ShinyJWAS: Shiny-based Application to Help Perform Whole-genome Bayesian Regression Analysis with JWAS package

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Summary

ShinyJWAS is a shiny web application (Chang, Cheng, Allaire, Xie, & McPherson, 2020) to help users to perform whole-genome Bayesian regression analysis with JWAS package (Cheng, Fernando, & Garrick, 2018), a well-documented software platform based on Julia and the interactive Jupyter notebook for analyses of general univariate and multivariate Bayesian mixed effects models. With the easy-to-use graphical user interface (GUI) (Figure 1), ShinyJWAS provides users a complete tutorial to the JWAS package for Bayesian analysis and a number of options to manage, explore, and visualize the data and results. The application provides interactive interfaces to generate scripts to run Bayesian analysis in JWAS, visualize phenotypic data, pedigree structure, and posterior distributions of parameters of interest, e.g., heritability, make Manhattan plots from GWAS, and perform convergence diagnosis of MCMC samples.

In conclusion, functions in ShinyJWAS free users from scripting by automating the Bayesian analysis process and provide interactive interfaces for data summarization, visualization, and diagnostic tests. More detailed documentation and tutorials can be found on the shiny app page: https://qtl-rocks.shinyapps.io/shinyjwas/ .
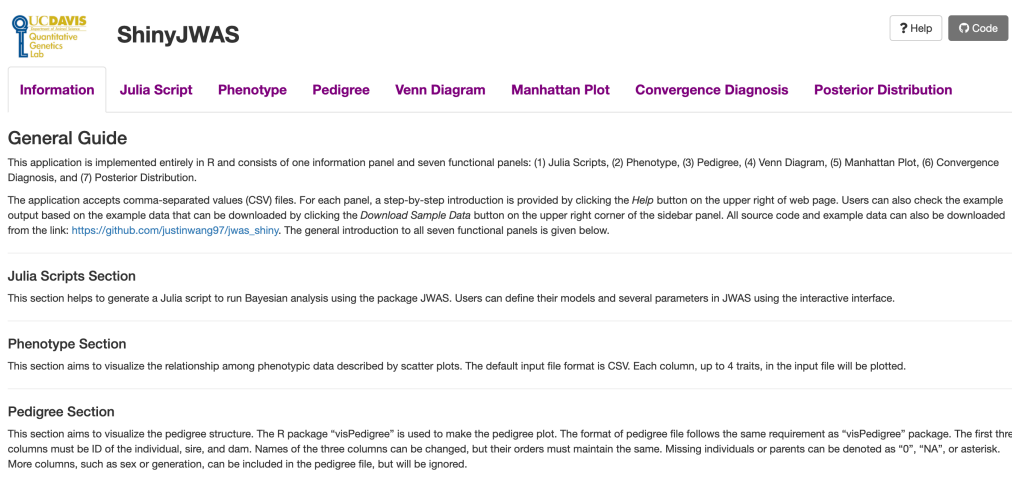
Figure 1: ShinyJWAS GUI.

Acknowledgements

References

Chang, W., Cheng, J., Allaire, J., Xie, Y., & McPherson, J. (2020). *Shiny: Web application framework for r*. Retrieved from https://CRAN.R-project.org/package=shiny

Cheng, H., Fernando, R., & Garrick, D. (2018). JWAS:Julia implementation of Whole-genome Analyses Software. *Proceedings of the World Congress on Genetics Applied to Livestock Production*.