tPRiors: Bayesian prevalence estimation with elicited priors

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September 1, 2022

Expectations

www.menti.com, code: 8378 1377

Why?

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

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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
- ∞ modelling strategies
- Single/Multiple populations - Apparent/True prevalence - No zero/Zero prior prevalence - Informative/ Non Informative

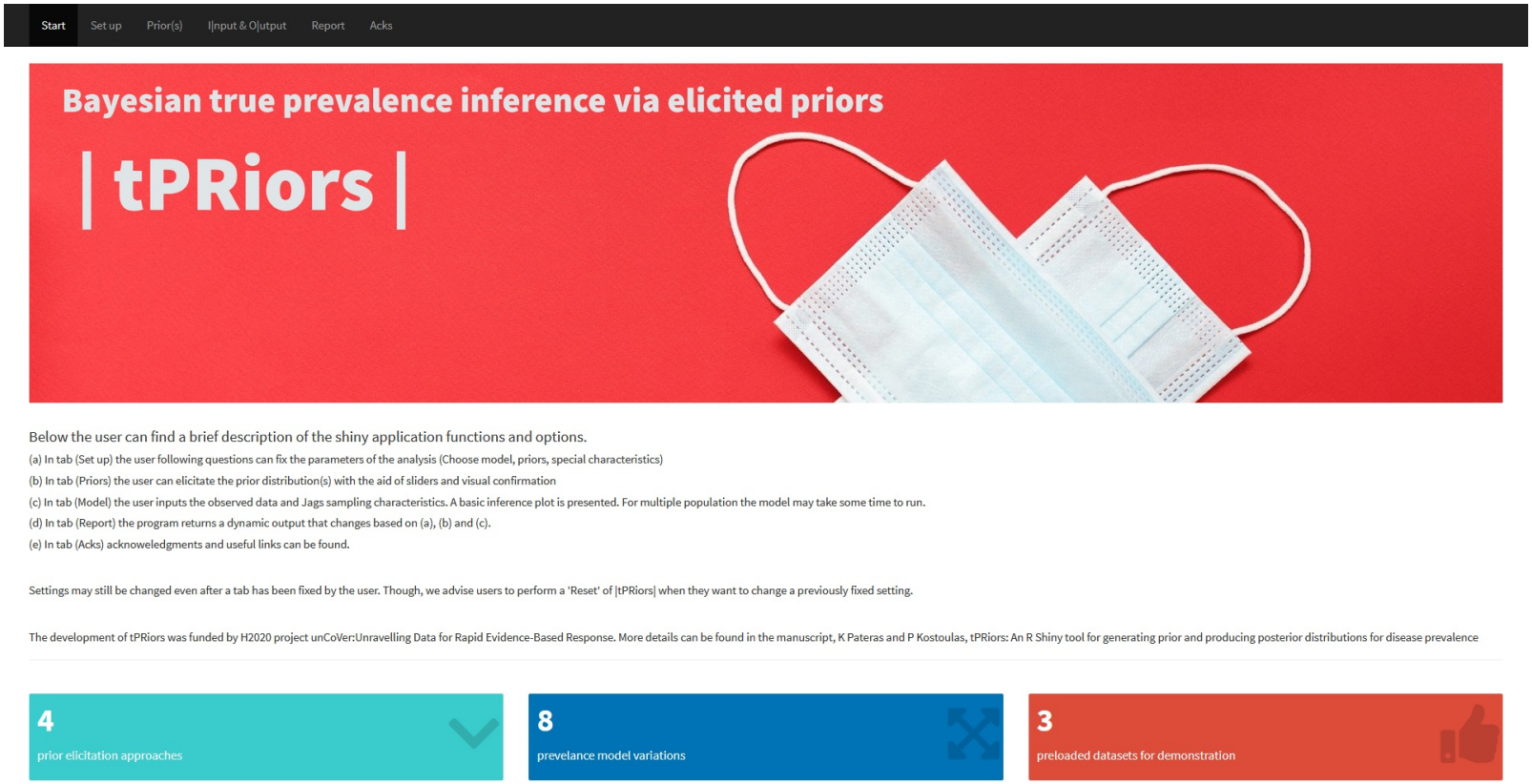
How?

