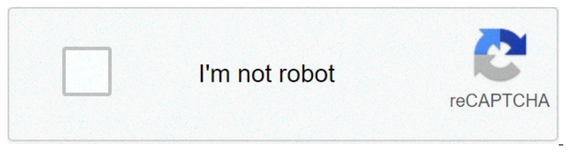

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Liftover hg19 to hg38

12.08.2020: Release Version 0.5.2 add a no-comp-allelesÃ ¢ flag for CrossMap.py vcf and CrossMap.py gvcf. If set, CrossMap does not check whether the alleleÃ ¢ A reference is different from alternative alleleÃ ¢ Ã ¢. 19/08/2020: version 0.5.1 Release In CrossMap.py region: maintain additional columns (columns after the column 3 Â °) BED of the original file after conversion. 08/14/2020: Version 0.5.0 Release of CrossMap.py region Added feature to convert large genomic regions. Unlike CrossMap.py bed function which divides large genomic regions, CrossMap.py region try to convert the large genomic region as a whole. 07.09.2020: Release Version 0.4.3 Structural variants VCF files often use INFO / headland to indicate the end of a cancellation. v0.4.3 update a coordinated Enda in INFO. 04.05.2020: Release version 0.4.2 converting GVCF support files. 24.03.2020: Release the Version 0.4.1 Deal with consecutive cards in the MAF input file. 10.09.2019: Release Version 0.3.8 The University of California owns the copyright in the UCSC chain files. As required by UCSC, all generated UCSC chain files will be permanently removed from the site and CrossMap distributions. 22.07.2019: Release the 0.3.6 version of MAF support (mutation record format). to fix an error TypeError: AlignmentHeader does not support voice allocation (use header.to_dict () Â ¢ When lifting BAM files on user does not need to downgrade to 0.13.0 pysam to lift file BAM 01/04 / .. 2019 :. release version 0.3.4 bug fix when chromosomal ID (the source genome) in the chain files do not have a chra prefix (such as a GRCh37ToHg19.over.chain.gzÃ ¢) This version also allows you to detect CrossMap if a VCF mapping has been reversed, and in that case complements reverse the alternative allele (Thanks to Andrew Yates) improve formulation 07/01/2019: .. version release 0.3.3 to 0.3.3 version is exactly the same a. version 0.3.2 the reason for releasing this version is that CrossMap-0.3.2.tar.gz was broken when uploading PyPI 12/14/18 :. version 0.3.2 Fix the key error problem (example KeyError output: Ã ¢ sequence ba 7_KI270803v1_altÃ ¢ Ã ¢ not PRESENTS). This error occurs when a locus from original group is mapped to a alternativeÃ ¢ Ã ¢, Ã ¢ unplacedÃ or ¢ Ã ¢ unlocalizedÃ contig in the mounting target, and this Ã ¢ ¢ contigÃ goal does not exist in your target_ref.fa. In version 0.3.2, as loci will be silently skipped and saved in a file .unmapÃ ¢ Ã ¢. 5/11/18: output version 0.3.0 v0.3.0 or more recently will support python3. Earlier versions support Python2.7. * Add pyBigWig as an addiction. PIP3 install CrossMap #Install CrossMap support install python3 PIP3 CrossMap --upgrade #upgrade CrossMap support install python3 PIP2 CrossMap #Install CrossMap Python2.7 support. * PIP2 install CrossMap --upgrade #upgrade CrossMap Python2.7 support. * CrossMap supports the following file formats. The output file format depends on the input Input_format output_format BED BED (Genome will be updated coordinates) BAM BAM (Genome coordinates, header section, all the SAM flag, insert size will be updated) CRAM BAM (requires pysam> = 0.8.2) SAM SAM (Genome coordinates, header section, all flags SAM, size insert will be updated) Wiggle bIGWIG bIGWIG bIGWIG GFF GFF (Genome coordinates will be updated for the target group) GTF GTF (Genome