Resource Summary Report

Generated by dkNET on Apr 29, 2025

RepeatFiller

RRID:SCR_017414
Type: Tool

Proper Citation

RepeatFiller (RRID:SCR_017414)

Resource Information

URL: https://github.com/hillerlab/GenomeAlignmentTools

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Description: Software tool to incorporate newly detected repeat overlapping alignments into pairwise alignment chains. It only aligns local genomic regions that are bounded by colinear aligning blocks, as provided in chains, which makes it feasible to consider all seeds including those that overlap repetitive regions. Used to improve genome alignments by incorporating previously undetected local alignments between repetitive sequences.

Resource Type: data processing software, image analysis software, alignment software, software resource, software application

Defining Citation: DOI:10.1101/696922

Keywords: Repeat, overlapping, alignment, pairwise, chain, local, genomic, region, colinear, block, sequence, undetected, bio.tools

Funding:

Availability: Free, Freely available

Resource Name: RepeatFiller

Resource ID: SCR_017414

Alternate IDs: biotools:RepeatFiller, BioTools:RepeatFiller

Alternate URLs: https://bio.tools/RepeatFiller, https://bio.tools/RepeatFiller, https://bio.tools/RepeatFiller

Record Creation Time: 20220129T080335+0000

Record Last Update: 20250429T055913+0000

Ratings and Alerts

No rating or validation information has been found for RepeatFiller.

No alerts have been found for RepeatFiller.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Du K, et al. (2024) Phylogenomic analyses of all species of swordtail fishes (genus Xiphophorus) show that hybridization preceded speciation. Nature communications, 15(1), 6609.

Szcze?niak MW, et al. (2024) CANTATAdb 3.0: An Updated Repository of Plant Long Non-Coding RNAs. Plant & cell physiology, 65(9), 1486.

Bukhman YV, et al. (2024) Chromosome level genome assembly of the Etruscan shrew Suncus etruscus. Scientific data, 11(1), 176.

Wang Y, et al. (2024) The evolution history of an allotetraploid mangrove tree analysed with a new tool Allo4D. Plant biotechnology journal, 22(6), 1491.

Feng T, et al. (2024) Curcumol Enhances the Sensitivity of Gastric Cancer to Cisplatin Resistance by Inducing Ferroptosis Through the P62/KEAP1/NRF2 Pathway. Integrative cancer therapies, 23, 15347354241294043.

Wolf M, et al. (2023) The genome of the pygmy right whale illuminates the evolution of rorquals. BMC biology, 21(1), 79.

Wang Y, et al. (2023) Prevalent Introgression Underlies Convergent Evolution in the Diversification of Pungitius Sticklebacks. Molecular biology and evolution, 40(2).

Xu MR, et al. (2023) Maternal dominance contributes to subgenome differentiation in allopolyploid fishes. Nature communications, 14(1), 8357.

Roscito JG, et al. (2022) Convergent and lineage-specific genomic differences in limb regulatory elements in limbless reptile lineages. Cell reports, 38(3), 110280.

Robledo-Ruiz DA, et al. (2022) Chromosome-length genome assembly and linkage map of a critically endangered Australian bird: the helmeted honeyeater. GigaScience, 11.

Hecker N, et al. (2020) A genome alignment of 120 mammals highlights ultraconserved element variability and placenta-associated enhancers. GigaScience, 9(1).

Pippel M, et al. (2020) A highly contiguous genome assembly of the bat hawkmoth Hyles vespertilio (Lepidoptera: Sphingidae). GigaScience, 9(1).

Osipova E, et al. (2019) RepeatFiller newly identifies megabases of aligning repetitive sequences and improves annotations of conserved non-exonic elements. GigaScience, 8(11).