Creating a universal SNP and small indel variant caller with deep neural networks

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Abstract

Next-generation sequencing (NGS) is a rapidly evolving set of technologies that can be used to determine the sequence of an individual's genome[1] by calling genetic variants present in an individual using billions of short, errorful sequence reads[2]. Despite more than a decade of effort and thousands of dedicated researchers, the hand-crafted and parameterized statistical models used for variant calling still produce thousands of errors and missed variants in each genome[3,4]. Here we show that a deep convolutional neural network[5] can call genetic variation in aligned next-generation sequencing read data by learning statistical relationships (likelihoods) between images of read pileups around putative variant sites and ground-truth genotype calls. This approach, called DeepVariant, outperforms existing tools, even winning the "highest performance" award for SNPs in a FDA-administered variant calling challenge. The learned model generalizes across genome builds and even to other species, allowing non-human sequencing projects to benefit from the wealth of human ground truth data. We further show that, unlike existing tools which perform well on only a specific technology, DeepVariant can learn to call variants in a variety of sequencing technologies and experimental designs, from deep whole genomes from 10X Genomics to Ion Ampliseq exomes. DeepVariant represents a significant step from expert-driven statistical modeling towards more automatic deep learning approaches for developing software to interpret biological instrumentation data.

Main Text

Calling genetic variants from NGS data has proven challenging because NGS reads are not only errorful (with rates from ~0.1-10%) but result from a complex error process that depends on properties of the instrument, preceding data processing tools, and the genome sequence itself[1,3,4,6]. State-of-the-art variant callers use a variety of statistical techniques to model these error processes and thereby accurately identify differences between the reads and the reference genome caused by real genetic variants and those arising from errors in the reads[3,4,6,7]. For example, the widely-used GATK uses logistic regression to model base errors, hidden Markov models to compute read likelihoods, and naive Bayes classification to identify variants, which are then filtered to remove likely false positives using a Gaussian mixture model

with hand-crafted features capturing common error modes[6]. These techniques allow the GATK to achieve high but still imperfect accuracy on the Illumina sequencing platform[3,4]. Generalizing these models to other sequencing technologies has proven difficult due to the need for manual retuning or extending these statistical models (see e.g. Ion Torrent[8,9]), a major problem in an area with such rapid technological progress[1].

Here we describe a variant caller for NGS data that replaces the assortment of statistical modeling components with a single, deep learning model. Deep learning is a revolutionary machine learning technique applicable to a variety of domains, including image classification[10], translation[11], gaming[12,13], and the life sciences[14–17]. This toolchain, which we call DeepVariant, (Figure 1) begins by finding candidate SNPs and indels in reads aligned to the reference genome with high-sensitivity but low specificity. The deep learning model, using the Inception-v2 architecture[5], emits probabilities for each of the three diploid genotypes at a locus using a pileup image of the reference and read data around each candidate variant (Figure 1). The model is trained using labeled true genotypes, after which it is frozen and can then be applied to novel sites or samples. Throughout the following experiments, DeepVariant was trained on an independent set of samples or variants to those being evaluated.

This deep learning model has no specialized knowledge about genomics or next-generation sequencing, and yet can learn to call genetic variants more accurately than state-of-the-art methods. When applied to the Platinum Genomes Project NA12878 data[18], DeepVariant produces a callset with better performance than the GATK when evaluated on the held-out chromosomes of the Genome in a Bottle ground truth set (Figure 2A). For further validation, we sequenced 35 replicates of NA12878 using a standard whole-genome sequencing protocol and called variants on 27 replicates using a GATK best-practices pipeline and DeepVariant using a model trained on the other eight replicates (see methods). Not only does DeepVariant produce more accurate results but it does so with greater consistency across a variety of quality metrics (Figure 2B). To further confirm the performance of DeepVariant, we submitted variant calls for a blinded sample, NA24385, to the Food and Drug Administration-sponsored variant calling Truth Challenge in May 2016 and won the "highest performance" award for SNPs by an independent team using a different evaluation methodology.

