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1183 – CLASSIVUS: a digital platform for reclassification of variants of uncertain significance in hereditary breast and ovarian cancer

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The identification of pathogenic variants in genes such as BRCA1 and BRCA2 is essential for guiding prevention and clinical management. However, variants of uncertain significance (VUS) remain a major challenge, limiting decision-making regarding surveillance, risk-reducing strategies, and family testing. Although international guidelines, such as those from the American College of Medical Genetics and Genomics (ACMG), provide criteria for variant classification, their application is often inconsistent across laboratories. This issue is further compounded by the underrepresentation of admixed populations, such as the Brazilian population, in global genomic databases, which hinders accurate interpretation. CLASSIVUS addresses these challenges by integrating multiple data sources into a unified environment, including population databases, in silico prediction tools, scientific literature, and standardized classification frameworks. The platform ensures transparency and traceability throughout the variant curation process while enabling periodic reassessment as new evidence emerges. Current developments include the automated ingestion of sequencing data, real-time querying of public databases, and assisted annotation workflows. These features aim to streamline analysis, reduce interobserver variability, and improve reproducibility. Additionally, the system provides structured reporting and complete documentation of classification decisions. By enhancing standardization and efficiency in variant interpretation, CLASSIVUS has the potential to reduce the number of inconclusive results, improving clinical decision-making for patients with hereditary cancer predisposition.

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