Resource Summary Report

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CHAoS

RRID:SCR_005174
Type: Tool

Proper Citation

CHAoS (RRID:SCR_005174)

Resource Information

URL: http://www.well.ox.ac.uk/~kgaulton/chaos.shtml

Proper Citation: CHAoS (RRID:SCR_005174)

Description: A Perl-based system for annotation of variants identified in high-throughput sequencing experiments. Functionality includes annotation of variants with information relating to population genetics, known transcripts, positional records, and sequence motif-based prediction. In addition, annotated variants can be summarized and extracted to facilitate downstream analysis. There is also basic support for gene-based biological annotation, and eventually will include tools for variant and genotype analysis and visualization.

Abbreviations: CHAoS

Synonyms: chaos - Annotation analysis and visualization of variants from high-throughput sequencing experiments

Resource Type: software resource

Keywords: annotation, analysis, visualization, variant, high-throughput sequencing, perl, population genetic, transcript, positional record, sequence, motif, genotype

Funding:

Availability: GNU General Public License, v2

Resource Name: CHAoS

Resource ID: SCR_005174

Alternate IDs: OMICS_00170

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250525T030856+0000

Ratings and Alerts

No rating or validation information has been found for CHAoS.

No alerts have been found for CHAoS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Patel N, et al. (2024) Training Robust T1-Weighted Magnetic Resonance Imaging Liver Segmentation Models Using Ensembles of Datasets with Different Contrast Protocols and Liver Disease Etiologies. Research square.

Patel N, et al. (2024) Training robust T1-weighted magnetic resonance imaging liver segmentation models using ensembles of datasets with different contrast protocols and liver disease etiologies. Scientific reports, 14(1), 20988.

Wang T, et al. (2024) Weakly supervised chest X-ray abnormality localization with non-linear modulation and foreground control. Scientific reports, 14(1), 29181.

Yoon S, et al. (2024) Accelerated muscle mass estimation from CT images through transfer learning. BMC medical imaging, 24(1), 271.

Moraitopoulou G, et al. (2024) No association between alexithymia and emotion recognition or theory of mind in a sample of adolescents enhanced for autistic traits. Autism : the international journal of research and practice, 28(8), 2066.

Mascheroni E, et al. (2022) The role of experience in parenting beliefs of British and Italian women during pregnancy. Infant mental health journal, 43(6), 835.

Li CF, et al. (2022) MultiR-Net: A Novel Joint Learning Network for COVID-19 segmentation and classification. Computers in biology and medicine, 144, 105340.

Koster N, et al. (2022) Understanding personality pathology in a clinical sample of youth: study protocol for the longitudinal research project 'APOLO'. BMJ open, 12(6), e054485.

Dubois-Comtois K, et al. (2021) Child Psychological Functioning During the COVID-19 Lockdown: An Ecological, Family-Centered Approach. Journal of developmental and behavioral pediatrics : JDBP, 42(7), 532.

Camhi SM, et al. (2021) Socioecological Factors Associated with an Urban Exercise Prescription Program for Under-Resourced Women: A Mixed Methods Community-Engaged Research Project. International journal of environmental research and public health, 18(16).

Woolhead VL, et al. (2021) Breed predispositions, clinical findings, and prognostic factors for death in dogs with nonregenerative immune-mediated anemia. Journal of veterinary internal medicine, 35(1), 252.

Kloenne M, et al. (2020) Domain-specific cues improve robustness of deep learning-based segmentation of CT volumes. Scientific reports, 10(1), 10712.

Rayce SB, et al. (2020) Concordance within parent couples' perception of parental stress symptoms among parents to 1-18-year-olds with physical or mental health problems. PloS one, 15(12), e0244212.

Sandholm N, et al. (2018) Confirmation of GLRA3 as a susceptibility locus for albuminuria in Finnish patients with type 1 diabetes. Scientific reports, 8(1), 12408.

Flannick J, et al. (2017) Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific data, 4, 170179.

Fuchsberger C, et al. (2016) The genetic architecture of type 2 diabetes. Nature, 536(7614), 41.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Mahajan A, et al. (2015) Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. PLoS genetics, 11(1), e1004876.

Sanges R, et al. (2013) Highly conserved elements discovered in vertebrates are present in non-syntenic loci of tunicates, act as enhancers and can be transcribed during development. Nucleic acids research, 41(6), 3600.

Jaffee SR, et al. (2012) Chaotic homes and children's disruptive behavior: a longitudinal cross-lagged twin study. Psychological science, 23(6), 643.