Like many variant calling algorithms, GATK relies on a model that assumes read errors are independent[6]. Though long-recognized as an invalid assumption[2], the true likelihood function that models multiple reads simultaneously is unknown[6,19,20]. Because DeepVariant presents an image of all of the reads relevant for a putative variant together, the convolutional neural network (CNN) is able to account for the complex dependence among the reads by virtue of being a universal approximator[21]. This manifests itself as a tight concordance between the estimated probability of error from the likelihood function and the observed error rate, as seen in Figure 2C where DeepVariant's CNN is well calibrated, strikingly more so than the GATK. That the CNN has approximated this true, but unknown, inter-dependent likelihood function is the essential technical advance enabling us to replace the hand-crafted statistical models in other approaches with a single deep learning model and still achieve such high performance in variant calling.

We further explored how well DeepVariant's CNN generalizes beyond its training data. First, a model trained with read data aligned to human genome build GRCh37 and applied to reads aligned to GRCh38 has similar performance (overall F1 = 99.45%) to one trained on GRCh38 and then applied to GRCh38 (overall F1 = 99.53%), thereby demonstrating that a model learned from one version of the human genome reference can be applied to other versions with effectively no loss in accuracy (Table S1). Second, models learned using human reads and ground truth data achieve high accuracy when applied to a mouse dataset[22] (F1 = 98.29%), out-performing training on the mouse data itself (F1 = 97.84%, Table S4). This last experiment is especially demanding as not only do the species differ but nearly all of the sequencing parameters do as well: 50x 2x148bp from an Illumina TruSeq prep sequenced on a HiSeq 2500 for the human sample and 27x 2x100bp reads from a custom sequencing preparation run on an Illumina Genome Analyzer II for mouse[22]. Thus, DeepVariant is robust to changes in sequencing depth, preparation protocol, instrument type, genome build, and even species. The practical benefits of this capability is substantial, as DeepVariant enables resequencing projects in non-human species, which often have no ground truth data to guide their efforts[22,23], to leverage the large and growing ground truth data in humans.

To further assess its capabilities, we trained DeepVariant to call variants in eight datasets from Genome in a Bottle[24] that span a variety of sequencing instruments and protocols, including whole genome and exome sequencing technologies, with read lengths from fifty to many thousands of basepairs (Table 1 and S6). We used the already processed BAM files to introduce additional variability as these BAMs differ in their alignment and cleaning steps. The results of this experiment all exhibit a characteristic pattern: the candidate variants have the highest sensitivity but a low PPV (mean 57.6%), which varies significantly by dataset. After retraining, all of the callsets achieve high PPVs (mean of 99.3%) while largely preserving the candidate callset sensitivity (mean loss of 2.3%). The high PPVs and low loss of sensitivity indicate that DeepVariant can learn a model that captures the technology-specific error processes in sufficient detail to separate real variation from false positives with high fidelity for many different sequencing technologies.

As we already shown above that DeepVariant performs well on Illumina WGS data, we analyze here the behavior of DeepVariant on two non-Illumina WGS datasets and two exome datasets from Illumina and Ion Torrent. The SOLID and Pacific Biosciences (PacBio) WGS datasets have high error rates in the candidate callsets. SOLID (13.9% PPV for SNPs, 96.2% for indels, and 14.3% overall) has many SNP artifacts from the mapping short, color-space reads. The PacBio dataset is the opposite, with many false indels (79.8% PPV for SNPs, 1.4% for indels, and 22.1% overall) due to this technology's high indel error rate. Training DeepVariant to call variants in an exome is likely to be particularly challenging. Exomes have far fewer variants (~20-30k)[25] than found in a whole-genome (~4-5M)[26]. The non-uniform coverage and sequencing errors from the exome capture or amplification technology also introduce many false positive variants[27]. For example, at 8.1% the PPV of our candidate variants for Ion Ampliseq is the lowest of all our datasets.