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

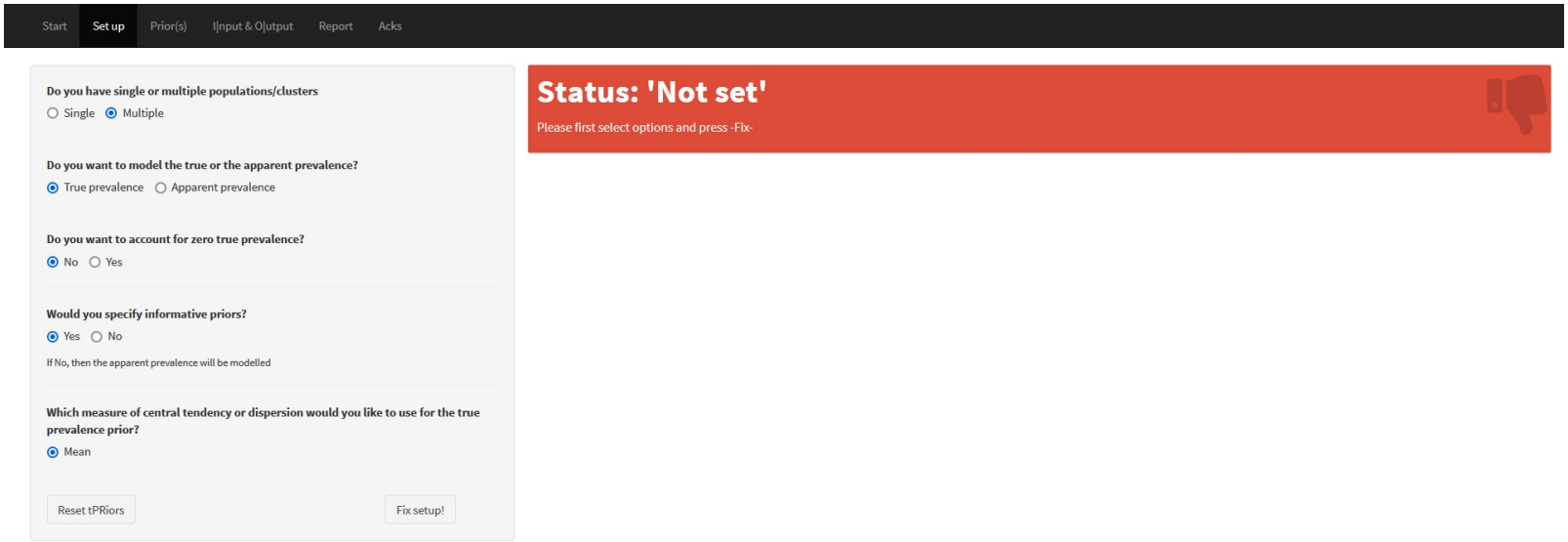
Easy Through the