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DEPARTMENT OF HEALTH AND HUMAN SERVICES

5/7/2021

Dear Editors,

We'd like to submit our manuscript, entitled "**SEMIPs: Structural Equation Modeling of In silico Perturbations**" for consideration as a Bioinformatics Application Note under the Gene Expression category. In this study, we developed an R Shiny app, termed "Structural Equation Modeling of In silico Perturbations (SEMIPs)" that allows users to infer causal inference of molecular interactions *in silico*. The app provides a user-friendly way for bench scientists to perform structural equation modeling on their data to generate hypotheses. The source code of this application was deposited in github and freely available to non-commercial users. The detailed instructions of this app are also provided in github and a case study in the supplemental materials.

We confirm that none of this material has been published or is under consideration elsewhere. In addition, all of the authors have approved the contents of this manuscript and have agreed to the Bioinformatics' submission policies.

Thank you for your consideration of our manuscript.

Sincerely,

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