Despite the low initial PPVs, the retrained models in DeepVariant separate errors from real variants with high accuracy in the WGS datasets (PPVs of 99.0% and 97.3% for SOLID and PacBio, respectively), though with a larger loss in sensitivity (candidates 82.5% and final 76.6%

for SOLID and 93.4% and 88.5% for PacBio) than other technologies. Despite the challenges the retrained deep learning model with limited data, the exome datasets also perform strikingly well, with a small reduction in sensitivity (from 91.9% to 89.3% and 94.0% to 92.6% for Ion and TruSeq candidates and final calls) for a substantial boost in PPV (from 8.1% to 99.7% and 65.3% to 99.3% for Ion and TruSeq). The performance of DeepVariant compares favorably to those of callsets submitted to the Genome in a Bottle project site using tools developed specifically for each NGS technology and to callsets produced by the GATK or samtools (Table S7).

The accuracy numbers presented here shouldn't be viewed as the maximum achievable by either the sequencing technology or DeepVariant. For consistency, we used the same model architecture, image representation, training parameters, and candidate variant criteria for each technology. Because DeepVariant achieves high PPVs for all technologies, the overall accuracy (F1), which is the harmonic mean of sensitivity and PPV, is effectively driven by the sensitivity of the candidate callset. Improvements to the data processing steps before DeepVariant and the algorithm used to identify candidate variants will likely translate into substantial improvements in overall accuracy, particularly for multi-allelic indels. Conversely, despite its effectiveness, representing variant calls as images and applying general image-classification models is certainly suboptimal, as we were unable to effectively encode all of the available information in the reads and reference into the four-channel image. The accuracy of DeepVariant will likely improve by transitioning to more expressive tensor-based[28] models specialized for genomic data.

Taken together, our results demonstrate that the deep learning approach employed by DeepVariant is able to learn a statistical model describing the relationship between the experimentally observed NGS reads and genetic variants in that data for potentially any sequencing technology. Technologies like DeepVariant change the problem of calling variants from a laborious process of expert-driven, technology-specific statistical modeling to a more automated process of optimizing a general model against data. With DeepVariant, creating a NGS caller for a new sequencing technology becomes a simpler matter of developing the appropriate preprocessing steps, training a deep learning model on sequencing data from samples with ground truth data, and applying this model to new, even non-human, samples.

At its core, DeepVariant (1) generates candidate entities with high sensitivity but low specificity, (2) represents the experimental data about each entity in a machine-learning compatible format and then (3) applies deep learning to assign meaningful biological labels to these entities. This general framework for inferring biological entities from raw, errorful, indirect experimental data is likely applicable to many other high-throughput instruments.

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a hosted service (https://cloud.google.com/genomics/deepvariant) and as open-source software based on the TensorFlow framework.

