Testimonials for Veridical

Veridical wins best paper award at two conferences!

Coby Viner presented the Veridical algorithm and software at the 2014 Compute Ontario 1st Annual Research Conference (Waterloo, Ontario, May 7, 2014) and at the 9th Annual Great Lakes Bioinformatics Conference (Cincinnati, Ohio, May 17). He received the *Best Oral Presentation* and *Best Highlights Presentation* award, respectively.

Stefania Bortoluzzi, Assistant Professor, Department of Biology, University of Padua, Italy:

"...the interpretation of genetic variants is a difficult and key issue in current research. The integration of genomic and transcriptomic data, namely the use of RNA-seq-based transcriptome characterization as a “molecular phenotype” of cells is useful and meaningful. "

Francesc Xavier Roca, Assistant Professor, Div. Molecular Genetics & Cell Biology, Nanyang Technological University, Singapore:

“This outstanding tool appears very useful to screen the wealth of transcriptomic data for effects in splicing due to mutations in disease samples, and I think that it will potentially be of interest for many if not all such RNAseq-based studies. In addition, this could spur further efforts to derive similar tools with improved efficiencies. Use of this method should help establish the importance of aberrant splicing in disease as well as the effects of genomic mutations at the RNA level. "

Dr. med. Sebastian Beer, Universitätsklinikum Leipzig, Germany:

"It's a great work you and your colleagues have performed. I was guided to your homepage by a couple of publication of yours."

Nathaniel Bryans, Software Development Engineer, Microsoft,

USA:

"I haven't yet had a chance to deep-dive the article, but from my first read it looks like an interesting and novel piece of software. Congrats . . ."

Yskert von Kodolitsch, Professor, Universitätsklinikum Hamburg-Eppendorf, Germany:

"that is sensational....looks like a break-through. People really should start using your prediction model."

Stylianos Antonarakis, Professor and Chairman, Department of Genetic Medicine and Development, University of Geneva Medical School:

"Very interesting and useful indeed!"

Liliana Florea, McKusick-Nathans Institute of Human Genetics, Johns Hopkins University:

"The idea is ingenious and novel as applied to mutations affecting splicing ... The software is fast and practical, being able to test thousands of variants in hundreds of samples within hours. This is the first software of its kind, and if accurate it will be a very valuable resource for clinical genomics."

Peter Robinson, Institute for Medical Genetics, Universitätsklinikum Charité, Berlin, Germany:

"The program fulfils an important need in the community, the results appear promising and will be of special interest to groups performing RNA-seq analysis in medical settings."