web - application

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

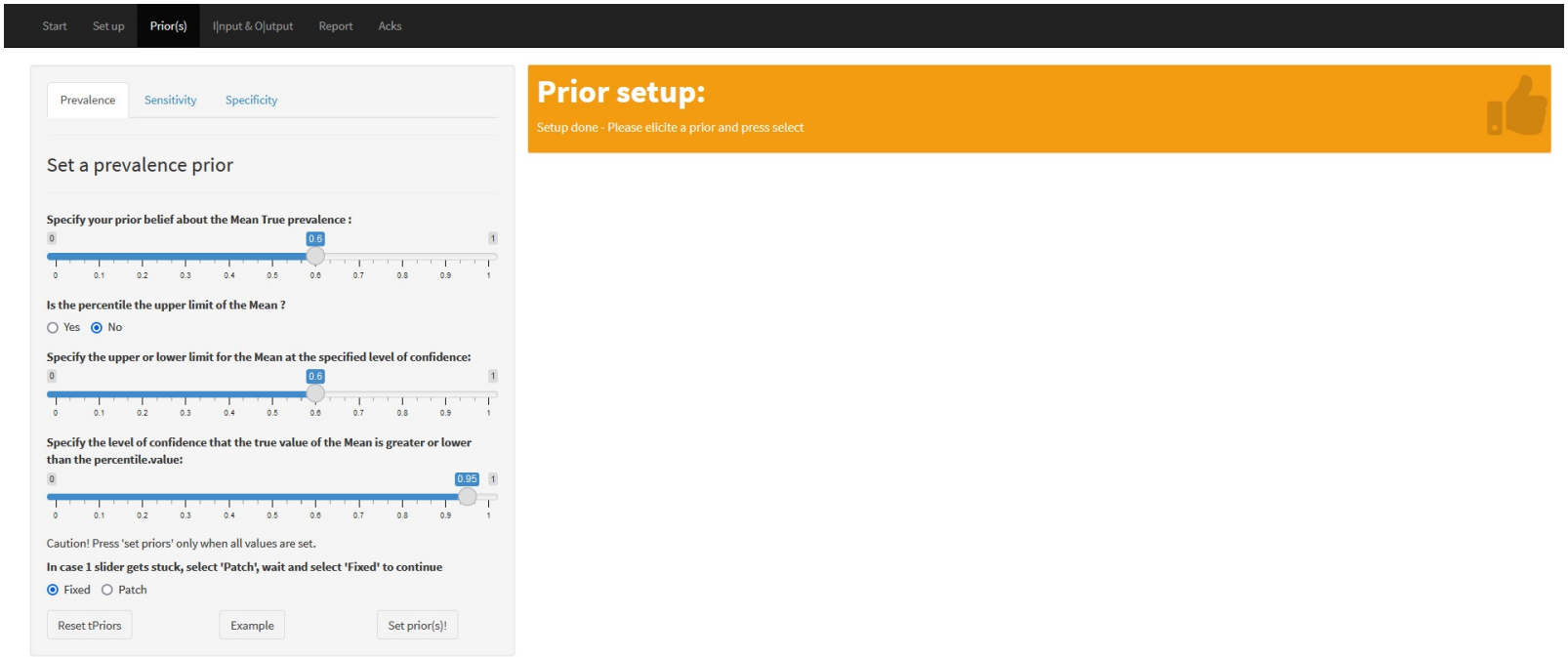