Figures

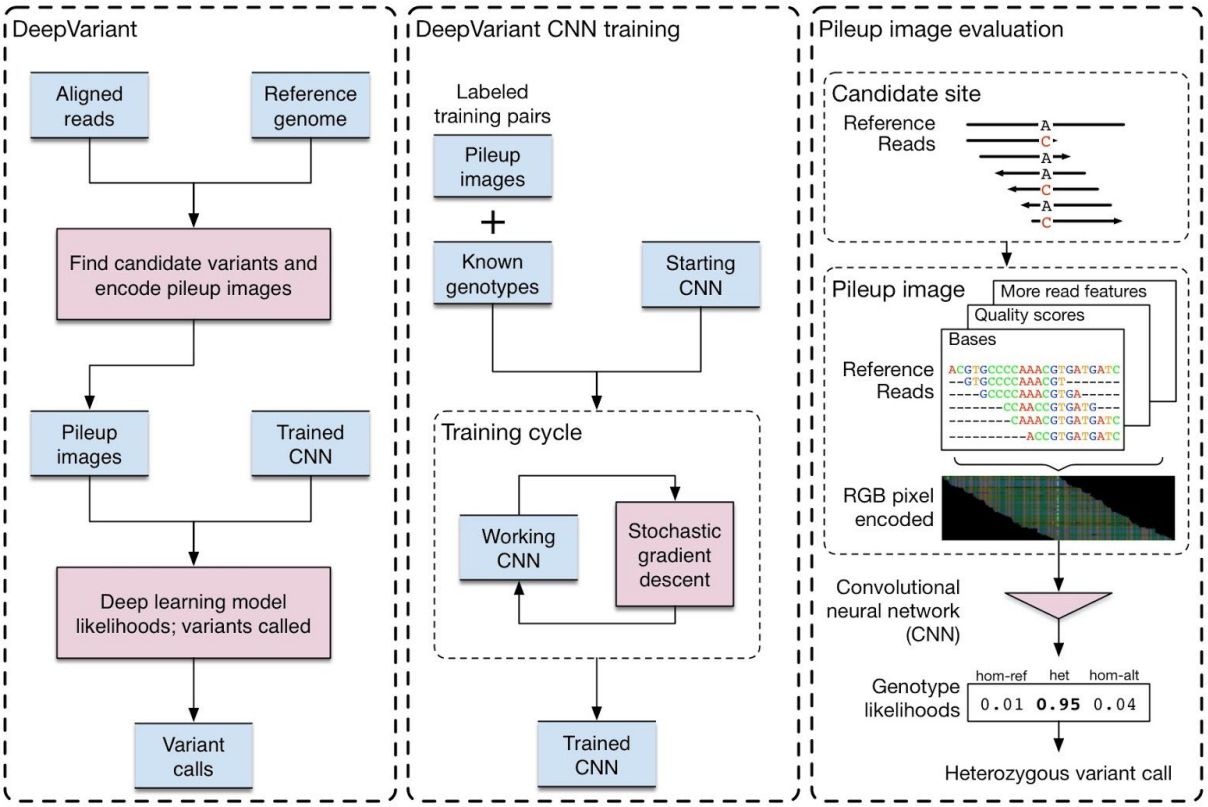
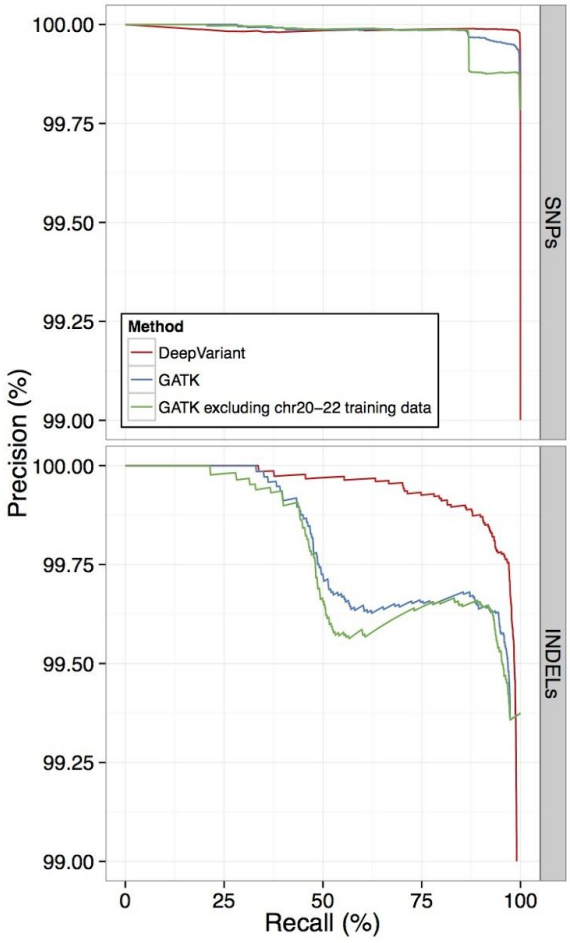


