Author's response to reviews

Title: Identification of a prognostic signature for old-age mortality by integrating genome-wide transcriptomic data with the conventional predictors: the Vitality 90+ Study

Authors:

Juulia Jylhävä (juulia.jylhava@uta.fi)
Jani Raitanen (jani.raitanen@uta.fi)
Saara Marttila (saara.marttila@uta.fi)
Antti Hervonen (antti.hervonen@uta.fi)
Marja Jylhä (marja.jylha@uta.fi)
Mikko A Hurme (mikko.a.hurme@uta.fi)

Version: 2 Date: 12 June 2014

Author's response to reviews:

Dear Sir/Madam,

please find enclosed our manuscript entitled "Identification of a prognostic signature for old-age mortality by integrating genome-wide transcriptomic data with the conventional predictors: the Vitality 90+ Study". In this manuscript we demonstrate that old age all-cause mortality predictions can be improved by utilizing a bioinformatic feature selection method that incorporates the whole-genome transcriptomic data with the conventional mortality-predicting (bio)markers. To the best of our knowledge, our study is the first one to describe the whole-genome transcriptomic landscape that precedes all-cause old-age mortality. The transcripts in the final mortality-predicting signature demonstrate that immunoinflammatory processes, control of the DNA damage response and cell cycle, and mitochondrial functions are decisive in old-age mortality. Moreover, the methodology presented could also serve for other purposes in which high-dimensional genomic data are used for predictive modeling in cohort studies.

All authors have red and approved the manuscript and the manuscript has not been, or is not, under consideration for publication in another journal, in whole or in part, in any language. The study protocol has been approved by the local ethics committee and an informed consent was obtained from all of the participants.

We have identified three potential reviewers who have expertise in prediction modeling using a whole-genome expression data.

Professor Ørnulf Borgan

The Faculty of Mathematics and Natural Sciences, Department of Mathematics,
University of Oslo, Norway
brogan@math.uio.no

Assistant Professor Glen Jickling, M.D., FRCPC
University of California, Davis, Medical Center, Sacramento, California.
glen.jickling@ucdmc.ucdavis.edu

Professor Lodewyk Wessels
Delft Bioinformatics Laboratory, Faculty of Electrical Engineering, Mathematics and Computer Science, Delft University of Technology, Mekelweg, Delft, The Netherlands
l.wessels@nki.nl

Sincerely,
Juulia Jylhävä
Department of Microbiology and Immunology
School of Medicine
University of Tampere, FIN-33014 Tampere, Finland
Phone: +358-3-3551 7723, Fax: +358-3-3551 6173
E-mail: juulia.jylhava@uta.fi