

On 5/07/2012 7:12 PM, P.E.M.Taschner@lumc.nl wrote:

Dear International Scientific Advisory Committee,

Many gene variant databases are using LOVD software (<http://www.lovd.nl>). Therefore, I would like to propose that the HVP initiates an activity to assess the quality of LOVD and work towards its recognition as a standard for gene variant database software. LOVD is open source software with a data structure mapped to the Gen2Phen data model for increased data interoperability. The latter will become more and more important with the increasing amount of data from next generation sequencing experiments.

The assessment might also take into account that LOVD might be set up locally and nationally during the first steps of creating the necessary IT infrastructure for HVP country nodes.

Thank you very much for your time and consideration.

Best regards,

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