Starting page



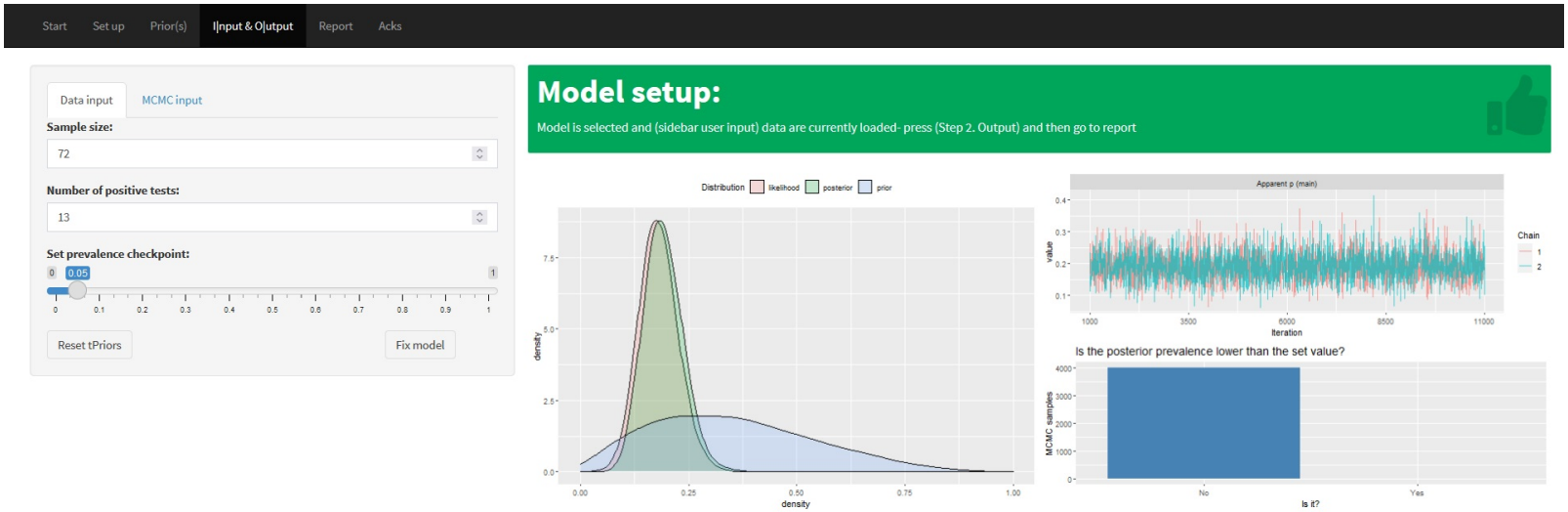
Set-up page



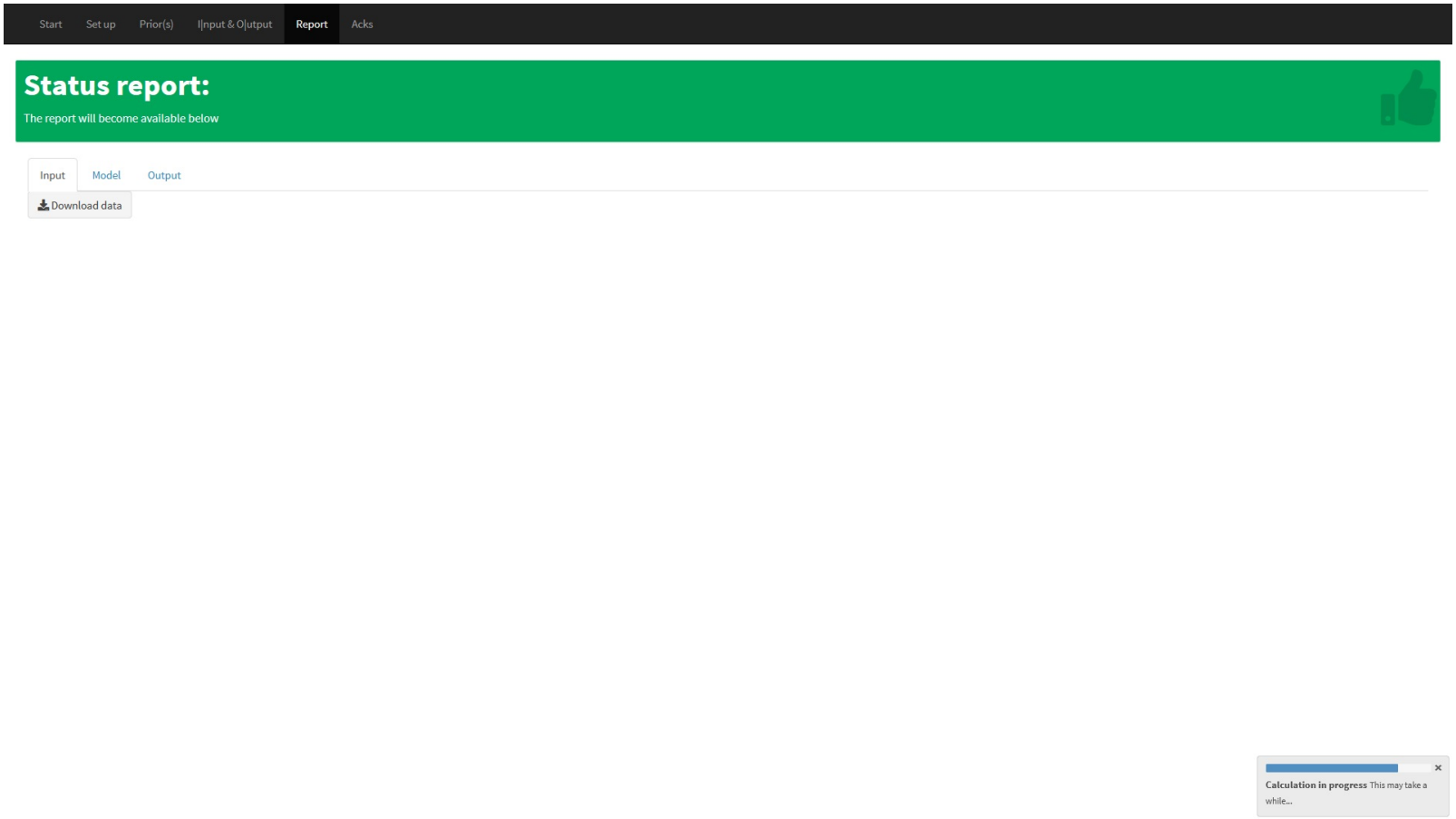