coordinates will be updated to the assembly target) VCF VCF (header section, genome coordinates, reference alleles will be updated) GVCF GVCF (header section, genome coordinates, reference alleles will be updated) MAF MAF (coordinates genome and reference alleles will be updated) Perform CrossMap.py no arguments will print a help message $ Program: CrossMap (V0.5.2) Description: CrossMap is a program to convert coordinated genome between different reference groups (for example from HG19 HG38 human or vice versa). Supported file formats include BAM, bed, a piece from ninety, Cram, GFF, GTF, GVCF, MAF (annotation format mutation), Sam, Wiggle, and VCF. Use: Use: [Options] Bam Converts Bam, Cram or Sam format files. Bed convert bed, bedgraph or other similar files to bed. Bigwig converts the â € chr2 238808038 242183529 map_ratio = 0.9622 if we increase -r to 0.99, this region will fail: $ crossmap.py region glch37_to_gch38.chain.gz test.bed -r -r 0.99 CHR2 239716679 243199373 Fail Map_Ratio = 0.9622 Sam (Sequence Alignment Map) Format is a generic format for storing sequencing alignments, and BAM is the binary and tablet version of Sam (Li et al., 2009). CRAM was designed to be an alternative based on efficient reference to the most aligned SAM / BAM file sizes (HTS) of level-thHTNINGPUT in SAM / BAM format and many HTS analysis tools work with SAM format / Bam. CrossMap updates the chromosomes, the coordinates of the genome, the header sections and all SAM flags accordingly. The crossmap version number is inserted in the header section, along with the names of the original Bam file and from the chain file. For pair sequencing, the insert size is also recalculated. The input bam file should be ordered and indexed correctly using SamTools (Li et al., 2009). The output format is determined by the input format and from the BAM output will be ordered and indexed automatically. Typing CrossMap.py Bam Without any topic Print Guide A message: Usage: crossmap.py bam [output_file] [Options] .. Note :: output_file is 'stdout', '-' or missing , CrossMap Write the BAM file in Stdout options: -M insert_size, --Mean = insert_Size Media Insert the size of the torque sequencing (BP). {default = -s insert_size_stdev, --stdev = insert_size_stdev stanadard Deviation of the insert size. {default = 30.0} -T insert_size_fold, --times = insert_size_fold to a mapped torque is considered as "correct torque" if both ends are mapped to a different wire and the distance between them is less than "-t '* Stdev from the average. {Default = 3.0} -a, --append-tag Add tag to each alignment. Example Convert Bam from HG19 to HG18: # Add optional tags using' -a '' -a ' Always use '-a' option) $ crossmap.py bam -a ../data/hg19tohg18.over.chain.gz test.hg19.bam test.hg18 insert size = 200.000000 insert size stdev = 30.000000 number of stdev from the media = 3.000000 Add Tags to each alignment = True @ 2016-10-07 15:29:06: Read chain_file: ../data/hg19tohg18.over.chain.gz @ 2016-10-07 15:29:07: Agover Bam file : test.hg19.bam ==> test.hg18.bam @ 2016-10-07 15:29:14: Done! @ 2016-10-07 15:29:14: order "test.hg18.bam" ... @ 2016-10-07 15:29:15: index "test.hg18.sorted.bam" ... Total alignments : 99914 QC failed: 0 R1 Unico, R2 Unico (uu): 96094 R1 Unique, R2 Unmapp (one): 3579 R1 Unique, Multiple R2 (UM): 0 R1 Multiple, Multiple R2 (mm): 0 R1 Multiple, R2 Unique (MU): 233 R1 multiples, R2 not mapped (MN): 8 R1 Unmap, R2 Unmap (NN): 0 