Mickaël Canouil, Ph.D.  
CNRS UMR 8199 – EGID  
Pôle Recherche - 1er étage Aile Ouest  
1, Place de Verdun  
59045 LILLE CEDEX FRANCE  
Tel: +33(0)3-74-00-81-29  
Email: mickael.canouil@cnrs.fr

Sanjay Shete, Ph.D.  
Editor-in-Chief,  
Genetic Epidemiology, The University of Texas,  
M. D. Anderson Cancer Center, Department of Epidemiology,  
P.O. Box 301439, Houston, TX 77230-1439 USA.   
Tel: (713) 745-2483;   
Email: sshete@mdanderson.org

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Dear Dr. Sanjay Shete,

Please find enclosed an original research article entitled “*Single Nucleotide Polymorphisms Associated with Fasting Plasma Glucose Trajectory and Type 2 Diabetes Incidence: A Joint Modelling Approach*” by Canouil M. et al. to consider for publication in *Genetic Epidemiology*.  
In recent years, developments of joint models for longitudinal and survival data have increased, especially in medical research to evaluate the efficacy of treatments on both outcomes (longitudinal and time-to event).

In this manuscript, we compare two approaches (i.e. joint likelihood and two-step inference) to model longitudinal and time-to event outcomes in a genetic context, where SNPs are used as “treatments” variable. We show through simulations and application to real data that the joint likelihood approach provides better estimations than two-step approach, but for a genome-wide scale use two-step approach show more suitable computation times and estimations close to the joint likelihood approach and thus could be used in a screening step prior to the joint likelihood approach.

We believe that this manuscript is appropriate for publication by Genetic Epidemiology because it provides a new tool in the field of genetic epidemiology which may help to better understand genetic factors, by distinguishing their effect on quantitative traits and on disease’s risk.

The manuscript has been seen and approved by all co-authors. No part of the manuscript has been published previously and the paper is not under consideration for publication elsewhere. We have no conflicts of interest to disclose.

Thank you for your consideration!  
Yours sincerely,

Mickaël Canouil, Ph.D.  
CNRS UMR 8199 – EGID