Prior page



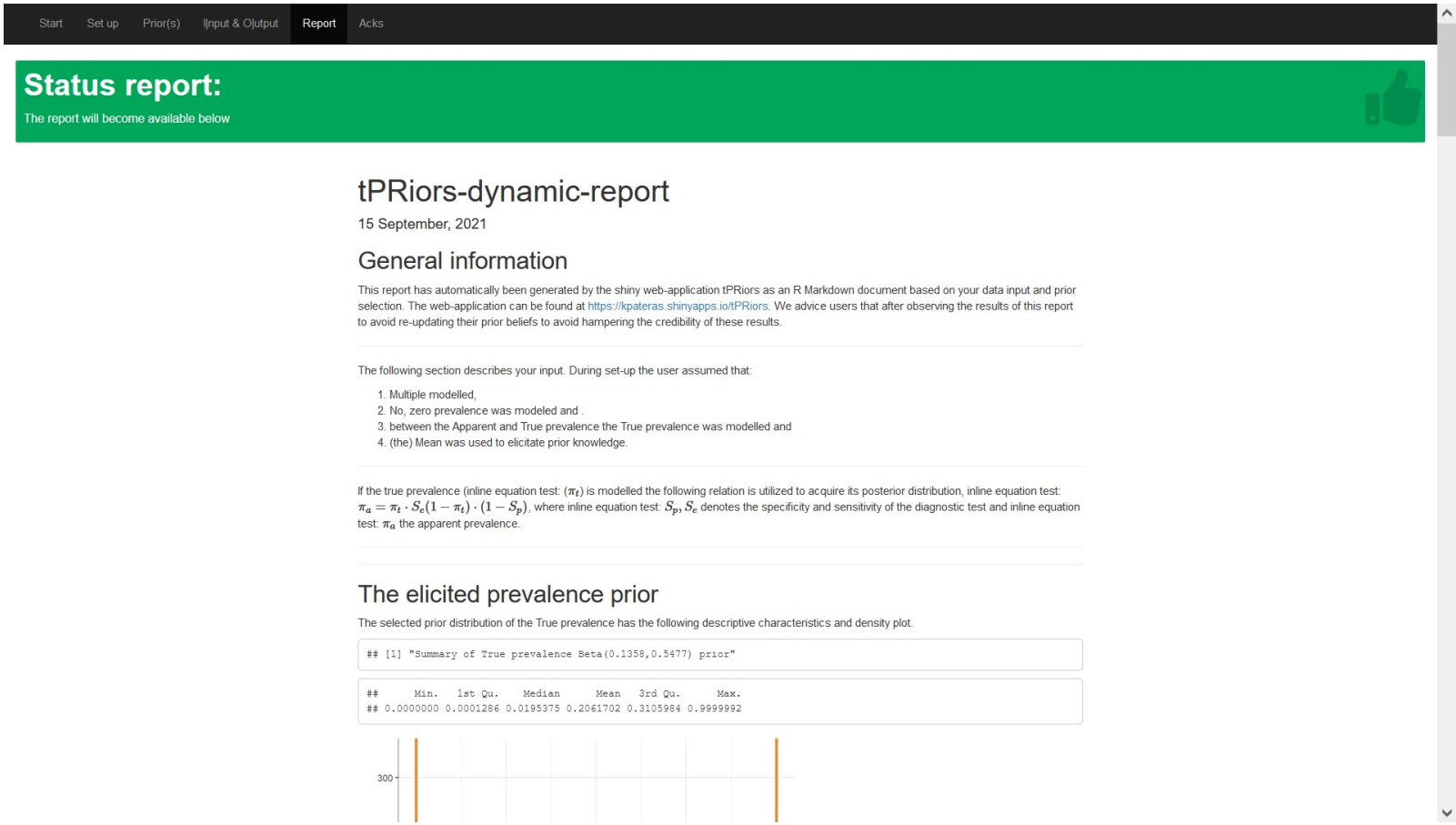
Input & Output page



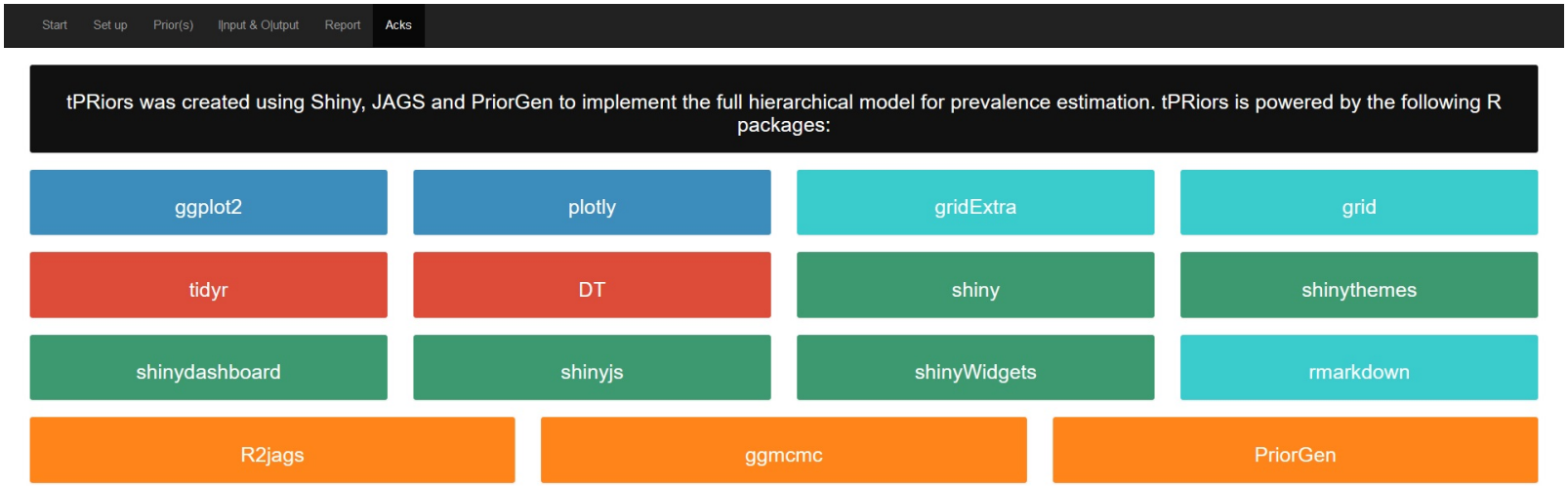
