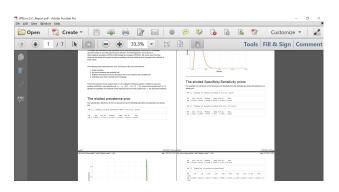
- 1 Meshing with MCMC input should not change inference.
- 2 Change input data to check the dynamics of posterior, prior, likelihood.

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1 Open "tPRiors_Ex1_Report.pdf", discuss

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Further analyses

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

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Exercise - Analysis and replication of results! (15-20')

- Check manuscript Perquin et al. 2008 GitHub/day3
- Calculate the posterior prevalence of dementia for 65+ participants
- Experts discuss that:
 - 1 the average risk for dementia is relatively low but depends on age range.
 - 2 Conducted test known to show high sensitivity and very high specificity.
 - 3 Work individually. Report posterior median and IQR of the true prevalence.

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 - 4 www.menti.com (1588 8807)

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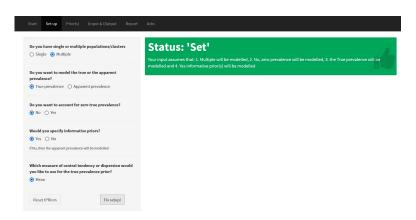
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Set-up page



- 1 Multiple True NonZero Informative
- 2 One elicitation measure, if non-informative is selected, $\psi \sim IG(0.1, 0.1)$.

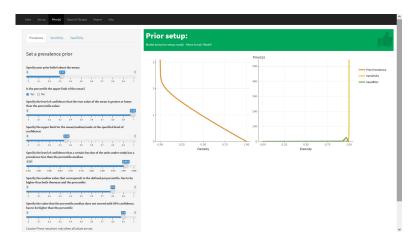


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- 1 Conditions applied, caution how to set values
- 2 If plotted, change one at a time, observe change (not suggested)



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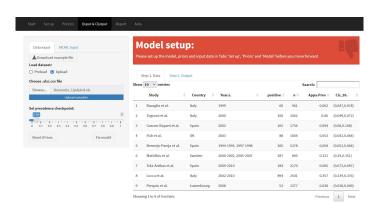
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Input & Output page



- 1 Load preselected data or upload .csv or .xls file. Must contain two columns named 1. positive and 2. n.
- 2 Download example file for a template.



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Input & Output page



- 1 Necessary step to check Step 2. Output before moving to report!
- 2 Diagnostics look cramped...



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Exercise - Analysis and replication of results! (15-20')

Download article Bacigalupo et al. 2018. Produce posterior box-plots for the study-specific prevalences of dementia using tPRiors and the multiple population models. Use similar SE and SP priors to previous example. 3 goals! Work in pairs but individually.

- Goal 1 is to produce the posterior study-level boxplot.
- Goal 2 is to save all information for reproducibility.
- Goal 3 is to re-produce the posterior study-level boxplot of your peer.

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Bibliography [1 more slide]

- Konstantinos Pateras, Polychronis Kostoulas. tPRiors: Bayesian prevalence estimation with elicited priors, Submitted
- Bagipulo et al. A Systematic Review and Meta-Analysis on the Prevalence of Dementia in Europe 2018
- Perguin et al and cognitive complaints in the context of high cognitive reserve: A population-based study. 2015
- Polychronis Kostoulas priorGen, R packages, 2019

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