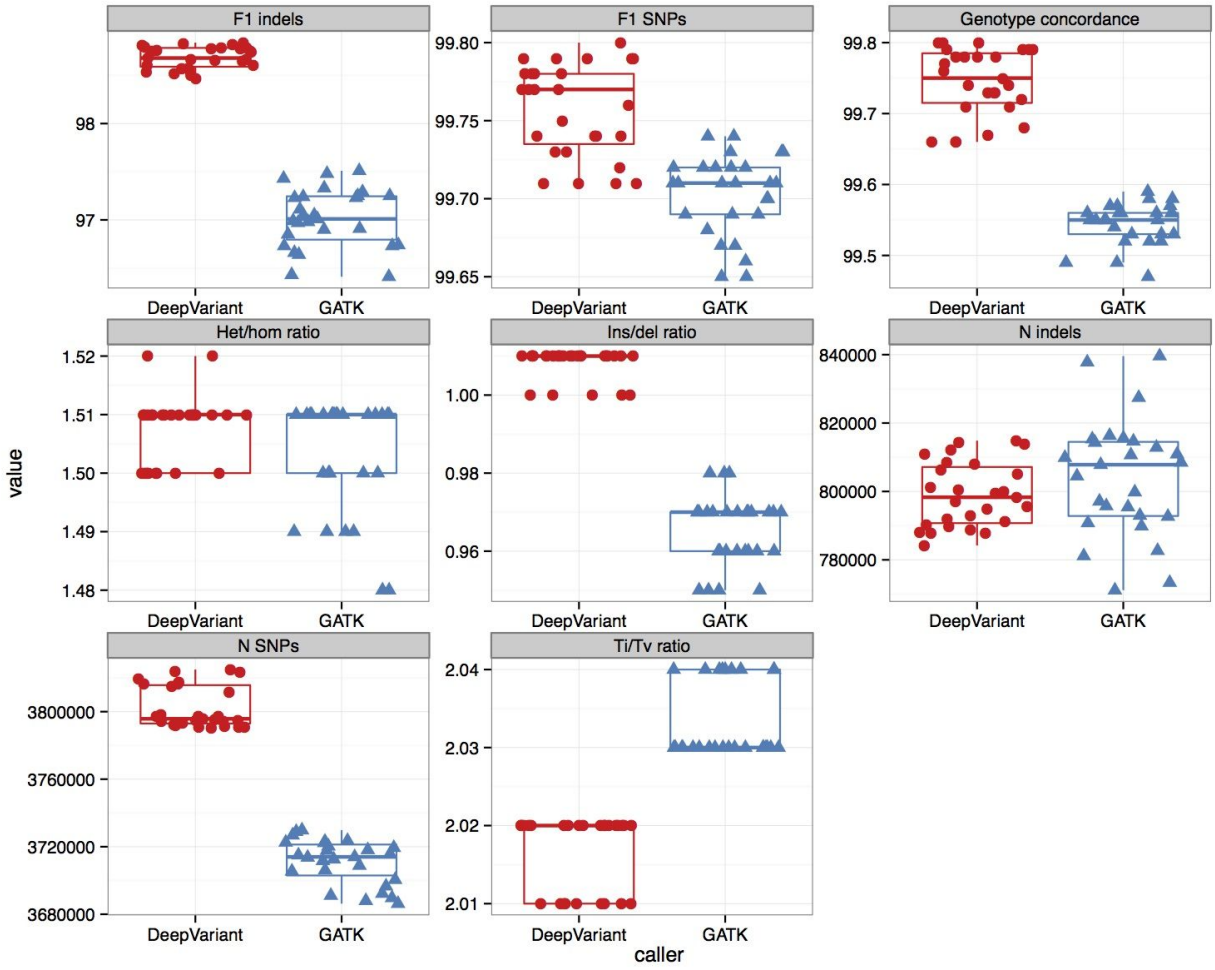
Figure 1: DeepVariant workflow overview. Before DeepVariant, NGS reads are first aligned to a reference genome and cleaned up with duplicate marking and, optionally, local assembly. (Left box) First, the aligned reads are scanned for sites that may be different from the reference genome. The read and reference data is encoded as an image for each candidate variant site. A trained convolutional neural network (CNN) calculates the genotype likelihoods for each site. A variant call is emitted if the most likely genotype is heterozygous or homozygous non-reference. (Middle box) Training the CNN reuses the DeepVariant machinery to generate pileup images for a sample with known genotypes. These labeled image + genotype pairs, along with an initial CNN which can be a random model, a CNN trained for other image classification tests, or a prior DeepVariant model, are used to optimize the CNN parameters to maximize genotype prediction accuracy using a stochastic gradient descent algorithm. After a maximum number of cycles or time has elapsed or the model's performance has convergence, the final trained model is frozen and can then be used for variant calling. (Right box) The reference and read bases, qualities scores, and other read features are encoded into an red-green-blue (RGB) pileup image at a

candidate variant. This encoded image is provided to the CNN to calculate of the genotype likelihoods for the three diploid genotype states of homozygous reference (hom-ref), heterozygous (het), or homozygous alternate (hom-alt). In this example a heterozygous variant call is emitted as the most probable genotype likelihood here is "het". In all panels blue boxes represent data and red boxes are processes. Details of all processes are given in the Supp. Mats.