Report page



Report page



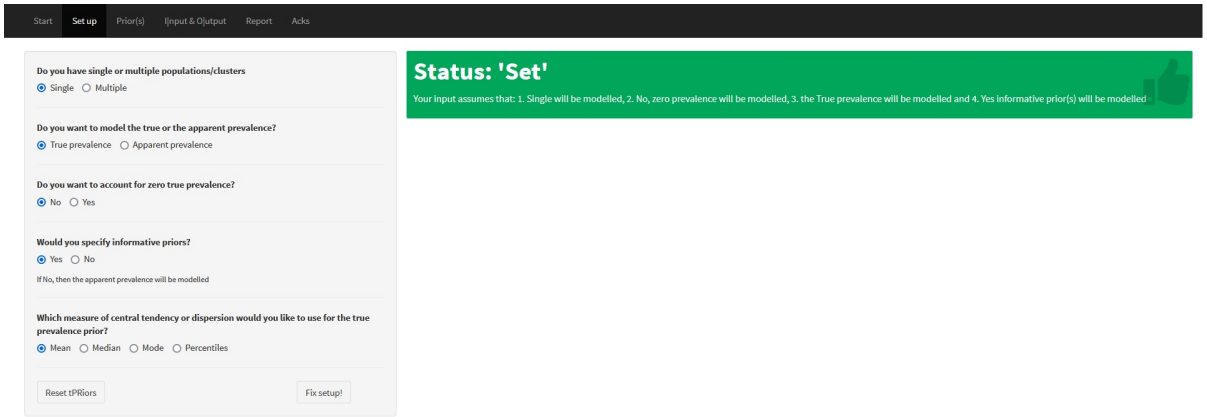
Acks page



Single population (30-60')