R1 Unmap, R2 Unique (NU): 0 R1 Unmap, R2 Multiplo (Nm): 0 # Bam / Sam The header sections have been updated: $ samtools view -h test.hg19.bam @sq sn: CHR1 LN: 249250621 @SQ SN: CHR2 LN: 243199373 @SQ SN: CHR3 LN: 198022430 ... @SQ SN: CHRX LN: 155270560 @SQ SN: CHRY LN: 59373566 @SQ SN: CHRM LN: 16571 @RG ID: sample_618545BE SM: sample_618545be lb: sample_618545be lb: sample_618545be lb: sample_618545be pl: light @pg id: bwa pn: bwa vn: 0.6.2-R126 $ samtools view -h -h test.hg18.bam @HD VN: 1.0 SO: Coordinate @SQ SN: CHR1 LN: 247249719 @SQ SN: CH10 LN: 135374737 @SQ SN: CHR11 LN: 134452384. .. @SQ SN: CHRX LN: 154913754 @sq sn: chrx_random ln: 1719168 @sq sn: chry ln: 57772954 @rg id: sample_618545be sm: sample_618 545be lb: sample_618545be pl: light @pg pn pn: id bwa id: bwa vn: 0.6.2- R126 @pg id: crossmap vn: 0.5.0 @co aolofover from the original file bam / sam: test.hg19.bam @co liftover is based on the chain file: ../test/hg19tohg18.over.chain.gz optional tag : QQC. QC has not succeeded. Nunmat. Originally not mapped or originally mapped but failed to raise itself to the new assembly. Mmultiple mapped. The alignment can be raised on more places. Uuniche mapped. The alignment can be raised up to 1 place. Tags for the sequencing of the torque include: QF = QC failed nn = both read1 and read2 not mapped nu = read1 not mapped, unique reading mapped nm = read1 not mapped, mapped multiple a = read1 uniquely mapped, read2 does not have uniquely mapped um = read1 uniquely mapped, reading2 mn multipla mn = read1 multip mapped, read2 not mapped mu = reading1 mlter mlter, read2 unique mapped mm = is reading1 and read 2 multiple mapped tags for single-end sequencing include : QF = QC WEALD SN = Smilke = Most mapped su = unique note note all alignments (mapped, partial mapped, not mapped, failed qc) will write to a file. Users can filter them by tags. The header section will be updated to the target group. The coordinates of the genome and all SAM flags in the Alignment section will be updated to the destination assembly. If the input is a CRAM file, the PYSAM version should> = 0.8.2 The optional fields in the Alignment section will not update. The Wiggle (Wig) format is useful for displaying continuous data such as GC content and high-speed sequencing data intensity readings. Bigwig is a wiggle file in self-defined binary format and has the advantage of supporting random access. The input wiggle data can be in VariableStep (for data with irregular intervals) or fixed (for data with regular intervals). Regardless of the input, the output files are always in Bedgraph format. We export files in Bedgraph format because it is more compact than Wiggle format, and above all, CrossMap transforms internally turns into blur in bedgraph to increase the speed speed. Typing the crossmap.py wig without any topic prints a help message: $ crossmap.py wig uses ----- crossmap.py wig Description --------- - Convert the â € CHR1 10000 2.568.561 MAP_RATIO = 0.9360 CHR1 145.394.955 145.807.817 -> CHR1 145.627.235 146.040.039 map_ratio = 0.9994 CHR1 146.527.987 147.394.444 -> CHR1 147.056.425 147.922 .330 map_ratio = 0.9989 CHR10 82.045.472 88.931.651 -> CHR10 80.285.716 87.171.894 map_ratio = 1.0000 CHR11 43.020.000 -> CHR11 43.918.450 45998449 map_ratio = 1.0000 CHR15 22.805.313 23.094.530 Fail Map_Ratio = 0.3607 CHR15 22.805.313 28.390.339 -> CHR15 22.598.414 28.145.193 map_ratio = 0.8967 CHR15 31.080.645 32.462.776 -> CHR15 30.788.442 32.170.575 map_ratio = 1.0000 CHR15 72.900.171 78.151.253 -> CHR15 72.607.830 77.858.911 map_ratio = 1.0000 CHR15 85722039 - > chr15 82,550,985 85,178,808 15,511,655 16,293,689 Mappa_Ratio = 0.9800 CH111 - > Ch116 15,417,798 16,199,832 22,431,889 Mappa_Ratio = 1.0000 CH1611950135 - > CH116 21,938,814 22,420,568 28,823,196 29,046,783 Map_Ratio = 1.0000 CH16 - > CH11 75 29035462 Mappa_Ratio = 1.0000 1.0000 29650840 30200773 -> chr16 29.639.519 30.189.452 map_ratio = 1.0000 chr17 1.247.834 1.303.556 -> chr17 1.344.540 1.400.262 map_ratio = 1.0000 chr17 2.496.923 2.588.909 -> chr17 2.593.629 2.685.615 map_ratio = 1.0000 chr17 16.812.771 20.211.017 -> chr17 16.909.457 20.307.704 map_ratio = 1.0000 chr17 29.107.491 30.265.075 -> chr17 30.780.473 31938056 map_ratio = 1.0000 chr17 34.815.904 36.217.432 Unmap chr17 43.705.356 44.164.691 -> chr17 45.627.990 46.087.325 map_ratio = 1.0000 ChR2 50.145.643 51.259.674 -> ChR2 49.918.505 51.032.536 map_ratio = 1.0000 ChR2 96.742.409 97.677.516 -> ChR2 96.076.661 97.011.779 map_ratio = 1.0000 ChR2 111.394.040 112.012.649 -> ChR2 110.636.463 111.255.072 map_ratio = 1.0000 ChR2 239.716.679 243.199.373 -> ChR2 238.808.038 242.183.529 map_ratio = 0,9622 chr22 19.037.332 21.466.726 Fail map_ratio = 0,8490 chr22 21.920.127 23.653.646 -> chr22 21.565.838 23.311.459 map_ratio = 0,9996 chr22 51.113.070 51.171.640 -> chr22 50.674.642 50.733.212 map_ratio = 1.0000 chr3 195.720.167 197.354.826 -> chr3 195.993.296 197.627.955 map_ratio = 1.0000 CHR4 1552030 2091303 -> CHR4 1550303 2089576 map_rat Io = 1.0000 CHR5 175.720.924 177.052.594 -> CHR5 176.293.921 177.625.593 map_ratio = 1.0000 chr7 72.744.915 74.142.892 -> chr7 73.330.912 74.728.554 map_ratio = 0,9997 chr8 8.098.990 11.872.558 -> chr8 8.241.468 12.015.049 map_ratio = 1.0000 chr9 140.513.444 140.730.578 -> chr9 137.618.992 137.836.126 map_ratio = 1.0000 Nota LETTO ingresso Il file dovrebbe avere almeno 3 colonne (crom, inizio, fine). Le colonne aggiuntive saranno mantenute cosÃ¬ com'Ã¨. Per accedere alla precisione di CrossMap, ha generato casualmente 10.000 intervalli di genoma (download da qui) con la dimensione dell'intervallo fisso di 200 BP da HG19. Quindi li abbiamo convertiti in HG18 utilizzando CrossMap e UCSC SOLLEVOVER Strumento con configurazioni predefinite. Confrontiamo CrossMap sullo strumento Agorover UCSC perchÃ© Ã¨ lo strumento piÃ¹ utilizzato per convertire le coordinate del genoma. CrossMap non Ã¨ riuscito a convertire 613 intervalli e lo strumento UCSC Liveover non Ã¨ riuscito a convertire 614 intervalli. Tutti gli intervalli falliti sono esattamente lo stesso ad eccezione di una regione (CHR2 90542908 90543108). UCSC non Ã¨ riuscito a convertirlo perchÃ© questa regione deve essere divisa due volte: originale (HG19) SPLIT (HG19) Target (HG19) CHR2 90542908 90543108 - CHR2 90542908 - CHR2 90542908 90542933 - CHR2 89906445 89906470 - CHR2 90542908 90543108 - CHR2 90542933 90543001 - CHR2 87414583 87414651 CHR2 90542908 90543108 - CHR2 90543010 90543108 - CHR2 87414276 87414374 - Per gli intervalli del genoma che sono stati convertiti con successo in HG18, le coordinate di avvio e fine sono esattamente la stessa tra conversione UCSC e conversione crossmap. Zhao, H., Sun, Z., Wang, J., Huang, H., Kocher, J.-P., & Wang, L. (2013). CrossMap: uno strumento versatile per la conversione delle coordinate tra assiemi genoma. 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