

Resource Summary Report

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

Defining Citation: [DOI:10.1101/696922](https://doi.org/10.1101/696922)

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

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: 20260808T190109+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 16 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Thomas WR, et al. (2026) Genomic comparisons and the adaptive basis of brain size plasticity and chromosomal instability in the Eurasian common shrew. *Molecular biology and evolution*, 43(2).

Du K, et al. (2025) Identification of the male-specific region on the guppy Y Chromosome from a haplotype-resolved assembly. *Genome research*, 35(3), 489.

Morales AE, et al. (2025) Bat genomes illuminate adaptations to viral tolerance and disease resistance. *Nature*, 638(8050), 449.

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.

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

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

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

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

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

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

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