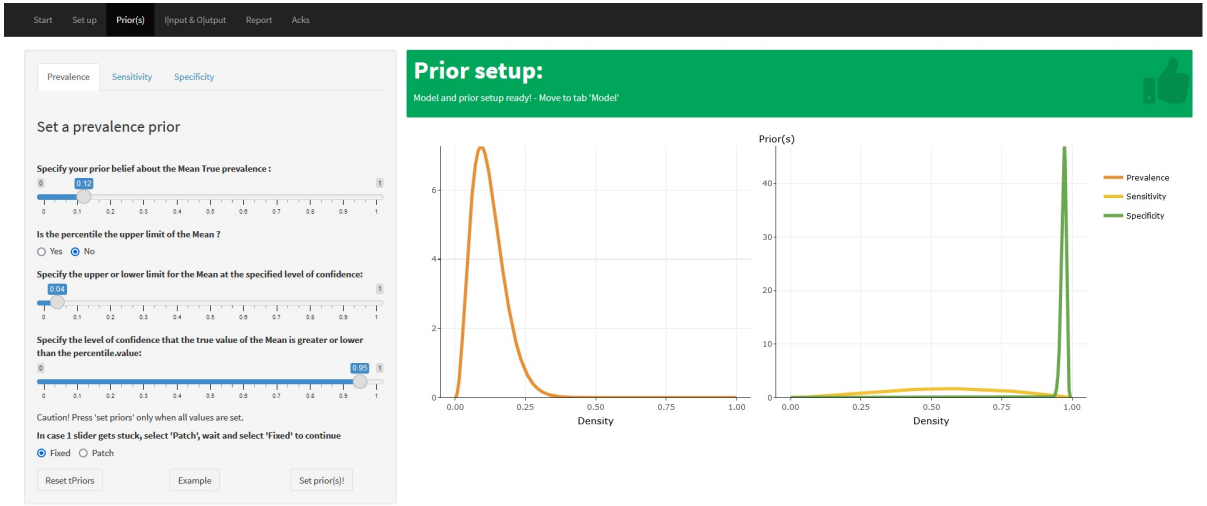
- Prevalence of a moderate adverse event (fatigue) of a vaccine.
- Observed 50 events in a sample of 1000.
- Prior information:
  1. A publication stated that average risk for fatigue is low.
  2. Experts report that fatigue is observed with very high sensitivity but moderate specificity.

Set-up page



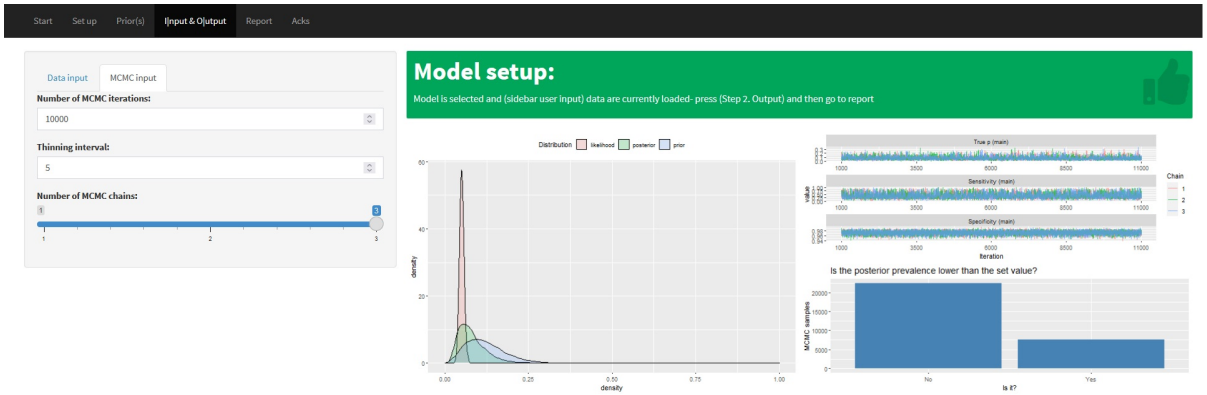
1. Single - True - No zero - Informative - Mean.
2. If Apparent (Se=Sp=1), if also Non-informative, then 3 prior prevalence choices available.
3. Currently, selected measure applies to all priors.

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

1. Check ESS, diagnostics, extra plots,
2. Check models, input data, output data
3. Use ggmcmc for clearer diagnostic plots
4. www.menti.com 3855 2899

Multiple populations (30-60')

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

tPRiors

- 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

- 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)