Group #22

**Deciphering DNA Repair Pathways through Structural Variant Analysis in Cancer Genomes**

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Abstract

Structural variants (SVs) are significant drivers of genomic instability in cancer, yet their detection is often hindered by a 40-60% discordance among computational callers and a slow manual validation bottleneck. To address this, we developed a high-confidence analysis framework that integrates an ensemble of five complementary callers with an AI vision-based SV classifier that automates expert manual review of IGV screenshots. The classifier utilizes large language models to apply a structured, feature-based scoring rubric to produce calibrated TRUE/FALSE calls with ≥90% accuracy. This discovery pipeline is further integrated with a targeted PacBio long-read sequencing branch used to verify complex rearrangements, such as Break-Induced Replication (BIR), which are often unresolvable using standard short-read methods. This system establishes a scalable, self-validating genomic ecosystem that provides a comprehensive and validated map of the complex genomic architectures driving cancer development.