

Genomics AI tool: Google's DeepVariant released as open source

A novel artificial intelligence tool that can accurately call out variants in sequencing data was released as [open source on the Google Cloud Platform](#) yesterday. The tool, called DeepVariant, was developed during a collaboration between the Google Brain team and researchers from fellow-Alphabet subsidiary, Verily Life Sciences. The release was announced in a press release cross-posted to [the Google Research blog](#) and [the Google Open Source blog](#).

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The Google Brain team and Verily wanted to develop a machine learning tool for variant calling that was capable of differentiating between accidental sequence changes and genetic mutations. To do so, they used millions of sequences collected by the GIAB project to teach their artificial intelligence, adjusting the parameters of the tool through a series of iterations.

Their work was rewarded last year when DeepVariant won the 2016 PrecisionFDA Truth Challenge for the Highest SNP Performance. Since then, the team believe that they have further reduced the error rate by 50%.

"DeepVariant is the first of what we hope will be many contributions that leverage Google's computing infrastructure and ML expertise to both better understand the genome and to provide deep learning-based genomics tools to the community," the press release concludes.

Read full, original post: [Google Releases DeepVariant AI As Open Source](#)