Synthetic Genomics Data Generation And Evaluation For The Use Case Of Benchmarking Somatic Variant Calling Algorithms

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MOTIVATION

- Variant calling plays an important in identifying genetic lesions.
- In the case of variants at <u>low frequency (≤10%)</u> identification becomes more challenging.
- The challenge that rises is the absence of a ground truth for reliable and consistent identification and benchmarking.





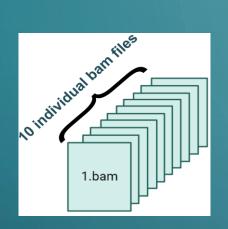






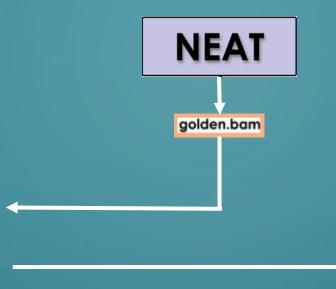


SYNTHETIC «GOLD STANDARD» DATASET GENERATION



x500 coverage

"Gold Standard" Variants of 100% Allele Frequency



Ground Truth.bam

x5000 coverage

"Gold Standard" Variants of <u>10%</u> Allele Frequency

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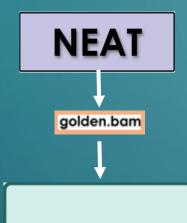






COMPARING ALGORITHMS

In-silico generated dataset that contains «Ground Truth» SNIPs and INDELs Results from GATK somatic variant calling algorithm







Mutect2

Ground Truth.bam



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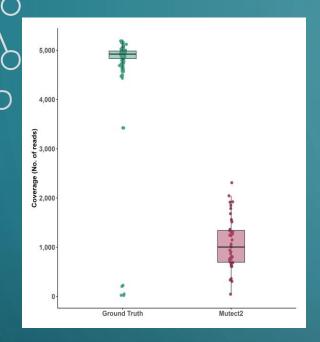
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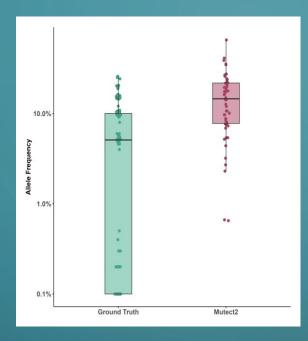




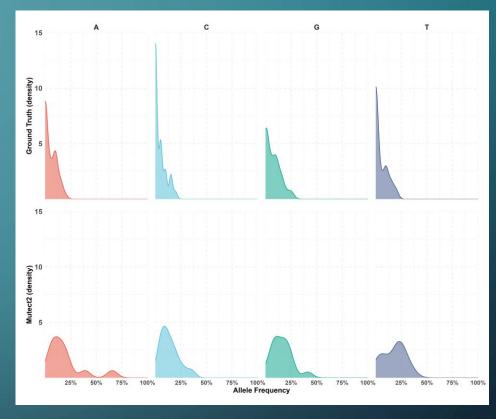
BENCHMARKING GATK-MUTECT2



Down-sampling of coverage of «Ground Truth» Variants



Differences in AF of «Ground Truth» Variants



Variance in AF Density plots of «Ground Truth»

Variants per DNA Base

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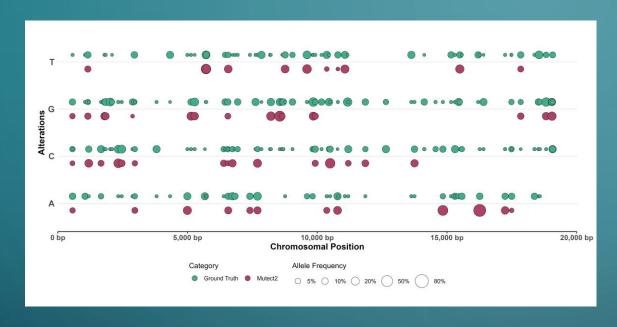
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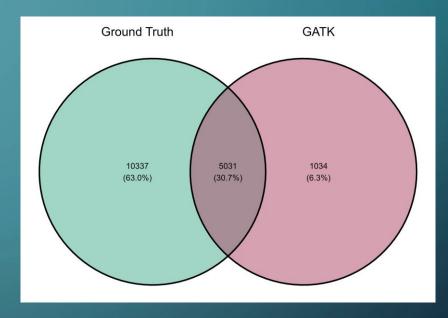






BENCHMARKING GATK-MUTECT2





Divergence in the identification of SNIPs and their AF of «Ground Truth» Variants

Venn plot of the Overall Variants

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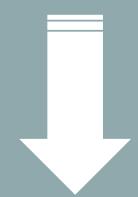




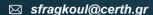
Highlights

- Generation of synthetic genomics data based on TP53 gene
- Define «Ground Truth»
 SNIPs and INDELs in order to benchmark
 somatic variant callers
- Investigate the impact of variant callers in variants at low frequencies

To learn more about our work please visit







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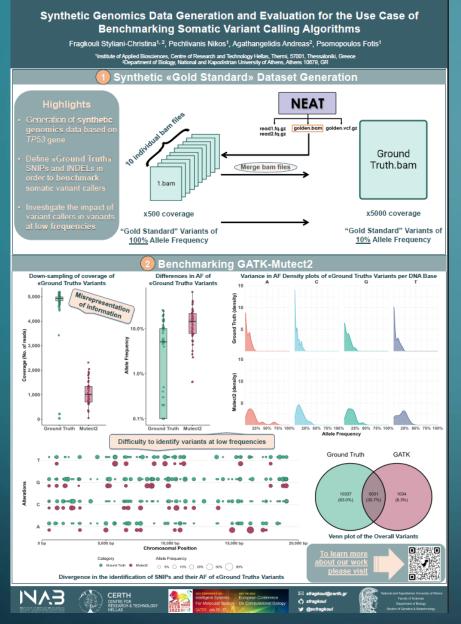
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Come say Hi:)

Monday 24th of July

Poster Session A

Track: BOSC

Poster: A-102



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