Resource Summary Report

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AVIA

RRID:SCR_005172
Type: Tool

Proper Citation

AVIA (RRID:SCR_005172)

Resource Information

URL: http://avia.abcc.ncifcrf.gov/apps/site/index

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Description: An interactive web-based tool to explore and interpret large sets of genomic variations (single nucleotide variations and insertion/deletions) to help guide and summarize genomic experiments. The tool is based on coupling a comprehensive annotation pipeline with a flexible visualization method. They leveraged the ANNOVAR (Wang et. al, 2010) framework for assigning functional impact to genomic variations by extending its list of reference annotation databases (RefSeq, UCSC, SIFT, Polyphen etc.) with additional in-house developed sources (Non-B DB, PolyBrowse). Further, because many users also have their own annotation sources, they have added the ability to supply their own files as well. The results can be obtained in tabular format or as tracks in whole genome circular views generated by the Circos application (Krzywinski et. al, 2009). Users can also select different sets of pre-computed tracks, including whole genome distributions of different genomic features (genes, exons, repeats), as well as variations analysis tracks for the 69 CGI public genomes for reference.

Abbreviations: AVIA

Synonyms: Annotation Visualization and Impact Analysis

Resource Type: data analysis service, analysis service resource, production service resource, service resource

Defining Citation: PMID:24215028

Keywords: genomic variation, single nucleotide variation, insertion, deletion, indel, genome, annotation, visualization, impact analysis, mirna snp, mirna, snp, subtractive analysis, protein

coding

Funding:

Availability: Acknowledgement requested

Resource Name: AVIA

Resource ID: SCR_005172

Alternate IDs: OMICS_00168

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250411T054953+0000

Ratings and Alerts

No rating or validation information has been found for AVIA.

No alerts have been found for AVIA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Silva GC, et al. (2023) The impact of Brazil's transport network on the spread of COVID-19. Scientific reports, 13(1), 2240.

Lyons EL, et al. (2023) Rare disease variant curation from literature: assessing gaps with creatine transport deficiency in focus. BMC genomics, 24(1), 460.

Czy?ycki J, et al. (2021) Analysis of the Displacement of Thin-Walled Workpiece Using a High-Speed Camera during Peripheral Milling of Aluminum Alloys. Materials (Basel, Switzerland), 14(16).

Sharifipour F, et al. (2021) Progression in pediatric glaucoma: lessons learnt from 8 years' follow-up. Medical hypothesis, discovery & innovation ophthalmology journal, 10(3), 138.

Sherman BT, et al. (2021) Genome-wide association study of high-sensitivity C-reactive protein, D-dimer, and interleukin-6 levels in multiethnic HIV+ cohorts. AIDS (London,

England), 35(2), 193.

Rossmann C, et al. (2019) Appropriation of Mobile Health for Diabetes Self-Management: Lessons From Two Qualitative Studies. JMIR diabetes, 4(1), e10271.

Pettingill P, et al. (2019) A causal role for TRESK loss of function in migraine mechanisms. Brain : a journal of neurology, 142(12), 3852.

González-Peñas J, et al. (2019) Enrichment of rare genetic variants in astrocyte gene enriched co-expression modules altered in postmortem brain samples of schizophrenia. Neurobiology of disease, 121, 305.

Lack J, et al. (2017) Circulating tumor cells capture disease evolution in advanced prostate cancer. Journal of translational medicine, 15(1), 44.