Panel A



Panel B



Panel C

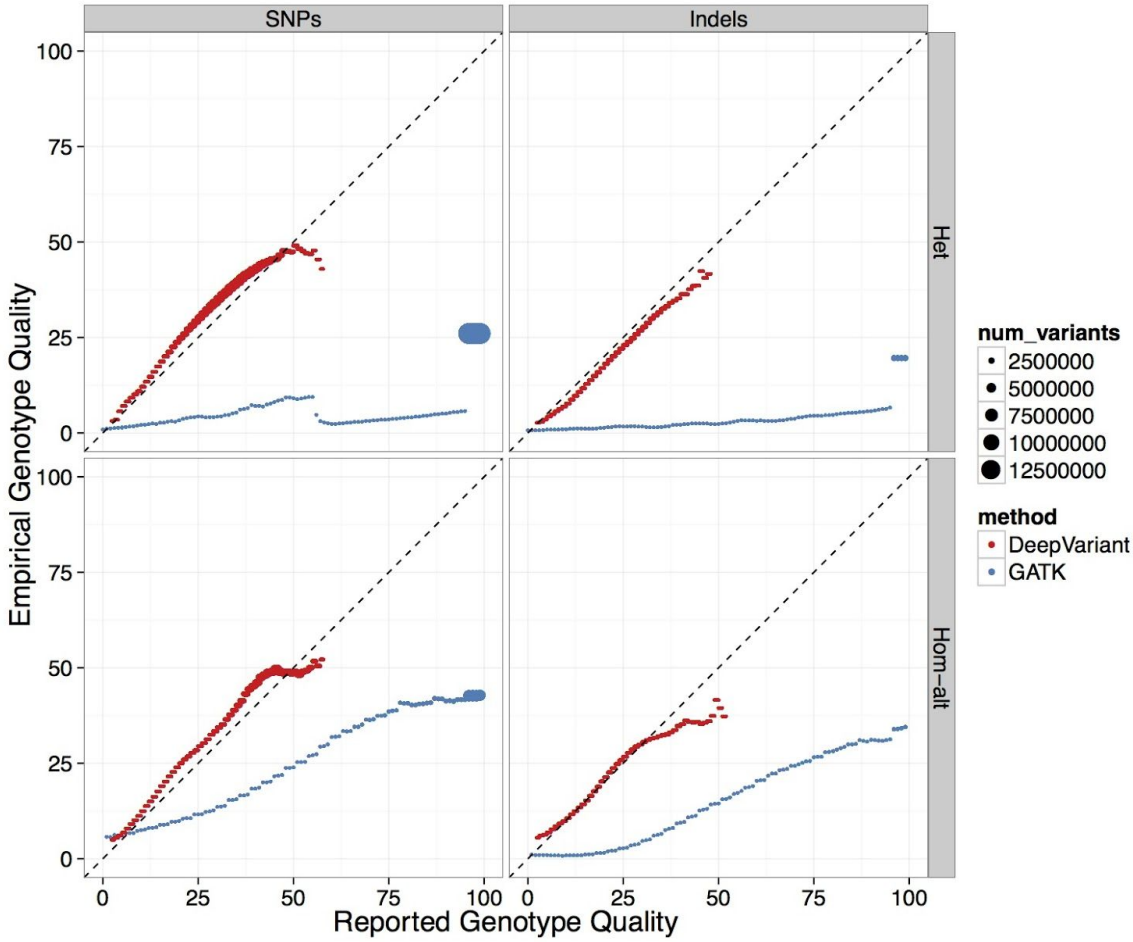


Figure 2: DeepVariant accuracy, consistency, and calibration relative to the GATK. (A) Precision-recall plot for DeepVariant (red) and GATK (green, blue) calls for the Genome in the Bottle benchmark sample NA12878 using 2x101 Illumina HiSeq data from the Platinum Genomes project. The GATK was run in two ways. In the first, GATK best-practices were followed and the variant filtering step (VQSR) was provided data for known variants on both the training and test chromosomes, allowing VQSR to use population variation information to better call variants on the test chromosomes. In the second, we removed all population variation information for the test chromosomes chr20-22, relying on the VQSR model learned only on the training chromosomes, which is more representative of the GATK's calling performance on novel variation. See Suppl. Mats for additional details and figures. (B) DeepVariant (red circles) and the GATK (blue triangles) were run on 27 independently sequenced replicates of NA12878 (PCR-free WGS 2x151 on an Illumina X10 with coverage from 24x-35x). Each panel shows the distribution of values for the given metric (panel label) for DeepVariant and the GATK. DeepVariant produces more accurate SNP and indel calls (F1) when compared to the Genome in a Bottle standard for NA12878 with a higher fraction of sites having the correct genotype assigned (Genotype concordance). DeepVariant finds a similar numbers of indels to the GATK, but has a more consistent ratio of insertions to deletions. DeepVariant finds more SNPs than GATK, at a slightly lower transition/transversion ratio (Ti/Tv ratio) and a similar ratio of heterozygous variants to homozygous alternative variants (Het/hom ratio). (C) Comparison of likelihoods assigned to heterozygous and homozygous alternate genotypes emitted by

DeepVariant and the GATK shows the likelihood model learned by DeepVariant is substantially better calibrated than that employed by the GATK. On the x-axis is the reported genotype quality (GQ) for calls for DeepVariant (red) and GATK (blue) compared to the observed error rate in each of these GQ bands (y-axis), for true heterozygous and homozygous variants (vertical facet) and SNPs and indels (horizontal facet) separately. The size of each calibration point reflects the number of variant calls used to estimate the empirical accuracy. The calibration curves were calculated using genotype likelihoods from the held-out evaluation data in eight sequenced replicates of NA12878. For example, the set of all Q30 heterozygous calls should be in aggregate accurate at a rate of 999 in 1000. Genotypes should be correct at a rate declared by their confidence; perfect calibration would follow the marked x=y line.

Tables

	Sensitivity		PPV		F1	
Dataset	Candidate variants	Called variants	Candidate variants	Called variants	Candidate variants	Called variants
10X Chromium 75x WGS	99.66%	98.73%	89.55%	99.91%	94.34%	99.32%
10X GemCode 34x WGS	97.03%	94.34%	75.19%	99.47%	84.73%	96.84%
Illumina HiSeq 31x WGS	99.88%	99.76%	95.14%	99.98%	97.45%	99.87%
Illumina HiSeq 60x WGS	99.95%	99.88%	90.90%	99.98%	95.21%	99.93%
Ion AmpliSeq exome	91.94%	89.28%	8.05%	99.70%	14.81%	94.21%
PacBio 40x WGS	93.36%	88.51%	22.14%	97.25%	35.79%	92.67%
SOLID SE 85x WGS	82.50%	76.62%	14.27%	99.01%	24.33%	86.39%
Illumina TruSeq exome	94.04%	92.58%	65.31%	99.31%	77.08%	95.83%
Mean	94.79%	92.46%	57.57%	99.33%	65.47%	95.63%
Median	94.79%	92.58%	65.31%	99.47%	77.08%	95.83%

Table 1: Training DeepVariant to call variants on a variety of sequencing technologies and experimental protocols. Datasets are labeled to indicate instrument, protocol, target area (WGS for whole genome, gene regions as exome), with sequencing depth shown for whole genome targets. For each dataset, a set of candidate variants were identified across the genome in the NGS reads (methods). The baseline Illumina model was retrained using the candidate variants with labeled genotypes on chromosomes 1-19. This retrained model was then used to assign genotype likelihoods to the candidate variants, keeping those confidently non-reference on the held-out chromosomes 20-22. The sensitivity, positive predictive value (PPV), and overall accuracy (F1) are shown for the candidate and called variants on chr20-22 only.

Online methods and supplementary materials

Are available in a separate supplementary materials document.

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